

10294.204.ST25.txt
SEQUENCE LISTING

<110> Novozymes A/S
Andersen, Jens Tønne
Clausen, Ib Groth
Jørgensen, Steen Troels
Olsen, Peter Bjarke
Rasmussen, Michael Dolberg

<120> Improved Bacillus Host Cell

<130> 10294.000

<160> 248

<170> PatentIn version 3.2

<210> 1

<211> 3405

<212> DNA

<213> Bacillus licheniformis

<220>

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<222> (501)..(2906)

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1 5 10
gct ttt att cta tta ttt gcg tta tcc aca ttc ctc acc gga gtg cag 581
Ala Phe Ile Leu Leu Phe Ala Leu Ser Thr Phe Leu Thr Gly Val Gln
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Ala Thr Ser Val Pro Asp Lys Lys Ser Pro Glu Leu Glu Lys Ala Glu
30 35 40
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Ile Tyr Gly Asp Ile Asp Val Thr Ser Asp Lys Gln Thr Thr Val Ile
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Val Glu Leu Lys Glu Lys Ser Leu Ala Glu Ala Lys Ala Asp Gly Glu
60 65 70 75
aaa caa acg aag gct tct cta aaa aca gct cga agc aaa gcg ctg aaa 773
Lys Gln Thr Lys Ala Ser Leu Lys Thr Ala Arg Ser Lys Ala Leu Lys
80 85 90

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gtc aag gaa gtt aaa gcg gtt tat cca aac gca act tac aaa cct gac Val Lys Glu Val Lys Ala Val Tyr Pro Asn Ala Thr Tyr Lys Pro Asp 125 130 135	917
agc gta aaa gga aaa gac gtg aca ctt gca gca gac gcc att tat cca Ser Val Lys Gly Lys Asp Val Thr Leu Ala Ala Asp Ala Ile Tyr Pro 140 145 150 155	965
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ggc tat gac ttt gtg gat aat gat tat gat cca cag gaa aca ccg aca Gly Tyr Asp Phe Val Asp Asn Asp Tyr Asp Pro Gln Glu Thr Pro Thr 205 210 215	1157
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gtg aaa gga aaa gtt gcg gtt atc cag aga ggc gtc ata cca ttt gtt Val Lys Gly Lys Val Ala Val Ile Gln Arg Gly Val Ile Pro Phe Val 400 405 410	1733
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gta ccg acc gtc aaa ttg tca aaa gaa gag ggc gaa aag ctt gtt caa Val Pro Thr Val Lys Leu Ser Lys Glu Glu Gly Glu Lys Leu Val Gln 445 450 455	1877
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 Lys Ser Leu Ala Glu Ala Lys Ala Asp Gly Glu Lys Gln Thr Lys Ala
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 Ser Leu Lys Thr Ala Arg Ser Lys Ala Leu Lys Thr Leu Lys Lys Ala
 85 90 95
 Lys Val Asn Arg Glu Tyr Asp Arg Val Phe Ser Gly Phe Ser Met Lys
 100 105 110
 Leu Pro Ala Ser Glu Ile Pro Lys Leu Leu Ala Val Lys Glu Val Lys
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 Asp Val Thr Leu Ala Ala Asp Ala Ile Tyr Pro Gln Met Asp Lys Ser
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 Ala Pro Phe Ile Gly Ala Asp Gln Ala Trp Lys Ser Gly Tyr Thr Gly
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 Pro Asp Leu Lys Asn Asn Phe Gly Pro Tyr Lys Gly Tyr Asp Phe Val
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 Asp Asn Asp Tyr Asp Pro Gln Glu Thr Pro Thr Gly Asp Pro Arg Gly
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 Gly Ala Thr Asp His Gly Thr His Val Ala Gly Thr Ile Ala Ala Asn
 225 230 235 240
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 Val Leu Gly Pro Gly Gly Ser Gly Thr Thr Glu Asn Val Ile Ala Gly
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Ile Glu Lys Ala Val Ala Asp Gly Ala Lys Val Met Asn Leu Ser Leu
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Val Ala Glu Ile Pro Leu Leu Leu Ile Val Lys Glu Pro Asp Tyr Pro
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Arg Val Thr Ser Val Thr Val Glu Pro Gly Ala Lys Gln Gly Ala Tyr
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Thr Ile Glu Ala Tyr Leu Pro Gly Gly Ala Glu Glu Leu Ala Phe Leu
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Val Tyr Asp Glu Asn Leu Asn Leu Leu Gly Gln Ala Gly Val Tyr Lys
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Asn Gln Gly Lys Gly Tyr Gln Ser Tyr Gln Trp Asn Gly Lys Ile Asn
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Ser Arg Leu Tyr Phe Gly Lys Arg Ala Lys Asp Ile Asn Thr Ala Glu
190 195 200

gct gca atg ctt gcc ggc att cca aag ggt cct tca gtt tat tcg ccc 1157
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205 210 215

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Phe Val Asn Glu Lys Lys Ala Lys Glu Arg Gln Glu Met Ile Leu Thr
220 225 230 235

atg atg gag aaa caa aac aag ctg acg gaa atg cag gcg gca gca ctg 1253
Met Met Glu Lys Gln Asn Lys Leu Thr Glu Met Gln Ala Ala Ala Leu
240 245 250

aaa aaa atg ccg ctc cgc ttt gaa aaa cag gat aag caa aca acc gaa 1301
Lys Lys Met Pro Leu Arg Phe Glu Lys Gln Asp Lys Gln Thr Thr Glu
255 260 265

aaa acc gct ccg tac ttt tat gac gaa gct gtt aaa gaa att tcg cga 1349
Lys Thr Ala Pro Tyr Phe Tyr Asp Glu Ala Val Lys Glu Ile Ser Arg
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Leu Leu Arg Leu Thr Pro Glu Gln Ala Glu Thr Gly Gly Tyr Asn Val
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Glu His Thr Ile Asp Ser Ser Ser Asp Ile Gln Ala Gly Phe Ala Ala
320 325 330

atc aac ccg tcc gac ggc agc gtt ctc gcg ctt gtc gga gga cgc gac 1541
Ile Asn Pro Ser Asp Gly Ser Val Leu Ala Leu Val Gly Gly Arg Asp
335 340 345

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Tyr Glu Lys Ser Pro Phe Asn Arg Val Thr Gln Ala Met Arg Gln Pro
350 355 360

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Gly Ser Thr Met Lys Pro Phe Leu Tyr Tyr Ser Ala Val Gln Asn Gly
365 370 375

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Phe Thr Pro Ala Thr Arg Met Arg Ser Ala Glu Thr Thr Phe Glu Leu
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Gly Gln Gly Ser Ala Tyr Ser Pro Ser Asn Tyr His Gly Tyr Tyr Ala
400 405 410

gac ggt ccg atc acg ctt ctg cag gca ctg gct ttg tcc gat aac att 1781
Asp Gly Pro Ile Thr Leu Leu Gln Ala Leu Ala Leu Ser Asp Asn Ile
415 420 425

tac gcc gtg aaa acc cac ctt ttc ctc ggc atg gac aaa ctg att gat 1829

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Tyr Ala Val Lys Thr His Leu Phe Leu Gly Met Asp Lys Leu Ile Asp
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gcc gca aag caa ttc ggc atc aac agc ccg ctg caa aaa gtg ccg tcg 1877
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 Leu Ala Leu Gly Thr Ser Pro Val Lys Pro Ile Glu Met Val Asn Gly
 460 465 470 475

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 Tyr Ala Met Phe Ala Asn Gly Gly Lys Lys Ile Glu Pro Ser Phe Ile
 480 485 490

acg aaa att acc gat ccg aac ggc aag gtt ctt tat gaa aaa ccg aag 2021
 Thr Lys Ile Thr Asp Pro Asn Gly Lys Val Leu Tyr Glu Lys Pro Lys
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 Thr Gly Arg Thr Ile Ala Asp Gln Leu Thr Arg Tyr Ala Gly Lys
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 Ser Gly Thr Thr Ser Thr Asp Ser Trp Met Ile Gly Phe Tyr Pro Gly
 560 565 570

ctt gct tca ggc gtg tgg acg gga tat gac aaa gag cgg aca atc gat 2261
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 575 580 585

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 590 595 600

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 Glu Lys Ala Leu Glu Asp Ala Pro Ala Ala Leu Met Pro Pro Glu
 605 610 615

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 Gly Val Lys Gly Met Tyr Ile Asp Pro Ala Thr Gly Tyr Ala Ala Ala
 620 625 630 635

ccc agc tgc ccg tcc aaa tat ttc gct tat ttt atc aaa ggt act gaa 2453
 Pro Ser Cys Pro Ser Lys Tyr Phe Ala Tyr Phe Ile Lys Gly Thr Glu
 640 645 650

ccc gag cag gtt tgc tat gga aag gaa atc tat aag gag caa aac gcc 2501
 Pro Glu Gln Val Cys Tyr Gly Lys Glu Ile Tyr Lys Glu Gln Asn Ala
 655 660 665

ggg cac gaa aag ccc gcc gct ccc ccc cat aag cgg caa aag tgg tgg 2549
 Gly His Glu Lys Pro Ala Ala Pro Pro His Lys Arg Gln Lys Trp Trp
 670 675 680

gaa aaa tgg ttt aaa aaa gga gaa taaacttttt agggggatag acgaaccccc 2603
 Glu Lys Trp Phe Lys Lys Gly Glu
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 <213> Bacillus licheniformis

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Ile Gln Val Pro Arg Ser Thr Val Leu Tyr Asp Gly Ser Gly Lys Gln
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Asn Ile Asn Pro Ala Val Ile Asp Ala Thr Leu Ala Val Glu Asp Arg
 85 90 95

Asn Phe Phe Arg His His Gly Phe Asp Tyr Met Arg Met Gly Gly Ala
 100 105 110

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 115 120 125

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 130 135 140

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 145 150 155 160

Asn Tyr Thr Lys Lys Asp Ile Leu Glu Gly Tyr Leu Asn Thr Ile Tyr
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 180 185 190

Gly Lys Arg Ala Lys Asp Ile Asn Thr Ala Glu Ala Ala Met Leu Ala

10294.204.ST25.txt

195

200

205

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 225 230 235 240

Asn Lys Leu Thr Glu Met Gln Ala Ala Ala Leu Lys Lys Met Pro Leu
 245 250 255

Arg Phe Glu Lys Gln Asp Lys Gln Thr Thr Glu Lys Thr Ala Pro Tyr
 260 265 270

Phe Tyr Asp Glu Ala Val Lys Glu Ile Ser Arg Leu Leu Arg Leu Thr
 275 280 285

Pro Glu Gln Ala Glu Thr Gly Gly Tyr Asn Val Phe Thr Thr Leu Asn
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Pro Arg Leu Gln Lys Ile Ala Glu Asp Thr Ile Glu His Thr Ile Asp
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 325 330 335

Gly Ser Val Leu Ala Leu Val Gly Gly Arg Asp Tyr Glu Lys Ser Pro
 340 345 350

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Ser Pro Val Lys Pro Ile Glu Met Val Asn Gly Tyr Ala Met Phe Ala
 Page 12

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 Met Lys Gly Leu Gln Asp Glu Gln Met Ile Ala Thr Ala Lys His Phe
 210 215 220
 Pro Gly His Gly Asp Thr Ala Val Asp Ser His Tyr Gly Leu Pro Leu
 225 230 235 240
 Val Pro His Asn Glu Lys Arg Leu Arg Ser Val Glu Leu Ala Pro Phe
 245 250 255
 Gln Lys Ala Ile Asp Ala Gly Ile Asp Met Ile Met Thr Ala His Val
 260 265 270
 Gln Phe Pro Ala Phe Asp Asp Thr Thr Tyr Lys Ser Lys Lys Asp Gly
 275 280 285
 Glu Asp Ile Met Val Pro Ala Thr Leu Ser Lys Lys Val Met Thr Asp
 290 295 300
 Leu Leu Arg Lys Asp Leu Ser Phe Lys Gly Val Val Val Thr Asp Ala
 305 310 315 320
 Leu Asn Met Lys Ala Ile Ser Asp Asn Phe Gly Gln Glu Glu Ala Val
 325 330 335
 Val Met Ala Val Lys Ala Gly Val Asp Ile Ala Leu Met Pro Ala Gln
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 Val Thr Ser Leu Glu Thr Glu Lys Asn Leu Ala Arg Val Phe Glu Ala
 355 360 365
 Leu Leu Thr Ala Val Lys Asn Gly Asp Ile Pro Met Glu Gln Ile Asp
 370 375 380
 Gln Ser Val Glu Arg Ile Leu Gln Leu Lys Ile Asp Arg Gly Ile Ile
 385 390 395 400
 Asp His Thr Gly Ser Glu Pro Leu Gln Lys Lys Ile Lys Tyr Ala Leu
 405 410 415
 Lys Thr Val Gly Ser Ser Lys His Met Lys Tyr Glu Lys Lys Met Ala
 420 425 430

10294.204.ST25.txt

Arg Asp Ser Ala Thr Ile Leu Lys Asn Asp Lys Ser Thr Leu Pro Phe
 435 440 445

Lys Pro Lys Lys Gly Asp Thr Val Leu Ile Leu Ala Pro Tyr Glu Glu
 450 455 460

Gln Thr Ala Ala Ile Ala Lys Thr Ile Ser Lys Ile Arg Lys Asn Ile
 465 470 475 480

Lys Val Val Glu Tyr Arg Phe Ala Glu Lys Thr Phe Glu Glu Glu Ile
 485 490 495

Gln Lys Lys Ile Asp Glu Ala Asp Tyr Val Ile Thr Gly Ser Tyr Val
 500 505 510

Ile Lys Asn Asp Pro Val Val Asn Asp Gly Val Ile Asp Asp Ser Ile
 515 520 525

Gln Asp Ser Ser Lys Trp Ala Thr Ala Phe Pro Arg Ala Ala Met Lys
 530 535 540

Tyr Ala Gln Ala Asn Gly Lys Lys Phe Val Leu Met Ser Leu Arg Asn
 545 550 555 560

Pro Tyr Asp Thr Ala Asn Phe Glu Glu Ala Glu Ala Val Ile Ala Val
 565 570 575

Tyr Gly Phe Lys Gly Tyr Ala Asn Gly Arg Phe Arg Gln Pro Asn Ile
 580 585 590

Pro Ala Gly Val Glu Ala Ile Phe Gly Lys Ala Lys Pro Lys Gly Thr
 595 600 605

Leu Pro Val Asp Ile Pro Ser Val Thr Arg Pro Gly Glu Thr Leu Tyr
 610 615 620

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Gly Gly Ser

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 <213> Bacillus licheniformis

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<400> 9

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tttgtttttc tttggcgtca tcatgtcaaa tgcgattttt gtcatcaatt tattttataa	240
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tatgacgaag gtcatgatta cactgagcat cgaaaaaaca gaaatgaaca ggcaaaactt	360
tttcatcgtt tttctgatgt actttacata ctcgcaggct tggattgtgc tcgtgattta	420
ttctttattc gtagaaatca agcaccgcct gttcaagcaa catggtacaa aacagaacga	480
tacaatcaaa agaaaagcgg gtg act ttt ttg aaa tat atc atc ata tgt ctg	533
Val Thr Phe Leu Lys Tyr Ile Ile Ile Cys Leu	
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Ala Ser Phe Leu Leu Ile Thr Ala Thr Gly Gln Ala Ala Ala Ala Lys	
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Asp Val Thr Val Asp Gly Ser Ile Leu Gly Glu Asn Ser Arg Glu Gln	
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Ala Lys Gln Gln Val Leu Thr Asn Asp Leu Leu Thr Leu Tyr Gly Ala	
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aaa gac agc gcc gag ctg acg tat caa ata ccg gcg ggc gcc tcc tct	725
Lys Asp Ser Ala Glu Leu Thr Tyr Gln Ile Pro Ala Gly Ala Ser Ser	
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acc cat cag cag ctt aca ctt aaa tac gag gcc tca gac ctt tta atc	773
Thr His Gln Gln Leu Thr Leu Lys Tyr Glu Ala Ser Asp Leu Leu Ile	
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Ser Pro Ser Ser Leu Thr Ala Glu Ile Asp Gly Glu Pro Val Lys Thr	
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Val Lys Leu Glu Gly Asn Asn Gly Lys Lys Thr Leu Lys Leu Ser Leu	
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Asn Lys Ser Gln Ser Ser Pro Gly Phe His Ser Leu Ser Leu Lys Phe	
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Tyr Gly Val Val His Glu Gly Val Cys Val Arg Gln Asp Ser Ser Gly	
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Asn Trp Ile Lys Ile Tyr Pro Asp Ser Arg Leu Asn Ile Gly Glu Lys	
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aac gaa tct aaa gga gcg gcg ctc gaa cat tat cct tat ccg ttc gcc	1061
Asn Glu Ser Lys Gly Ala Ala Leu Glu His Tyr Pro Tyr Pro Phe Ala	
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cag tcc ggc agc tcc gtg gaa aaa acg gca atc gtc att ccg gac cat	1109
Gln Ser Gly Ser Ser Val Glu Lys Thr Ala Ile Val Ile Pro Asp His	
190 195 200	

10294.204.ST25.txt																
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Pro	Ser	Ser	Ala	Glu	Ile	Glu	Ala	Ala	Val	Lys	Thr	Glu	Ala	Tyr	Leu	
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aaa	acg	ggt	gac	aac	agc	atc	agc	acg	aag	atc	ttg	ggt	gaa	tct	gac	1205
Lys	Thr	Val	Asp	Asn	Ser	Ile	Ser	Thr	Lys	Ile	Leu	Gly	Glu	Ser	Asp	
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ctg	gcg	aag	atc	gac	agg	ccg	acg	att	gtg	atc	ggc	ggt	cac	cat	cac	1253
Leu	Ala	Lys	Ile	Asp	Arg	Pro	Thr	Ile	Val	Ile	Gly	Val	His	His	His	
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Trp	Ser	Gly	Lys	Val	Lys	Lys	Leu	Leu	Lys	Gln	Ala	Lys	Leu	Glu	Ala	
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Lys	Glu	Asp	Lys	Leu	Leu	Leu	Ala	Lys	Arg	Met	Leu	Lys	Ala	Lys	Asp	
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Lys	Gln	Gln	Pro	Val	Leu	Phe	Ala	Ala	Ala	Ala	Ser	Asp	Asp	Val	Leu	
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Ser	Glu	Lys	Ile	Ser	Val	Ile	Thr	Asp	Lys	Thr	Tyr	Ala	Ala	Gln	Leu	
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Ser	Gly	Asp	Thr	Leu	Ala	Ile	Gly	Lys	Leu	Gln	Gln	His	Ser	Lys	Arg	
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Gly	Gly	Ser	Lys	Leu	Thr	Leu	Glu	Asp	Phe	Gly	Ala	Gly	Asp	Leu	Thr	
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Ile	Gly	Ser	Gly	Gln	Thr	Ser	Ser	Glu	His	Phe	Tyr	Tyr	Pro	Ala	Pro	
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Ala	Leu	Leu	Asp	Lys	Asn	Gln	Pro	Ala	Lys	Leu	Ser	Leu	Ala	Met	Lys	
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aaa	tcg	aaa	acg	att	caa	aag	cag	gcc	ggc	caa	agc	gac	tta	gct	gcg	1685
Lys	Ser	Lys	Thr	Ile	Gln	Lys	Gln	Ala	Gly	Gln	Ser	Asp	Leu	Ala	Ala	
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gaa	cag	gcg	gag	ctg	aag	gtc	atg	atc	aat	ggc	cag	cct	cat	tcc	gtc	1733
Glu	Gln	Ala	Glu	Leu	Lys	Val	Met	Ile	Asn	Gly	Gln	Pro	His	Ser	Val	
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Gly	Leu	Asp	Asp	Ile	Gly	Lys	Glu	Asp	Lys	Asn	Gly	Phe	Tyr	His	Val	
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tct	tta	aaa	gtc	gat	ccg	aaa	ctt	ttg	caa	aaa	agc	cgt	tac	att	gat	1829
Ser	Leu	Lys	Val	Asp	Pro	Lys	Leu	Leu	Gln	Lys	Ser	Arg	Tyr	Ile	Asp	
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Ile	Gln	Phe	Ala	Ala	Ser	Gly	Leu	Lys	Glu	Asn	Asn	Pro	Cys	Tyr	Ala	
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10294.204.ST25.txt

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gca gca acc gtt gtg aat gaa acg gac agc cat cag cta ttt aca aac Ala Ala Thr Val Val Asn Glu Thr Asp Ser His Gln Leu Phe Thr Asn 640 645 650	2453
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atc ata gcg gca gcg gtt att ttg atc ttg aca acg gca agg cgc aga Ile Ile Ala Ala Ala Val Ile Leu Ile Leu Thr Thr Ala Arg Arg Arg 685 690 695	2597
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10294.204.ST25.txt

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<213> Bacillus licheniformis

<400> 10

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 35 40 45

Leu Thr Asn Asp Leu Leu Thr Leu Tyr Gly Ala Lys Asp Ser Ala Glu
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Leu Thr Tyr Gln Ile Pro Ala Gly Ala Ser Ser Thr His Gln Gln Leu
 65 70 75 80

Thr Leu Lys Tyr Glu Ala Ser Asp Leu Leu Ile Ser Pro Ser Ser Leu
 85 90 95

Thr Ala Glu Ile Asp Gly Glu Pro Val Lys Thr Val Lys Leu Glu Gly
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Asn Asn Gly Lys Lys Thr Leu Lys Leu Ser Leu Asn Lys Ser Gln Ser
 115 120 125

Ser Pro Gly Phe His Ser Leu Ser Leu Lys Phe Tyr Gly Val Val His
 130 135 140

Glu Gly Val Cys Val Arg Gln Asp Ser Ser Gly Asn Trp Ile Lys Ile
 145 150 155 160

Tyr Pro Asp Ser Arg Leu Asn Ile Gly Glu Lys Asn Glu Ser Lys Gly
 165 170 175

Ala Ala Leu Glu His Tyr Pro Tyr Pro Phe Ala Gln Ser Gly Ser Ser
 180 185 190

Val Glu Lys Thr Ala Ile Val Ile Pro Asp His Pro Ser Ser Ala Glu
 195 200 205

Ile Glu Ala Ala Val Lys Thr Glu Ala Tyr Leu Lys Thr Val Asp Asn
 210 215 220

Ser Ile Ser Thr Lys Ile Leu Gly Glu Ser Asp Leu Ala Lys Ile Asp
 225 230 235 240

Arg Pro Thr Ile Val Ile Gly Val His His His Trp Ser Gly Lys Val
 245 250 255

10294.204.ST25.txt

Lys Lys Leu Leu Lys Gln Ala Lys Leu Glu Ala Lys Glu Asp Lys Leu
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 275 280 285
 Leu Phe Ala Ala Ala Ala Ser Asp Asp Val Leu Ser Glu Lys Ile Ser
 290 295 300
 Val Ile Thr Asp Lys Thr Tyr Ala Ala Gln Leu Ser Gly Asp Thr Leu
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 Ala Ile Gly Lys Leu Gln Gln His Ser Lys Arg Gly Gly Ser Lys Leu
 325 330 335
 Thr Leu Glu Asp Phe Gly Ala Gly Asp Leu Thr Ile Gly Ser Gly Gln
 340 345 350
 Thr Ser Ser Glu His Phe Tyr Tyr Pro Ala Pro Ala Leu Leu Asp Lys
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 Asn Gln Pro Ala Lys Leu Ser Leu Ala Met Lys Lys Ser Lys Thr Ile
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 385 390 395 400
 Lys Val Met Ile Asn Gly Gln Pro His Ser Val Gly Leu Asp Asp Ile
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 Gly Lys Glu Asp Lys Asn Gly Phe Tyr His Val Ser Leu Lys Val Asp
 420 425 430
 Pro Lys Leu Leu Gln Lys Ser Arg Tyr Ile Asp Ile Gln Phe Ala Ala
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 Ser Gly Leu Lys Glu Asn Asn Pro Cys Tyr Ala Val Asn Glu Asp Lys
 450 455 460
 Trp Ile Phe Ile Asp Lys Gln Ser Ala Leu Ser Tyr His Val Ser Asp
 465 470 475 480
 Thr Ser Ala Ser Ala Asp Phe Gln Ala Trp Pro Leu Pro Tyr Ala Gly
 485 490 495
 Asp His Asn Asn Lys Thr Leu Met Ile Leu Pro Asp Asn Ala Asp Gln
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 Ser Lys Ile Asp Glu Leu Ser Leu Val Val Gly Ser Phe Gly Ser Glu
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10294.204.ST25.txt

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Asp Val Lys Gly Arg Asn Val Ile Phe Ile Gly Ser Val Asp Gln Phe
 545 550 555 560

Ser Leu Leu Lys Glu Lys Thr Ala Glu Leu Ala Val Pro Thr Ala Lys
 565 570 575

Asn Gly Thr Phe Asp Val Ser Ser Phe Gln Met Leu Asn Glu Thr Thr
 580 585 590

Lys Gln Val Ala Phe Thr Gln Thr Ser Leu Trp Asp Ser Asn Tyr Ser
 595 600 605

Met Ala Val Phe Ala Pro Phe Lys Gly Gln Gly Thr Ala Val Thr Lys
 610 615 620

Glu Met Ile Asn Phe Leu Asn Ser Asn Asp Phe Ala Ala Thr Val Val
 625 630 635 640

Asn Glu Thr Asp Ser His Gln Leu Phe Thr Asn His Gln Gln Leu Thr
 645 650 655

Ala Lys Ser Ala Glu Thr Lys Thr Asp Asp Lys Gln Glu Ser Asn Gln
 660 665 670

Gln His Val Leu Tyr Ile Ala Ile Leu Ile Val Ile Ile Ala Ala Ala
 675 680 685

Val Ile Leu Ile Leu Thr Thr Ala Arg Arg Arg Lys Arg Lys Ala Asn
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Ala Gly Gly Gly Ile Asp Glu
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 <222> (519)..(1958)

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 atccatctat gtttgagcct gtgcacggct ctgctccgga catcatctga tagcgagtca 180
 tcatcggaaa aggaatcgcc aatccgatcg gccaaatttg gacggcaaaa atgatgctcg 240

10294.204.ST25.txt

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gcaacaaaac atagtgcagg cagaagagga ggtatagg atg aat cag aag att gtg	536
Met Asn Gln Lys Ile Val	
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tct gtg ctc atc att gcg ctc agc ctg tta tgc ggc ttg gta aca ggc	584
Ser Val Leu Ile Ile Ala Leu Ser Leu Leu Cys Gly Leu Val Thr Gly	
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gcc ggc ccg att ccg tta cat gat gtc gtt tca aaa gca tca gcg gct	632
Ala Gly Pro Ile Pro Leu His Asp Val Val Ser Lys Ala Ser Ala Ala	
25 30 35	
gaa gaa gct gca gcc aaa agc acc gct aga aac gaa ttg gag aaa att	680
Glu Glu Ala Ala Ala Lys Ser Thr Ala Arg Asn Glu Leu Glu Lys Ile	
40 45 50	
gag aaa gca tat gac ctg att tca aat gaa tat gtg gag cag gtc gac	728
Glu Lys Ala Tyr Asp Leu Ile Ser Asn Glu Tyr Val Glu Gln Val Asp	
55 60 65 70	
agg gaa aaa ctg ttg gaa gga gcc ata cag ggc atg ctt tca aca ttg	776
Arg Glu Lys Leu Leu Glu Gly Ala Ile Gln Gly Met Leu Ser Thr Leu	
75 80 85	
aat gac cca tac tcg gtc tat atg gat aaa cag acg gca aag cgg ttt	824
Asn Asp Pro Tyr Ser Val Tyr Met Asp Lys Gln Thr Ala Lys Arg Phe	
90 95 100	
tca gat tcc ctt gat tcc tct ttt gaa gga atc ggt gca gaa atc gga	872
Ser Asp Ser Leu Asp Ser Ser Phe Glu Gly Ile Gly Ala Glu Ile Gly	
105 110 115	
atg gaa gac aga aaa atc att atc gtt tct cct ttt aaa cag tct ccg	920
Met Glu Asp Arg Lys Ile Ile Ile Val Ser Pro Phe Lys Gln Ser Pro	
120 125 130	
gca gag aaa gcc gga tta aag ccg aac gat gaa atc att agc atc gac	968
Ala Glu Lys Ala Gly Leu Lys Pro Asn Asp Glu Ile Ile Ser Ile Asp	
135 140 145 150	
ggc gat tcc atg agc gga atg gat ttg aat gac gcc gta tta aag atc	1016
Gly Asp Ser Met Ser Gly Met Asp Leu Asn Asp Ala Val Leu Lys Ile	
155 160 165	
aga ggc aaa aag gga tcg acg gtt aca ctg aaa gtt cac cga ccc gga	1064
Arg Gly Lys Lys Gly Ser Thr Val Thr Leu Lys Val His Arg Pro Gly	
170 175 180	
atg aaa gac cag ctg aca ttt acg att aag cgc gat gaa atc ccg ctg	1112
Met Lys Asp Gln Leu Thr Phe Thr Ile Lys Arg Asp Glu Ile Pro Leu	
185 190 195	
gaa acg gtg ttt gct tcc ata aag aaa gta cag gat aaa cct gtc ggc	1160
Glu Thr Val Phe Ala Ser Ile Lys Lys Val Gln Asp Lys Pro Val Gly	
200 205 210	
tat atc gca ata tct tcc ttt tcc gaa cat acg gca aaa gat ttt act	1208
Tyr Ile Ala Ile Ser Ser Phe Ser Glu His Thr Ala Lys Asp Phe Thr	
215 220 225 230	

10294.204.ST25.txt

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Ala Glu Leu Lys Lys 235 Leu Glu Lys Lys Gly 240 Ile Lys Gly Leu Val 245 Leu	
gat gta aga gga aat ccg ggc ggg tac ttg caa agc gtg gaa gac att	1304
Asp Val Arg Gly 250 Asn Pro Gly Gly Tyr 255 Leu Gln Ser Val Glu 260 Asp Ile	
tta aaa cat ttt gtg aca aaa gat cat ccg tat ata caa atc gcc gaa	1352
Leu Lys His 265 Phe Val Thr Lys Asp 270 His Pro Tyr Ile Gln 275 Ile Ala Glu	
aga aac gga aat aaa aaa caa tac ttc tca aaa tta aaa gag aaa aaa	1400
Arg Asn Gly Asn Lys Lys 280 Gln Tyr Phe Ser Lys 290 Leu Lys Glu Lys Lys	
cca tac cct gtg agc gtg atc acg gac aag ggc agc gct tcg gct tcg	1448
Pro Tyr Pro Val Ser Val 300 Ile Thr Asp Lys Gly 305 Ser Ala Ser Ala Ser 310	
gaa att ctt gca ggc gca tta aaa gaa gcc gag ggc tac gac gtg gtt	1496
Glu Ile Leu Ala Gly 315 Ala Leu Lys Glu Ala 320 Glu Gly Tyr Asp Val 325 Val	
ggc gat cct tcc ttt gga aag gga acc gtc cag cag gcg gtg ccg atg	1544
Gly Asp Pro Ser 330 Phe Gly Lys Gly Thr 335 Val Gln Gln Ala Val 340 Pro Met	
gga gac ggt agc aat att aag ctg acg ctg tac aaa tgg ctg aca cct	1592
Gly Asp Gly 345 Ser Asn Ile Lys Leu Thr Leu Tyr Lys Trp 355 Leu Thr Pro	
aaa gga aat tgg atc cat aag cag ggc att cag ccg acc gtt cca gtc	1640
Lys Gly Asn Trp Ile His Lys 365 Gln Gly Ile Gln Pro Thr Val Pro Val	
acg cag cct gca tat ttc tcg gcg ggg cct tta cag ctg aaa gaa ccc	1688
Thr Gln Pro Ala Tyr Phe 380 Ser Ala Gly Pro Leu 385 Gln Leu Lys Glu Pro 390	
ctc aag ccg gat atg aac aac aat gaa att aag cgg gcg cag ttc ctg	1736
Leu Lys Pro Asp Met 395 Asn Asn Asn Glu Ile Lys Arg Ala Gln Phe 405 Leu	
ctg aaa gga ctc ggg ttt gtc ccc ggc cgg gaa gac ggc tat tac aat	1784
Leu Lys Gly Leu 410 Gly Phe Val Pro Gly 415 Arg Glu Asp Gly Tyr 420 Tyr Asn	
gaa agc aca aaa aaa gcc gtc atg gcg ttt cag gca gca aac aag ctg	1832
Glu Ser Thr 425 Lys Lys Ala Val Met Ala Phe Gln Ala Ala 435 Asn Lys Leu	
aag caa aca ggg atc att gac caa aaa acg gca aat aca atg aac ctg	1880
Lys Gln Thr Gly Ile Ile Asp 445 Gln Lys Thr Ala Asn 450 Thr Met Asn Leu	
cgg att gag gag aaa aag atg gat gaa aag aac gat ctt cag ctg caa	1928
Arg Ile Glu Glu Lys 460 Met Asp Glu Lys Asn 465 Asp Leu Gln Leu 470	
gcc gca tta aaa gtg ctg ttt aac aaa aag tgagggcacg ggatgtcctc	1978
Ala Ala Leu Lys Val 475 Leu Phe Asn Lys Lys 480	
acttttttta ttctcagaaa gttaaattctc aatcttttta cctaaaattt ttgctttttc	2038
ataaaaaaaaa cattcataat gaatagaatt gacccgataa cataagtata tgggagactt	2098

10294.204.ST25.txt

tataaggatg taaagatgca gtaaaaatgt aactttttgca agttgtataa cataggaaaa 2158
 ctttttataaa tagaaccaaa gcttttttcaa gaattataat gtgtgcattt tttttgcgga 2218
 gaatgtagc gctgttttgcg ttcttcgtct ctgttggtgg agtcgtctga cgcttgcgct 2278
 tttcttatat ataaataata aatgggggta cacgattgaa aagggcaagt attgtgagag 2338
 agaaaaata ctatgaatta gtggagcagt taaaagtctg atcacaagac gttacgtttt 2398
 ccgctacaaa ggcagtagga ttgcttatgc tgt 2431

<210> 12
 <211> 480
 <212> PRT
 <213> Bacillus licheniformis

<400> 12

Met Asn Gln Lys Ile Val Ser Val Leu Ile Ile Ala Leu Ser Leu Leu
 1 5 10 15

Cys Gly Leu Val Thr Gly Ala Gly Pro Ile Pro Leu His Asp Val Val
 20 25 30

Ser Lys Ala Ser Ala Ala Glu Glu Ala Ala Ala Lys Ser Thr Ala Arg
 35 40 45

Asn Glu Leu Glu Lys Ile Glu Lys Ala Tyr Asp Leu Ile Ser Asn Glu
 50 55 60

Tyr Val Glu Gln Val Asp Arg Glu Lys Leu Leu Glu Gly Ala Ile Gln
 65 70 75 80

Gly Met Leu Ser Thr Leu Asn Asp Pro Tyr Ser Val Tyr Met Asp Lys
 85 90 95

Gln Thr Ala Lys Arg Phe Ser Asp Ser Leu Asp Ser Ser Phe Glu Gly
 100 105 110

Ile Gly Ala Glu Ile Gly Met Glu Asp Arg Lys Ile Ile Ile Val Ser
 115 120 125

Pro Phe Lys Gln Ser Pro Ala Glu Lys Ala Gly Leu Lys Pro Asn Asp
 130 135 140

Glu Ile Ile Ser Ile Asp Gly Asp Ser Met Ser Gly Met Asp Leu Asn
 145 150 155 160

Asp Ala Val Leu Lys Ile Arg Gly Lys Lys Gly Ser Thr Val Thr Leu
 165 170 175

Lys Val His Arg Pro Gly Met Lys Asp Gln Leu Thr Phe Thr Ile Lys
 180 185 190

10294.204.ST25.txt

Arg Asp Glu Ile Pro Leu Glu Thr Val Phe Ala Ser Ile Lys Lys Val
 195 200 205
 Gln Asp Lys Pro Val Gly Tyr Ile Ala Ile Ser Ser Phe Ser Glu His
 210 215 220
 Thr Ala Lys Asp Phe Thr Ala Glu Leu Lys Lys Leu Glu Lys Lys Gly
 225 230 235 240
 Ile Lys Gly Leu Val Leu Asp Val Arg Gly Asn Pro Gly Gly Tyr Leu
 245 250 255
 Gln Ser Val Glu Asp Ile Leu Lys His Phe Val Thr Lys Asp His Pro
 260 265 270
 Tyr Ile Gln Ile Ala Glu Arg Asn Gly Asn Lys Lys Gln Tyr Phe Ser
 275 280 285
 Lys Leu Lys Glu Lys Lys Pro Tyr Pro Val Ser Val Ile Thr Asp Lys
 290 295 300
 Gly Ser Ala Ser Ala Ser Glu Ile Leu Ala Gly Ala Leu Lys Glu Ala
 305 310 315 320
 Glu Gly Tyr Asp Val Val Gly Asp Pro Ser Phe Gly Lys Gly Thr Val
 325 330 335
 Gln Gln Ala Val Pro Met Gly Asp Gly Ser Asn Ile Lys Leu Thr Leu
 340 345 350
 Tyr Lys Trp Leu Thr Pro Lys Gly Asn Trp Ile His Lys Gln Gly Ile
 355 360 365
 Gln Pro Thr Val Pro Val Thr Gln Pro Ala Tyr Phe Ser Ala Gly Pro
 370 375 380
 Leu Gln Leu Lys Glu Pro Leu Lys Pro Asp Met Asn Asn Asn Glu Ile
 385 390 395 400
 Lys Arg Ala Gln Phe Leu Leu Lys Gly Leu Gly Phe Val Pro Gly Arg
 405 410 415
 Glu Asp Gly Tyr Tyr Asn Glu Ser Thr Lys Lys Ala Val Met Ala Phe
 420 425 430
 Gln Ala Ala Asn Lys Leu Lys Gln Thr Gly Ile Ile Asp Gln Lys Thr
 435 440 445
 Ala Asn Thr Met Asn Leu Arg Ile Glu Glu Lys Lys Met Asp Glu Lys
 450 455 460

Asn 465 Asp Leu Gln Leu Gln 470 Ala Ala Leu Lys Val 475 Leu Phe Asn Lys Lys 480

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<210> 13
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<212> DNA
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<220>
<221> CDS
<222> (977) ..(2383)
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Gly Thr Pro Thr Asp Ala Thr Ile Gln Ser Leu Leu Pro His Leu Glu	
80 85 90	
aaa ggc gac att ttg att gac ggc gga aat aca tat tat aaa gat acg	1300
Lys Gly Asp Ile Leu Ile Asp Gly Gly Asn Thr Tyr Tyr Lys Asp Thr	
95 100 105	
cag aga aga aac agg gag ctg gcc gaa agc ggc att cac ttc atc ggc	1348
Gln Arg Arg Asn Arg Glu Leu Ala Glu Ser Gly Ile His Phe Ile Gly	
110 115 120	
acc ggc gtt tcc ggc ggt gaa gaa ggc gct ctg aaa ggg ccg tct atc	1396
Thr Gly Val Ser Gly Gly Glu Glu Gly Ala Leu Lys Gly Pro Ser Ile	
125 130 135 140	
atg cca ggc gga caa aag gaa gcc cat gag ctt gtc aag ccg att ctt	1444
Met Pro Gly Gly Gln Lys Glu Ala His Glu Leu Val Lys Pro Ile Leu	
145 150 155	
gaa gct att tct gcc aag gtg gac ggc gaa ccg tgt acg aca tac atc	1492
Glu Ala Ile Ser Ala Lys Val Asp Gly Glu Pro Cys Thr Thr Tyr Ile	
160 165 170	
ggt cct gac ggc gcc ggc cat tat gta aaa atg gtt cat aac ggc atc	1540
Gly Pro Asp Gly Ala Gly His Tyr Val Lys Met Val His Asn Gly Ile	
175 180 185	
gaa tac ggc gat atg cag ctg atc tca gaa tcc tac ttt att ttg aaa	1588
Glu Tyr Gly Asp Met Gln Leu Ile Ser Glu Ser Tyr Phe Ile Leu Lys	
190 195 200	
cac att gtc ggt ctg tca tca gat gag ctt cac gaa gtc ttt tcc gag	1636
His Ile Val Gly Leu Ser Ser Asp Glu Leu His Glu Val Phe Ser Glu	
205 210 215 220	
tgg aat aag gga gag ctt gac agc tat ctg atc gaa atc acg gct gat	1684
Trp Asn Lys Gly Glu Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala Asp	
225 230 235	
att ttc acg aaa aaa gac gag gaa acc ggc aag ccg ctt gtt gac gtc	1732
Ile Phe Thr Lys Lys Asp Glu Glu Thr Thr Gly Lys Pro Leu Val Asp Val	
240 245 250	
atc ctc gat aaa gca ggt caa aaa ggc aca gga aaa tgg aca agc caa	1780
Ile Leu Asp Lys Ala Gly Gln Lys Gly Thr Gly Lys Trp Thr Ser Gln	
255 260 265	
agc gct ctt gac ctg ggc gtt ccg ctt cca atc att acg gaa tct gtt	1828
Ser Ala Leu Asp Leu Gly Val Pro Leu Pro Ile Ile Thr Glu Ser Val	
270 275 280	
ttc gcc cgc ttc atc tct tcc atg aaa gag gag cgc gtc aaa gcg agc	1876
Phe Ala Arg Phe Ile Ser Ser Met Lys Glu Glu Arg Val Lys Ala Ser	
285 290 295 300	
aag ctt ctg gca gga cct gaa gcg aaa cct gcc gct gag aac aaa gaa	1924
Lys Leu Leu Ala Gly Pro Glu Ala Lys Pro Ala Ala Glu Asn Lys Glu	
305 310 315	
gag ctg atc gaa gcg gtc aga aaa gcg ctc ttc atg agc aaa atc tgt	1972
Glu Leu Ile Glu Ala Val Arg Lys Ala Leu Phe Met Ser Lys Ile Cys	
320 325 330	
tct tac gcc caa ggc ttt gct caa atg aaa gcc gca tca gaa gaa tac	2020
Ser Tyr Ala Gln Gly Phe Ala Gln Met Lys Ala Ala Ser Glu Glu Tyr	
335 340 345	

10294.204.ST25.txt

ggc tgg gat ttg aaa tac ggc gat atc gcg atg att ttc cgc gga gga 2068
 Gly Trp Asp Leu Lys Tyr Gly Asp Ile Ala Met Ile Phe Arg Gly Gly
 350 355 360
 tgc atc atc cgc gcg gcg ttc ctg caa aaa atc aaa gaa gcg tat gac 2116
 Cys Ile Ile Arg Ala Ala Phe Leu Gln Lys Ile Lys Glu Ala Tyr Asp
 365 370 375 380
 cgc gat cca gag ctt gac aac ctg ctt ctt gac ccg tac ttc aaa aat 2164
 Arg Asp Pro Glu Leu Asp Asn Leu Leu Leu Asp Pro Tyr Phe Lys Asn
 385 390 395
 atc gtt gaa agc tat cag gga gcc ctg cgc aaa acg att tct ctt gcg 2212
 Ile Val Glu Ser Tyr Gln Gly Ala Leu Arg Lys Thr Ile Ser Leu Ala
 400 405 410
 gtt gaa caa gga att cct gta cct tgc ttc tca agc gct ctc gct tac 2260
 Val Glu Gln Gly Ile Pro Val Pro Cys Phe Ser Ser Ala Leu Ala Tyr
 415 420 425
 ttt gac agc tac cgc act gca acc ctg ccg gcc aac ctg att cag gcg 2308
 Phe Asp Ser Tyr Arg Thr Ala Thr Leu Pro Ala Asn Leu Ile Gln Ala
 430 435 440
 cag cgc gac tac ttt ggc gcc cat acg tat gag cgt aca gat aaa gaa 2356
 Gln Arg Asp Tyr Phe Gly Ala His Thr Tyr Glu Arg Thr Asp Lys Glu
 445 450 455 460
 ggc att ttc cac act gag tgg atg aaa taagatgtaa aaccgcaagc 2403
 Gly Ile Phe His Thr Glu Trp Met Lys
 465
 tgaaaagctt gcggtttttt tgatttttcgg aaggatgcat gtttaagcgg ttgtgtggaa 2463
 acctactcaa aagtgagttt caataaggag gaatcaaccc atgtatccaa gtttagaggg 2523
 aaaaacggtc gttatcaca 2542

<210> 14
 <211> 469
 <212> PRT
 <213> Bacillus licheniformis

<400> 14

Met Ala Lys Gln Gln Ile Gly Val Val Gly Leu Ala Val Met Gly Lys
1 5 10 15

Asn Leu Ala Leu Asn Ile Glu Ser Arg Gly Phe Ser Val Ser Val Tyr
20 25 30

Asn Arg Ser Ser Glu Lys Thr Glu Glu Phe Leu Lys Glu Ala Glu Gly
35 40 45

Lys Asn Val Val Gly Thr Tyr Ser Ile Glu Glu Phe Val Glu Ser Leu
50 55 60

Glu Lys Pro Arg Lys Ile Leu Leu Met Val Lys Ala Gly Thr Pro Thr
65 70 75 80

Asp Ala Thr Ile Gln Ser Leu Leu Pro His Leu Glu Lys Gly Asp Ile
85 90 95

10294.204.ST25.txt

Leu Ile Asp Gly Gly Asn Thr Tyr Tyr Lys Asp Thr Gln Arg Arg Asn
 100 105 110
 Arg Glu Leu Ala Glu Ser Gly Ile His Phe Ile Gly Thr Gly Val Ser
 115 120 125
 Gly Gly Glu Glu Gly Ala Leu Lys Gly Pro Ser Ile Met Pro Gly Gly
 130 135 140
 Gln Lys Glu Ala His Glu Leu Val Lys Pro Ile Leu Glu Ala Ile Ser
 145 150 155 160
 Ala Lys Val Asp Gly Glu Pro Cys Thr Thr Tyr Ile Gly Pro Asp Gly
 165 170 175
 Ala Gly His Tyr Val Lys Met Val His Asn Gly Ile Glu Tyr Gly Asp
 180 185 190
 Met Gln Leu Ile Ser Glu Ser Tyr Phe Ile Leu Lys His Ile Val Gly
 195 200 205
 Leu Ser Ser Asp Glu Leu His Glu Val Phe Ser Glu Trp Asn Lys Gly
 210 215 220
 Glu Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala Asp Ile Phe Thr Lys
 225 230 235 240
 Lys Asp Glu Glu Thr Gly Lys Pro Leu Val Asp Val Ile Leu Asp Lys
 245 250 255
 Ala Gly Gln Lys Gly Thr Gly Lys Trp Thr Ser Gln Ser Ala Leu Asp
 260 265 270
 Leu Gly Val Pro Leu Pro Ile Ile Thr Glu Ser Val Phe Ala Arg Phe
 275 280 285
 Ile Ser Ser Met Lys Glu Glu Arg Val Lys Ala Ser Lys Leu Leu Ala
 290 295 300
 Gly Pro Glu Ala Lys Pro Ala Ala Glu Asn Lys Glu Glu Leu Ile Glu
 305 310 315 320
 Ala Val Arg Lys Ala Leu Phe Met Ser Lys Ile Cys Ser Tyr Ala Gln
 325 330 335
 Gly Phe Ala Gln Met Lys Ala Ala Ser Glu Glu Tyr Gly Trp Asp Leu
 340 345 350
 Lys Tyr Gly Asp Ile Ala Met Ile Phe Arg Gly Gly Cys Ile Ile Arg
 355 360 365

10294.204.ST25.txt

Ala Ala Phe Leu Gln Lys Ile Lys Glu Ala Tyr Asp Arg Asp Pro Glu
370 375 380

Leu Asp Asn Leu Leu Leu Asp Pro Tyr Phe Lys Asn Ile Val Glu Ser
385 390 395 400

Tyr Gln Gly Ala Leu Arg Lys Thr Ile Ser Leu Ala Val Glu Gln Gly
405 410 415

Ile Pro Val Pro Cys Phe Ser Ser Ala Leu Ala Tyr Phe Asp Ser Tyr
420 425 430

Arg Thr Ala Thr Leu Pro Ala Asn Leu Ile Gln Ala Gln Arg Asp Tyr
435 440 445

Phe Gly Ala His Thr Tyr Glu Arg Thr Asp Lys Glu Gly Ile Phe His
450 455 460

Thr Glu Trp Met Lys
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<210> 15
<211> 2030
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1391)

<400> 15
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ctgaaatcga cgtgttgatc ccgggcgcca aacgcgctga tcagctgatc gacaacctca 180
aaacggcaga agtcaatctg tctcaagagg acattgattt catcgaccgg ctgtttgccc 240
gctaaatgat caggaaacct atcttaaaag ataggtttct ttatttttaa aatcctgttg 300
acagcgcttc catttttgat atgataggaa agaagttaat acaagtgacg gagaatggga 360
gattcacaat aagaccctct tgtgccaggg gtttttttgt ggatctcttt ttcttcgtca 420
tctaagaggg ggcgaaagca atcgtaatga atagacggca cttttattct gtataacagc 480
ttgaaaggag agatcatgtt atg aaa aga cta gtc cgc agc atc ttc ctt ata 533
Met Lys Arg Leu Val Arg Ser Ile Phe Leu Ile
1 5 10
acg gcc gca atc gct gct ttt ggt ttt gga ttc agc ggg cat gcg gag 581
Thr Ala Ala Ile Ala Ala Phe Gly Phe Gly Phe Ser Gly His Ala Glu
15 20 25
gcg gca agc cat tcc cag ccg cag ctc aat ccg aac aag cta cta aat 629
Ala Ala Ser His Ser Gln Pro Gln Leu Asn Pro Asn Lys Leu Leu Asn
30 35 40

10294.204.ST25.txt

gtc gcg cac cgc ggc gca tcg ggg cat gct ccc gag cac acg ctt ttg Val Ala His Arg Gly Ala Ser Gly His Ala Pro Glu His Thr Leu Leu 45 50 55	677
gct tat aag ctt gga caa aaa atg aaa ggc gat tac ata gaa atc gat Ala Tyr Lys Leu Gly Gln Lys Met Lys Gly Asp Tyr Ile Glu Ile Asp 60 65 70 75	725
ctt caa atg aca aaa gac ggc cac ttg gtc gcc atg cac gat gag aca Leu Gln Met Thr Lys Asp Gly His Leu Val Ala Met His Asp Glu Thr 80 85 90	773
ttg gat cgt acg act aat ggt acg ggt ttt gtc aaa gac tat acg ctg Leu Asp Arg Thr Thr Asn Gly Thr Gly Phe Val Lys Asp Tyr Thr Leu 95 100 105	821
aaa gaa atc aaa gag ctt gat gca ggc tcc tgg ttt aac gaa gca tat Lys Glu Ile Lys Glu Leu Asp Ala Gly Ser Trp Phe Asn Glu Ala Tyr 110 115 120	869
cct gag cgg gca aaa ccg gag tac gcc ggg ctg aaa gtg ccc acc ctt Pro Glu Arg Ala Lys Pro Glu Tyr Ala Gly Leu Lys Val Pro Thr Leu 125 130 135	917
gaa gaa atc atc caa aca ttc ggg aga agc gcg cgc tac tat atc gaa Glu Glu Ile Ile Gln Thr Phe Gly Arg Ser Ala Arg Tyr Tyr Ile Glu 140 145 150 155	965
aca aaa tca ccg gaa gac tat gat cat atg gaa gaa aag ctc ctg gac Thr Lys Ser Pro Glu Asp Tyr Asp His Met Glu Glu Lys Leu Leu Asp 160 165 170	1013
atc ctg aag caa tac aaa ttg acc gga gca gac att cat tca agc aaa Ile Leu Lys Gln Tyr Lys Leu Thr Gly Ala Asp Ile His Ser Ser Lys 175 180 185	1061
gtc atc att caa tct ttt agt cct gaa agc tta aaa atc att cat aac Val Ile Ile Gln Ser Phe Ser Pro Glu Ser Leu Lys Ile Ile His Asn 190 195 200	1109
gct aat cca aac att ccg cta gtg caa tta tta tgg tac gac aaa cct Ala Asn Pro Asn Ile Pro Leu Val Gln Leu Leu Trp Tyr Asp Lys Pro 205 210 215	1157
gct gcc att act gac gcc gaa tta aaa caa tat caa tct tac agc gtc Ala Ala Ile Thr Asp Ala Glu Leu Lys Gln Tyr Gln Ser Tyr Ser Val 220 225 230 235	1205
gga ctc ggc atg aac ttt gac cgc att ggc cgg gca tac gtg caa aag Gly Leu Gly Met Asn Phe Asp Arg Ile Gly Arg Ala Tyr Val Gln Lys 240 245 250	1253
att cga cgc acc ggc atg ctg gtc cat cct tat act gtg aat aaa aaa Ile Arg Arg Thr Gly Met Leu Val His Pro Tyr Thr Val Asn Lys Lys 255 260 265	1301
gaa gat atg aag cgg ctg ctc gat tgg gga gcg acc gga atg ttc acc Glu Asp Met Lys Arg Leu Leu Asp Trp Gly Ala Thr Gly Met Phe Thr 270 275 280	1349
aac ttt ccg gac cgg ctg cgc gat gtt ttg cgc gaa aag aag Asn Phe Pro Asp Arg Leu Arg Asp Val Leu Arg Glu Lys Lys 285 290 295	1391
taaatgaata aagaagggga ataccatggtt aaaactgttt aagccagcac cgccgattga	1451
gcggctgccg gaagatcaaa ttgattcgga atataagaaa ttcagactgc aagtttttct	1511

10294.204.ST25.txt

cggcacatcttc atcgggttatg cggcatacta ttttaattcgc aaaaattttct cgcttgccat 1571
 gccttattttg atcgaagagg gcttttcaaa gtcggcgctc ggctttgcct tgtccgctct 1631
 atccatctct tacgggctga gcaagttcgt gatggccacg atatcggacc ggagcaatcc 1691
 gaggatgttc ctgcccgcgc gtttgatcct ttccgctgtc atcagcctct tgatgggggtt 1751
 tgttcctttt ttcacctcat cgatcgccat tatgtttatc atgctgttct taaacggctg 1811
 gttccagggc atgggatggc cgccgtcagg gcgtgtcctt gtccactggg tcagcgtcag 1871
 cgaaagggga aataaaaccg ccatatggaa tgtcgcccac aatgtcggcg ggggactgat 1931
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 ctatgaaggt gtgtttattt tgccggcctt ggtcgccat 2030

<210> 16
 <211> 297
 <212> PRT
 <213> Bacillus licheniformis

<400> 16

Met Lys Arg Leu Val Arg Ser Ile Phe Leu Ile Thr Ala Ala Ile Ala
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Ala Phe Gly Phe Gly Phe Ser Gly His Ala Glu Ala Ala Ser His Ser
20 25 30

Gln Pro Gln Leu Asn Pro Asn Lys Leu Leu Asn Val Ala His Arg Gly
35 40 45

Ala Ser Gly His Ala Pro Glu His Thr Leu Leu Ala Tyr Lys Leu Gly
50 55 60

Gln Lys Met Lys Gly Asp Tyr Ile Glu Ile Asp Leu Gln Met Thr Lys
65 70 75 80

Asp Gly His Leu Val Ala Met His Asp Glu Thr Leu Asp Arg Thr Thr
85 90 95

Asn Gly Thr Gly Phe Val Lys Asp Tyr Thr Leu Lys Glu Ile Lys Glu
100 105 110

Leu Asp Ala Gly Ser Trp Phe Asn Glu Ala Tyr Pro Glu Arg Ala Lys
115 120 125

Pro Glu Tyr Ala Gly Leu Lys Val Pro Thr Leu Glu Glu Ile Ile Gln
130 135 140

Thr Phe Gly Arg Ser Ala Arg Tyr Tyr Ile Glu Thr Lys Ser Pro Glu
145 150 155 160

Asp Tyr Asp His Met Glu Glu Lys Leu Leu Asp Ile Leu Lys Gln Tyr

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<210> 17
<211> 2308
<212> DNA
<213> Bacillus licheniformis
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<220>
<221> CDS
<222> (501)..(1814)

[illegible]

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aca tcg aca aca gac gaa gcg acg ctc acc gat ata ccg gtc aaa tcg Thr Ser Thr Thr Asp Glu Ala Thr Leu Thr Asp Ile Pro Val Lys Ser	45	55	677
ttt tat gat gat gaa aac tac gtc gta aca ggc gtg ccg cag acg gtg Phe Tyr Asp Asp Glu Asn Tyr Val Val Thr Gly Val Pro Gln Thr Val	60	70	725
aat gtc acg att aaa ggc ccg acc gga acc gtc aag aag gtc aga caa Asn Val Thr Ile Lys Gly Pro Thr Gly Thr Val Lys Lys Val Arg Gln	80	85	773
gtg aag gat ttt gag att tat gcc gac atg caa aac ctg aaa aca ggc Val Lys Asp Phe Glu Ile Tyr Ala Asp Met Gln Asn Leu Lys Thr Gly	95	100	821
agg cat aaa gtc gag ctg aag gcc aga aat gtt gcc gac ggc ctc act Arg His Lys Val Glu Leu Lys Ala Arg Asn Val Ala Asp Gly Leu Thr	110	115	869
ctg acc atc aat cca tcg gtg aca acc gtg acg atc gaa gaa aaa acg Leu Thr Ile Asn Pro Ser Val Thr Thr Val Thr Ile Glu Glu Lys Thr	125	130	917
acg aag gaa ttc ccg gtc gag gtt gat ttt tat aat aaa aac aaa atg Thr Lys Glu Phe Pro Val Glu Val Asp Phe Tyr Asn Lys Asn Lys Met	140	145	965
aaa gac ggc tac acg ccg gag ctg ccg atc atc aac ccg aaa aac gtc Lys Asp Gly Tyr Thr Pro Glu Leu Pro Ile Ile Asn Pro Lys Asn Val	160	165	1013
agc gtc acc ggc tca aaa gcc gtg atc gac aga atc cag aac atc aag Ser Val Thr Gly Ser Lys Ala Val Ile Asp Arg Ile Gln Asn Ile Lys	175	180	1061
gcg acg atc aat tta gag ggc gtc gac cag acg gtt gaa aaa gaa gcc Ala Thr Ile Asn Leu Glu Gly Val Asp Gln Thr Val Glu Lys Glu Ala	190	195	1109
aag ctt aca gta tac gac aag gac gga aat gtc ctg ccg gtt gaa gtc Lys Leu Thr Val Tyr Asp Lys Asp Gly Asn Val Leu Pro Val Glu Val	205	210	1157
agc cct tcc gtc gtt aaa atc acc gtt ccg gtg acg agc ccg agc aaa Ser Pro Ser Val Val Lys Ile Thr Val Pro Val Thr Ser Pro Ser Lys	220	225	1205
aag att ccg gtc aaa gtt gac cgg aaa ggc agc ctt ccg gac ggc atc Lys Ile Pro Val Lys Val Asp Arg Lys Gly Ser Leu Pro Asp Gly Ile	240	245	1253
agc att tcc agc ctc gat ata agt ccg gga gag gtg acc gtc tac ggg Ser Ile Ser Ser Leu Asp Ile Ser Pro Gly Glu Val Thr Val Tyr Gly	255	260	1301
ccg caa aat gtt ctt gat tcg tta gaa ttt gtc gag gcc gac gag att Pro Gln Asn Val Leu Asp Ser Leu Glu Phe Val Glu Ala Asp Glu Ile	270	275	1349
gat tta agt aaa ata aag gat gat act gaa ttg gaa gcc ggc att aaa Asp Leu Ser Lys Ile Lys Asp Asp Thr Glu Leu Glu Ala Gly Ile Lys			1397

10294.204.ST25.txt

285 290 295

gtg ccg gac ggc gct aaa aag gtg tca ccc gaa aaa gtg aaa atc aag 1445
Val Pro Asp Gly Ala Lys Lys Val Ser Pro Glu Lys Val Lys Ile Lys 315
300 305

gtg aaa gtt gac aag gaa gaa gag aaa aaa ctg aaa aac gtt tca att 1493
Val Lys Val Asp Lys Glu Glu Glu Lys Lys Leu Lys Asn Val Ser Ile 330
320 325

aaa acc gcg ggc ctg aat gac agc cgg gat ctt gaa ttt ctc gat ccg 1541
Lys Thr Ala Gly Leu Asn Asp Ser Arg Asp Leu Glu Phe Leu Asp Pro 345
335 340

aag tca ggc aag ctg gat atc acg gca aag ggc tcg aca gcc gcg atc 1589
Lys Ser Gly Lys Leu Asp Ile Thr Ala Lys Gly Ser Thr Ala Ala Ile 360
350 355

gaa aaa ctc cag cct tcc gac gtc gag ctc tat gtc aat gtg gcg gat 1637
Glu Lys Leu Gln Pro Ser Asp Val Glu Leu Tyr Val Asn Val Ala Asp 375
365 370

ctc gat gac ggc gag cac aat gta aag ctg gaa gta aac ggt ccg cag 1685
Leu Asp Asp Gly Glu His Asn Val Lys Leu Glu Val Asn Gly Pro Gln 395
380 385

aac atg aca tgg tcg ctg ccg cgg caa agc att cga gtg aaa atc tca 1733
Asn Met Thr Trp Ser Leu Pro Arg Gln Ser Ile Arg Val Lys Ile Ser 410
400 405

tct caa aca acc caa aac gaa aaa aac aat ggt cag gat gaa gaa gaa 1781
Ser Gln Thr Thr Gln Asn Glu Lys Asn Asn Gly Gln Asp Glu Glu Glu 425
415 420

gag aat cat tct gaa aag gat tca caa cct tca tgaatcaaaa aggagcgata 1834
Glu Asn His Ser Glu Lys Asp Ser Gln Pro Ser 435
430

ttaatgggca agtatttttggt tacagacggt gtaagaggcg tggcaaacag tgaacttaca 1894

cctgagctgg ccttttaaagt cggacgcttt ggcggatatg tcctaacaaa agataaggag 1954

cgtcccaagg ttctgatcgg ccgtgacacg cgcatttcag ggcatatgct ggaaggggcc 2014

cttgtagcag gccttctttc gataggagca gaagtcatgc gtctcggcgt gatttcgacg 2074

cccggagtcg catatttgac gaaggctatg gacgcggagg cgggtgtgat gatttcgcgt 2134

tcccacaacc ctgtccagga caacggaatt aagtttttcg gcggcgacgg ctttaagctt 2194

tccgatgaac aggagcttga aatcgagcgt ctgatggatc agccggaaga tcacctgcca 2254

aggcctgtag gcgctgatct gggcatggtg aacgactact ttgaaggcgg acag 2308

<210> 18
<211> 438
<212> PRT
<213> Bacillus licheniformis

<400> 18

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20 25 30

10294.204.ST25.txt

Thr Pro Lys Lys Pro Gly Glu Ser Phe Phe Pro Thr Ser Thr Thr Asp
 35 40 45
 Glu Ala Thr Leu Thr Asp Ile Pro Val Lys Ser Phe Tyr Asp Asp Glu
 50 55 60
 Asn Tyr Val Val Thr Gly Val Pro Gln Thr Val Asn Val Thr Ile Lys
 65 70 75 80
 Gly Pro Thr Gly Thr Val Lys Lys Val Arg Gln Val Lys Asp Phe Glu
 85 90 95
 Ile Tyr Ala Asp Met Gln Asn Leu Lys Thr Gly Arg His Lys Val Glu
 100 105 110
 Leu Lys Ala Arg Asn Val Ala Asp Gly Leu Thr Leu Thr Ile Asn Pro
 115 120 125
 Ser Val Thr Thr Val Thr Ile Glu Glu Lys Thr Thr Lys Glu Phe Pro
 130 135 140
 Val Glu Val Asp Phe Tyr Asn Lys Asn Lys Met Lys Asp Gly Tyr Thr
 145 150 155 160
 Pro Glu Leu Pro Ile Ile Asn Pro Lys Asn Val Ser Val Thr Gly Ser
 165 170 175
 Lys Ala Val Ile Asp Arg Ile Gln Asn Ile Lys Ala Thr Ile Asn Leu
 180 185 190
 Glu Gly Val Asp Gln Thr Val Glu Lys Glu Ala Lys Leu Thr Val Tyr
 195 200 205
 Asp Lys Asp Gly Asn Val Leu Pro Val Glu Val Ser Pro Ser Val Val
 210 215 220
 Lys Ile Thr Val Pro Val Thr Ser Pro Ser Lys Lys Ile Pro Val Lys
 225 230 235 240
 Val Asp Arg Lys Gly Ser Leu Pro Asp Gly Ile Ser Ile Ser Ser Leu
 245 250 255
 Asp Ile Ser Pro Gly Glu Val Thr Val Tyr Gly Pro Gln Asn Val Leu
 260 265 270
 Asp Ser Leu Glu Phe Val Glu Ala Asp Glu Ile Asp Leu Ser Lys Ile
 275 280 285
 Lys Asp Asp Thr Glu Leu Glu Ala Gly Ile Lys Val Pro Asp Gly Ala
 290 295 300

10294.204.ST25.txt

Lys Lys Val Ser Pro Glu Lys Val Lys Ile Lys Val Lys Val Asp Lys
305 310 315 320

Glu Glu Glu Lys Lys Leu Lys Asn Val Ser Ile Lys Thr Ala Gly Leu
325 330 335

Asn Asp Ser Arg Asp Leu Glu Phe Leu Asp Pro Lys Ser Gly Lys Leu
340 345 350

Asp Ile Thr Ala Lys Gly Ser Thr Ala Ala Ile Glu Lys Leu Gln Pro
355 360 365

Ser Asp Val Glu Leu Tyr Val Asn Val Ala Asp Leu Asp Asp Gly Glu
370 375 380

His Asn Val Lys Leu Glu Val Asn Gly Pro Gln Asn Met Thr Trp Ser
385 390 395 400

Leu Pro Arg Gln Ser Ile Arg Val Lys Ile Ser Ser Gln Thr Thr Gln
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Asn Glu Lys Asn Asn Gly Gln Asp Glu Glu Glu Glu Asn His Ser Glu
420 425 430

Lys Asp Ser Gln Pro Ser
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cggcaagcgt ttttccccgt gtaaccggga cccttctgat ctgataatct cccatgagat 180
cgaccgcttt tcaatgaatg tttaacttta ccgtaatgat agaagggcc tttggatatg 240
aacgattcat cgaagcgatc ccgtcttata aagaagtgtt tggcacagac gaaaagggtgt 300
ggacaaaagc atcgccgctc tcatacataa acaactcaaa attgccgccg gcctatcttg 360
tgacccgctg ggaagaccct gccgtttaca agttcgcgga aaccgcaaac aaagcgaagg 420
caacggaatt tgtgtatcaa gtcaacagct tatctcacag tgatttaaac aagatgttcg 480
gctctccaga tgcaccggca gaagcgcaga atctgacaaa agcggttatg gcgttttttag 540
agaaggaaaa taaatagatc aaacggccga ctcggcttcc tacatgtact tgctgaaagg 600

10294.204.ST25.txt

atataaacag ctgttaaact agcagagaaa ggccgaaaat gttaaattcg gcctcttctc 660
 acacttgga ccccttact cataagacat cgatctgaaa attcccaaaa tataaaciaa 720
 acattaataa aatcaagcca tttgattaac aaattttacga tacgatcata tagaacttga 780
 tgattgggaa aagcattttg agagaagatt aagagcaagg gagatatgat gtgagaatga 840
 aacgattaag g atg agg aag cat tta ctg ata gct gtc tgt act ttg gca 890
 Met Arg Lys His Leu Leu Ile Ala Val Cys Thr Leu Ala
 1 5 10
 ctt ctt cta agt tcc ccg att gta agc gat gcg agc ccg gca act aaa 938
 Leu Leu Leu Ser Ser Pro Ile Val Ser Asp Ala Ser Pro Ala Thr Lys
 15 20 25
 cca aca act gca gat tcg ccg caa tct tcc gga ttt ttc gta gac cat 986
 Pro Thr Thr Ala Asp Ser Pro Gln Ser Ser Gly Phe Phe Val Asp His
 30 35 40 45
 tac aaa aat aat atc tct gcc aat acg acg gcg gaa tcc aat cct gtc 1034
 Tyr Lys Asn Asn Ile Ser Ala Asn Thr Thr Ala Glu Ser Asn Pro Val
 50 55 60
 atc ggc ctg ctt tcc gaa ttt aat aaa ctt tgg act ccc gga aag aca 1082
 Ile Gly Leu Leu Ser Glu Phe Asn Lys Leu Trp Thr Pro Gly Lys Thr
 65 70 75
 tgg aat acc ggt act aaa ctg aac agc agg gtg ctg gat gcc aac att 1130
 Trp Asn Thr Gly Thr Lys Leu Asn Ser Arg Val Leu Asp Ala Asn Ile
 80 85 90
 caa aaa gtc gtg gat att gct gaa cgc cgc acg atg ctt gag gaa aat 1178
 Gln Lys Val Val Asp Ile Ala Glu Arg Arg Thr Met Leu Glu Glu Asn
 95 100 105
 gct gcc tat ttt gat gat ccg ccg agc cag agc tac agt ata att gac 1226
 Ala Ala Tyr Phe Asp Asp Arg Arg Ser Gln Ser Tyr Ser Ile Ile Asp
 110 115 120 125
 ggc ctc ggc aag ctt gcc ggc gtc tat cga atg aac gcg gga gcg acg 1274
 Gly Leu Gly Lys Leu Ala Gly Val Tyr Arg Met Asn Ala Gly Ala Thr
 130 135 140
 aca acg atc acc agc att ccg gca gat gcc tcg att aga aaa tac aat 1322
 Thr Thr Ile Thr Ser Ile Pro Ala Asp Ala Ser Ile Arg Lys Tyr Asn
 145 150 155
 gat gaa gga acc aat tcg ggc agc acc agc tct gaa ctt gga aat gtc 1370
 Asp Glu Gly Thr Asn Ser Gly Ser Thr Ser Ser Glu Leu Gly Asn Val
 160 165 170
 gta agt ttg gtc aat act tta cgc ggc aac tat tct tca tcg aat ccg 1418
 Val Ser Leu Val Asn Thr Leu Arg Gly Asn Tyr Ser Ser Ser Asn Pro
 175 180 185
 gct aaa agc tat ttc aac tat ccc cgc ccg ttt cgc tgg aaa gac aat 1466
 Ala Lys Ser Tyr Phe Asn Tyr Pro Arg Pro Phe Arg Trp Lys Asp Asn
 190 195 200 205
 tcg atc att gtt cca acg ctt atc ccc gtc atc aat cct gat ccg aac 1514
 Ser Ile Ile Val Pro Thr Leu Ile Pro Val Ile Asn Pro Asp Pro Asn
 210 215 220
 aaa gac gga ggt ttt cca agc gga cac acg aac gcc gca tat ctc agc 1562
 Lys Asp Gly Gly Phe Pro Ser Gly His Thr Asn Ala Ala Tyr Leu Ser
 225 230 235

10294.204.ST25.txt

gct ttt gct atg gcc tat gcg ata ccg gag cgt tat cag gag ctg ctg 1610
Ala Phe Ala Met Ala Tyr Ala Ile Pro Glu Arg Tyr Gln Glu Leu Leu
240 245 250

act cgc gct tca gaa ctc ggt cat aac cgg att gtt gcc ggt atg cat 1658
Thr Arg Ala Ser Glu Leu Gly His Asn Arg Ile Val Ala Gly Met His
255 260 265

tcc ccg ctg gac gtc atg ggg gga cga gta atg gca aca gct ttg tct 1706
Ser Pro Leu Asp Val Met Gly Gly Arg Val Met Ala Thr Ala Leu Ser
270 275 280 285

gca gca atc ctg tct gac ccc gca aat gaa aga ttg aag aaa acg gct 1754
Ala Ala Ile Leu Ser Asp Pro Ala Asn Glu Arg Leu Lys Lys Thr Ala
290 295 300

ttt gat gaa gcc cgc cgt aaa tta tta acg caa acc ggt aca gct gaa 1802
Phe Asp Glu Ala Arg Arg Lys Leu Leu Thr Gln Thr Gly Thr Ala Glu
305 310 315

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Asp Arg Tyr Ser Asp Tyr Glu Lys Asn Lys Lys Gln Tyr Thr Glu Arg
320 325 330

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Leu Thr Tyr Gly Phe Arg Gln Met Asn Lys Thr Ala Lys Pro Met Ala
335 340 345

gtt cca aag gga gcc gaa gtc ctg ctg gaa aca cgt ttt cct tac ctt 1946
Val Pro Lys Gly Ala Glu Val Leu Leu Glu Thr Arg Phe Pro Tyr Leu
350 355 360 365

gac aaa aag cag cgc cgt tcg gtt tta gcc act acc ggt ctt ccg gcc 1994
Asp Lys Lys Gln Arg Arg Ser Val Leu Ala Thr Thr Gly Leu Pro Ala
370 375 380

ggc tac cct gtt ctt gat gat cga gaa gga tgg gga agg ctt aat ctc 2042
Gly Tyr Pro Val Leu Asp Asp Arg Glu Gly Trp Gly Arg Leu Asn Leu
385 390 395

ttt tcc gcg gca gat ggg tat ggg gct ttt acc aaa aat gtt acc gtg 2090
Phe Ser Ala Ala Asp Gly Tyr Gly Ala Phe Thr Lys Asn Val Thr Val
400 405 410

acc atg gat tcc gca aaa ggc ggc ttc cat aca gcc gat cgc tgg cgc 2138
Thr Met Asp Ser Ala Lys Gly Gly Phe His Thr Ala Asp Arg Trp Arg
415 420 425

aac gac atc tcc ggc acc gga aag ctg acc aaa aaa ggg aca ggc gct 2186
Asn Asp Ile Ser Gly Thr Thr Gly Lys Leu Thr Lys Lys Gly Thr Gly Ala
430 435 440 445

ttg aag ctg gaa ggg gat aat aca tat tcc ggc ggt aca cgg att gat 2234
Leu Lys Leu Glu Gly Asp Asn Thr Tyr Ser Gly Gly Thr Arg Ile Asp
450 455 460

caa gga aca ctt gag ggc ggt tcg gag aca gct ttc ggg aga ggt gat 2282
Gln Gly Thr Leu Glu Gly Gly Ser Glu Thr Ala Phe Gly Arg Gly Asp
465 470 475

gtt gca cta aac gga ggc atc ctt aag gaa gat gcg ccg gga aaa ctg 2330
Val Ala Leu Asn Gly Gly Ile Leu Lys Glu Asp Ala Pro Gly Lys Leu
480 485 490

atc atc gaa gga gac tac aaa caa tct gct aaa gga ata ctt gaa ctt 2378
Ile Ile Glu Gly Asp Tyr Lys Gln Ser Ala Lys Gly Ile Leu Glu Leu
495 500 505

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cag ctc agc ggc aaa aaa gat cag ttg aaa att aag gga aaa gca aga 2426
 Gln Leu Ser Gly Lys Lys Asp Gln Leu Lys Ile Lys Gly Lys Ala Arg
 510 515 520 525
 ttg aaa ggg aca ttg cgt ctc aat ttt acg gac aat tac gta ccg gct 2474
 Leu Lys Gly Thr Leu Arg Leu Asn Phe Thr Asp Asn Tyr Val Pro Ala
 530 535 540
 gac gga tcg gcg atc ata acc ttc cgc aag cgt cat gga tca ttt tct 2522
 Asp Gly Ser Ala Ile Ile Thr Phe Arg Lys Arg His Gly Ser Phe Ser
 545 550 555
 tcc gtc gag acc agt gga ttg cca agc aag tat aaa gtg aag atc atc 2570
 Ser Val Glu Thr Ser Gly Leu Pro Ser Lys Tyr Lys Val Lys Ile Ile
 560 565 570
 tat aaa tcc aac agt att cag ttg aaa gtt gag caa aaggggagaa 2616
 Tyr Lys Ser Asn Ser Ile Gln Leu Lys Val Glu Gln 585
 575 580
 gctgatctgc aagagg 2632

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 <213> Bacillus licheniformis

<400> 20

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 20 25 30

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 35 40 45

Asn Ile Ser Ala Asn Thr Thr Ala Glu Ser Asn Pro Val Ile Gly Leu
 50 55 60

Leu Ser Glu Phe Asn Lys Leu Trp Thr Pro Gly Lys Thr Trp Asn Thr
 65 70 75 80

Gly Thr Lys Leu Asn Ser Arg Val Leu Asp Ala Asn Ile Gln Lys Val
 85 90 95

Val Asp Ile Ala Glu Arg Arg Thr Met Leu Glu Glu Asn Ala Ala Tyr
 100 105 110

Phe Asp Asp Arg Arg Ser Gln Ser Tyr Ser Ile Ile Asp Gly Leu Gly
 115 120 125

Lys Leu Ala Gly Val Tyr Arg Met Asn Ala Gly Ala Thr Thr Thr Ile
 130 135 140

Thr Ser Ile Pro Ala Asp Ala Ser Ile Arg Lys Tyr Asn Asp Glu Gly
 Page 49

10294.204.ST25.txt
155

160

145

150

Thr Asn Ser Gly Ser Thr Ser Ser Glu Leu Gly Asn Val Val Ser Leu
 165 170 175
 Val Asn Thr Leu Arg Gly Asn Tyr Ser Ser Ser Asn Pro Ala Lys Ser
 180 185 190
 Tyr Phe Asn Tyr Pro Arg Pro Phe Arg Trp Lys Asp Asn Ser Ile Ile
 195 200 205
 Val Pro Thr Leu Ile Pro Val Ile Asn Pro Asp Pro Asn Lys Asp Gly
 210 215 220
 Gly Phe Pro Ser Gly His Thr Asn Ala Ala Tyr Leu Ser Ala Phe Ala
 225 230 235 240
 Met Ala Tyr Ala Ile Pro Glu Arg Tyr Gln Glu Leu Leu Thr Arg Ala
 245 250 255
 Ser Glu Leu Gly His Asn Arg Ile Val Ala Gly Met His Ser Pro Leu
 260 265 270
 Asp Val Met Gly Gly Arg Val Met Ala Thr Ala Leu Ser Ala Ala Ile
 275 280 285
 Leu Ser Asp Pro Ala Asn Glu Arg Leu Lys Lys Thr Ala Phe Asp Glu
 290 295 300
 Ala Arg Arg Lys Leu Leu Thr Gln Thr Gly Thr Ala Glu Asp Arg Tyr
 305 310 315 320
 Ser Asp Tyr Glu Lys Asn Lys Lys Gln Tyr Thr Glu Arg Leu Thr Tyr
 325 330 335
 Gly Phe Arg Gln Met Asn Lys Thr Ala Lys Pro Met Ala Val Pro Lys
 340 345 350
 Gly Ala Glu Val Leu Leu Glu Thr Arg Phe Pro Tyr Leu Asp Lys Lys
 355 360 365
 Gln Arg Arg Ser Val Leu Ala Thr Thr Gly Leu Pro Ala Gly Tyr Pro
 370 375 380
 Val Leu Asp Asp Arg Glu Gly Trp Gly Arg Leu Asn Leu Phe Ser Ala
 385 390 395 400
 Ala Asp Gly Tyr Gly Ala Phe Thr Lys Asn Val Thr Val Thr Met Asp
 405 410 415
 Ser Ala Lys Gly Gly Phe His Thr Ala Asp Arg Trp Arg Asn Asp Ile

10294.204.ST25.txt

420

425

430

Ser Gly Thr Gly Lys Leu Thr Lys Lys Gly Thr Gly Ala Leu Lys Leu
 435 440 445

Glu Gly Asp Asn Thr Tyr Ser Gly Gly Thr Arg Ile Asp Gln Gly Thr
 450 455 460

Leu Glu Gly Gly Ser Glu Thr Ala Phe Gly Arg Gly Asp Val Ala Leu
 465 470 475 480

Asn Gly Gly Ile Leu Lys Glu Asp Ala Pro Gly Lys Leu Ile Ile Glu
 485 490 495

Gly Asp Tyr Lys Gln Ser Ala Lys Gly Ile Leu Glu Leu Gln Leu Ser
 500 505 510

Gly Lys Lys Asp Gln Leu Lys Ile Lys Gly Lys Ala Arg Leu Lys Gly
 515 520 525

Thr Leu Arg Leu Asn Phe Thr Asp Asn Tyr Val Pro Ala Asp Gly Ser
 530 535 540

Ala Ile Ile Thr Phe Arg Lys Arg His Gly Ser Phe Ser Ser Val Glu
 545 550 555 560

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 565 570 575

Asn Ser Ile Gln Leu Lys Val Glu Gln
 580 585

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 <213> Bacillus licheniformis

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 <222> (501)..(2276)

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 ttccacggtg tgagaacgct cccttctttt aatctatttt ttatttaatt aaattgtagg 180
 ttgtaagcca gtcaataaca ttgttcactt tcaacaaaaa caaaagtaac attatacatt 240
 ttagacaaaa ggcgtcgtt aaaaatgatt catcgataga agctggcctt atgactcttt 300
 tttaaaacta acttggagta cccaatttaa cttcccgaat aaacaggaag cttcacaat 360
 gttgatataa cagtgttttt aacgttttaa aaactaaagg tgcattgacaa gcgaccttaa 420

10294.204.ST25.txt

gataagcttt ctttctcttt gaaaattcaa aaatcctccg atatatatag cgaacgccgc 480

taaaaaagga ggagagccgg atg aaa aag tta tgg aaa atc gcg gtt tcg gct 533
Met Lys Lys Leu Trp Lys Ile Ala Val Ser Ala
1 5 10

gca atg ttc gtc ggt ttt ttc gca aat tca ccc cgc att caa gcg gaa 581
Ala Met Phe Val Gly Phe Phe Ala Asn Ser Pro Arg Ile Gln Ala Glu
15 20 25

agc aat aag cag gaa aac gag gtc att gtt gta tat aaa aat acc agc 629
Ser Asn Lys Gln Glu Asn Glu Val Ile Val Val Tyr Lys Asn Thr Ser
30 35 40

gga aaa gaa acc gtc atc gaa cag gca gac acg gta gaa cac gtt tac 677
Gly Lys Glu Thr Val Ile Glu Gln Ala Asp Thr Val Glu His Val Tyr
45 50 55

cgg cac att ccc gca gcc gct gtc act gcg gac gac aaa aca gtg cgc 725
Arg His Ile Pro Ala Ala Val Thr Ala Asp Asp Lys Thr Val Arg
60 65 70 75

gaa ctt gaa cac gat ccc gac gtc ctg tat gtc gaa gac aac ctc ccg 773
Glu Leu Glu His Asp Pro Asp Val Leu Tyr Val Glu Asp Asn Leu Pro
80 85 90

gta gct gct gcc gac agc acc gct cta aaa gct ttc tcc agc agc aca 821
Val Ala Ala Ala Asp Ser Thr Ala Leu Lys Ala Phe Ser Ser Ser Thr
95 100 105

gcg caa aac gcc tcc gcg ttt tca cag tgg aac atc aag ctg att caa 869
Ala Gln Asn Ala Ser Ala Phe Ser Gln Trp Asn Ile Lys Leu Ile Gln
110 115 120

gcc gca ctg gct tgg aat aaa ggt ttg acc gga aaa cag gtg aag atc 917
Ala Ala Leu Ala Trp Asn Lys Gly Leu Thr Gly Lys Lys Gln Val Lys Ile
125 130 135

gcg gtt att gac agc ggg att tcc ccc cat gag gag ctg tcg atc gcc 965
Ala Val Ile Asp Ser Gly Ile Ser Pro His Glu Glu Leu Ser Ile Ala
140 145 150 155

ggc ggt gca tcg atg gtc ggc tat acc gct tca tac cgt gac gat aat 1013
Gly Gly Ala Ser Met Val Gly Tyr Thr Ala Ser Tyr Arg Asp Asp Asn
160 165 170

ggc cac gga acc cat gtt gcc gga atc atc gga gcg aag cat aac gga 1061
Gly His Gly Thr His Val Ala Gly Ile Ile Gly Ala Lys His Asn Gly
175 180 185

cgg ggg atc gac ggc atc gcg ccc ggc gcg cag ctg tat gcc gta aaa 1109
Arg Gly Ile Asp Gly Ile Ala Pro Gly Ala Gln Leu Tyr Ala Val Lys
190 195 200

gcg ctg gac cgg aat ggt gcg ggg gat ctg aaa ggt atc tta caa ggc 1157
Ala Leu Asp Arg Asn Gly Ala Gly Asp Leu Lys Gly Ile Leu Gln Gly
205 210 215

atc gat tgg tcg atc caa cac gga atc gat atc atc aat atg agc ctc 1205
Ile Asp Trp Ser Ile Gln His Gly Ile Asp Ile Ile Asn Met Ser Leu
220 225 230 235

gtc gtt tca ggc gac agt caa gtt ctc cac gat gcg gta gat aaa gca 1253
Val Val Ser Gly Asp Ser Gln Val Leu His Asp Ala Val Asp Lys Ala
240 245 250

tac aaa cgg gga atc att tta gtc gga gcg agc gga aat gcc gga aac 1301
Tyr Lys Arg Gly Ile Ile Leu Val Gly Ala Ser Gly Asn Ala Gly Asn

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255	260	265		
gga aaa tcc gtt tat tac ccg gcc gcc tac agc agc gtc att gcc gtc Gly Lys Ser Val Tyr Tyr Pro Ala Ala Tyr Ser Ser Val Ile Ala Val	270	275	280	1349
tcg gca acc aat gaa aaa aat cag atc gcc tca ttt acc aac acc cgg Ser Ala Thr Asn Glu Lys Asn Gln Ile Ala Ser Phe Thr Asn Thr Arg	285	290	295	1397
agc gcc gta tcg tat tcc gct ccg agc aca tct att atc aat aca tcg Ser Ala Val Ser Tyr Ser Ala Pro Ser Thr Ser Ile Ile Asn Thr Ser	300	305	310	1445
ggc aat cgc gga tat gca atc gga agc tgc act gca caa ggg aca ccc Gly Asn Arg Gly Tyr Ala Ile Gly Ser Cys Thr Ala Gln Gly Thr Pro	320	325	330	1493
gac gtc acc tgc gtg atc gca ctt atg aaa cag ctg cac cca acc gct Asp Val Thr Cys Val Ile Ala Leu Met Lys Gln Leu His Pro Thr Ala	335	340	345	1541
tca aat gct gag ctg cgc aag aaa atg cag ttt tat aca agc gat ttg Ser Asn Ala Glu Leu Arg Lys Lys Met Gln Phe Tyr Thr Ser Asp Leu	350	355	360	1589
ggc gct ccc ggt cgt gat cat ttg ttc ggc tac cga tta atc cgc ttc Gly Ala Pro Gly Arg Asp His Leu Phe Gly Tyr Arg Leu Ile Arg Phe	365	370	375	1637
aaa gag gtc aca cag cca ttg gaa aaa gcg caa aaa gcc gtc gga caa Lys Glu Val Thr Gln Pro Leu Glu Lys Ala Gln Lys Ala Val Gly Gln	380	385	390	1685
gcg gaa aag aca aag aaa aaa gcg gac att caa acc gca caa aaa gcg Ala Glu Lys Thr Lys Lys Lys Ala Asp Ile Gln Thr Ala Gln Lys Ala	400	405	410	1733
atc gaa ccg ctc cct gca gac gca gat aaa ccc gct ttg aaa aag aga Ile Glu Pro Leu Pro Ala Asp Ala Asp Lys Pro Ala Leu Lys Lys Arg	415	420	425	1781
ctc aat act gtt aaa gag cag ctt aaa aaa aca gcc gaa agc aaa gtg Leu Asn Thr Val Lys Glu Gln Leu Lys Lys Thr Ala Glu Ser Lys Val	430	435	440	1829
aaa ctc gct gag aag caa aaa aag aaa acc aat gcc gac tcc gcc caa Lys Leu Ala Glu Lys Gln Lys Lys Lys Thr Asn Ala Asp Ser Ala Gln	445	450	455	1877
aaa gcg gtc aac gaa ctc gac agc ggc act ttc aaa acg aat ttg caa Lys Ala Val Asn Glu Leu Asp Ser Gly Thr Phe Lys Thr Asn Leu Gln	460	465	470	1925
aaa cgg atc aac gcg gtc cgt tca agc ctc ttg aag acc gca aag cag Lys Arg Ile Asn Ala Val Arg Ser Ser Leu Leu Lys Thr Ala Lys Gln	480	485	490	1973
gcc gtt gcc aaa gct gaa aaa gcg gca aca gac tca aac ctc ggc aaa Ala Val Ala Lys Ala Glu Lys Ala Ala Thr Asp Ser Asn Leu Gly Lys	495	500	505	2021
gcg caa aaa gcg atc aat gag ctt ccc gcc gga aaa gac aaa tca aat Ala Gln Lys Ala Ile Asn Glu Leu Pro Ala Gly Lys Asp Lys Ser Asn	510	515	520	2069
ctg caa aaa agg ctg aac acc gcg aaa aag caa gca gct gca gcc tat Leu Gln Lys Arg Leu Asn Thr Ala Lys Lys Gln Ala Ala Ala Tyr				2117

10294.204.ST25.txt
535

525 530 535 2165
aat aaa aaa gtt tct gca gca aag gcc aaa gtc aaa acg gcc gaa caa
Asn Lys Lys Val Ser Ala Ala Lys Ala Lys Val Lys Thr Ala Glu Gln
540 545 550 555

2213
aag aga acg aaa aaa aca aaa tca gca gcg caa tca gca gta ggc aag
Lys Arg Thr Lys Lys Thr Lys Ser Ala Ala Gln Ser Ala Val Gly Lys
560 565 570

2261
ctg aaa gca tcc gcc gaa aaa acg aag ctg caa aaa cgg atc aat gcc
Leu Lys Ala Ser Ala Glu Lys Thr Lys Leu Gln Lys Arg Ile Asn Ala
575 580 585

2316
att aag ctg aag tag tacggaaaaa agcccggaat catccgggcc ttttaatttt
Ile Lys Leu Lys
590

2376
catatttagc aaatgcgtca ttattgatgc tgttgtacta attgacattt cgggctcgtc

2436
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2496
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2556
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2616
cttctcctct ccggtcactt cctgcagtgt aaaatcccct gtcaagtccc ctccggcggt

2676
gacggccittt aagtcgtcca gataaggctc tttgatcttt ttttcgttga tatacagctg

2736
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2772
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20 25 30

Asn Glu Val Ile Val Val Tyr Lys Asn Thr Ser Gly Lys Glu Thr Val
35 40 45

Ile Glu Gln Ala Asp Thr Val Glu His Val Tyr Arg His Ile Pro Ala
50 55 60

Ala Ala Val Thr Ala Asp Asp Lys Thr Val Arg Glu Leu Glu His Asp
65 70 75 80

Pro Asp Val Leu Tyr Val Glu Asp Asn Leu Pro Val Ala Ala Ala Asp
85 90 95

Ser Thr Ala Leu Lys Ala Phe Ser Ser Thr Ala Gln Asn Ala Ser
100 105 110

10294.204.ST25.txt

Ala Phe Ser Gln Trp Asn Ile Lys Leu Ile Gln Ala Ala Leu Ala Trp
115 120 125

Asn Lys Gly Leu Thr Gly Lys Gln Val Lys Ile Ala Val Ile Asp Ser
130 135 140

Gly Ile Ser Pro His Glu Leu Ser Ile Ala Gly Gly Ala Ser Met
145 150 155 160

Val Gly Tyr Thr Ala Ser Tyr Arg Asp Asn Gly His Gly Thr His
165 170 175

Val Ala Gly Ile Ile Gly Ala Lys His Asn Gly Arg Gly Ile Asp Gly
180 185 190

Ile Ala Pro Gly Ala Gln Leu Tyr Ala Val Lys Ala Leu Asp Arg Asn
195 200 205

Gly Ala Gly Asp Leu Lys Gly Ile Leu Gln Gly Ile Asp Trp Ser Ile
210 215 220

Gln His Gly Ile Asp Ile Ile Asn Met Ser Leu Val Val Ser Gly Asp
225 230 235 240

Ser Gln Val Leu His Asp Ala Val Asp Lys Ala Tyr Lys Arg Gly Ile
245 250 255

Ile Leu Val Gly Ala Ser Gly Asn Ala Gly Asn Gly Lys Ser Val Tyr
260 265 270

Tyr Pro Ala Ala Tyr Ser Ser Val Ile Ala Val Ser Ala Thr Asn Glu
275 280 285

Lys Asn Gln Ile Ala Ser Phe Thr Asn Thr Arg Ser Ala Val Ser Tyr
290 295 300

Ser Ala Pro Ser Thr Ser Ile Ile Asn Thr Ser Gly Asn Arg Gly Tyr
305 310 315 320

Ala Ile Gly Ser Cys Thr Ala Gln Gly Thr Pro Asp Val Thr Cys Val
325 330 335

Ile Ala Leu Met Lys Gln Leu His Pro Thr Ala Ser Asn Ala Glu Leu
340 345 350

Arg Lys Lys Met Gln Phe Tyr Thr Ser Asp Leu Gly Ala Pro Gly Arg
355 360 365

Asp His Leu Phe Gly Tyr Arg Leu Ile Arg Phe Lys Glu Val Thr Gln
370 375 380

10294.204.ST25.txt

Pro Leu Glu Lys Ala Gln Lys Ala Val Gly Gln Ala Glu Lys Thr Lys
385 390 395 400

Lys Lys Ala Asp Ile Gln Thr Ala Gln Lys Ala Ile Glu Pro Leu Pro
405 410 415

Ala Asp Ala Asp Lys Pro Ala Leu Lys Lys Arg Leu Asn Thr Val Lys
420 425 430

Glu Gln Leu Lys Lys Thr Ala Glu Ser Lys Val Lys Leu Ala Glu Lys
435 440 445

Gln Lys Lys Lys Thr Asn Ala Asp Ser Ala Gln Lys Ala Val Asn Glu
450 455 460

Leu Asp Ser Gly Thr Phe Lys Thr Asn Leu Gln Lys Arg Ile Asn Ala
465 470 475 480

Val Arg Ser Ser Leu Leu Lys Thr Ala Lys Gln Ala Val Ala Lys Ala
485 490 495

Glu Lys Ala Ala Thr Asp Ser Asn Leu Gly Lys Ala Gln Lys Ala Ile
500 505 510

Asn Glu Leu Pro Ala Gly Lys Asp Lys Ser Asn Leu Gln Lys Arg Leu
515 520 525

Asn Thr Ala Lys Lys Gln Ala Ala Ala Ala Tyr Asn Lys Lys Val Ser
530 535 540

Ala Ala Lys Ala Lys Val Lys Thr Ala Glu Gln Lys Arg Thr Lys Lys
545 550 555 560

Thr Lys Ser Ala Ala Gln Ser Ala Val Gly Lys Leu Lys Ala Ser Ala
565 570 575

Glu Lys Thr Lys Leu Gln Lys Arg Ile Asn Ala Ile Lys Leu Lys
580 585 590

<210> 23
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<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (513)..(1856)

<400> 23
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tttggccatg gggggcgcag gacaagtagg cgccgctttt gcatctatt tcaaaacgaa 120

10294.204.ST25.txt

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aaaagcaaaag ctaaaaagag ccattgccgg cggactgccg tcaggcctgc tcggcatcgg 180
cgaaccgctc atattcggtg taacccttcc gctcggacgt ccgttttttaa ccgcgtgcct 240
cggggccgga gtaggcggag catttcaagc gtatttcaaa attgcgaccg tatcgatagg 300
cgtatcaggg ctccctttgt cgtttttggg tcatacccac caagttcttt tgtatatattct 360
cggtttgttt atttcctatg ctgccggcct tgtcttaaca tactcctttg gtttcaagga 420
cgatatggca gttgaatttg attaaacggt tgtttaaaat ttcccactat gcaattttta 480
acagaaagga gtgaagcaag ctgaaaaagt tt atg atc agt gcg gcc gcg tcc 533
                               Met Ile Ser Ala Ala Ala Ser
                               1                               5

cta ttg ctg ctg aca tgc ttt ttt ccg ctt ccg tcc aca gca cag act 581
Leu Leu Leu Leu Thr Cys Phe Phe Pro Leu Pro Ser Thr Ala Gln Thr
                               10                               15                               20

gcc atc ggg aac gag aca aaa cag ccg ctg aca tat cct gtt tta acg 629
Ala Ile Gly Asn Glu Thr Lys Gln Arg Leu Thr Tyr Pro Val Leu Thr
                               25                               30                               35

aaa gcg aaa acg cct gaa gaa gcc ggt ttt tct tcg aaa aag ctt aaa 677
Lys Ala Lys Thr Pro Glu Glu Ala Gly Phe Ser Ser Lys Lys Leu Lys
40                               45                               50                               55

gct gtg gac cgt ctg atc gaa cag gat gtc aaa gcg ggc ttt ccc ggc 725
Ala Val Asp Arg Leu Ile Glu Gln Asp Val Lys Ala Gly Phe Pro Gly
60                               65                               70

gct gcc ctt att ttg att aaa gac gga aaa atc atc aaa aaa gaa gtc 773
Ala Ala Leu Ile Leu Ile Lys Asp Gly Lys Ile Ile Lys Lys Glu Val
75                               80                               85

tac ggc tac aag cag aaa tac aac ggc ctc ata gcg ctc aaa cat cca 821
Tyr Gly Tyr Lys Gln Lys Tyr Asn Gly Leu Ile Ala Leu Lys His Pro
90                               95                               100

aaa aaa atg aaa gca aac acg atg ttc gac cta gcc tcc aat aca aaa 869
Lys Lys Met Lys Ala Asn Thr Met Phe Asp Leu Ala Ser Asn Thr Lys
105                               110                               115

atg tat gcc gtc aat ttt gcc ttg cag cat tta gtg agc acc gga aag 917
Met Tyr Ala Val Asn Phe Ala Leu Gln His Leu Val Ser Thr Gly Lys
120                               125                               130                               135

ctt gac ttg aac aaa aac att tct caa tat ctc cct gat ttc aaa gat 965
Leu Asp Leu Asn Lys Asn Ile Ser Gln Tyr Leu Pro Asp Phe Lys Asp
140                               145                               150

cac ccg gaa gac gat gta aag gga aaa aac ccg ctc cgc gtg att gat 1013
His Pro Glu Asp Asp Val Lys Gly Lys Asn Arg Leu Arg Val Ile Asp
155                               160                               165

ttg ctt cat cat aac gca ggc ttc cct gca agc tgg aat tat tac gac 1061
Leu Leu His His Asn Ala Gly Phe Pro Ala Ser Trp Asn Tyr Tyr Asp
170                               175                               180

ccg aaa tca gcc gga cac ctc tac tct caa tca ccg agc aaa acg ctt 1109
Pro Lys Ser Ala Gly His Leu Tyr Ser Gln Ser Arg Ser Lys Thr Leu
185                               190                               195

gaa tat ctt gtg aaa acc ccc ttg gca tat gaa ccc ggc aca aag caa 1157
Glu Tyr Leu Val Lys Thr Pro Leu Ala Tyr Glu Pro Gly Thr Lys Gln
200                               205                               210                               215

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10294.204.ST25.txt

att tac agt gac atc gac tat atg ctc ctc ggg ctg atc att gaa aaa Ile Tyr Ser Asp Ile Asp Tyr Met Leu Leu Gly Leu Ile Ile Glu Lys 220 225 230	1205
atc aca aac gag cgt tta gat acc ttt gtt gaa aac cgg ttt tac cgg Ile Thr Asn Glu Arg Leu Asp Thr Phe Val Glu Asn Arg Phe Tyr Arg 235 240 245	1253
cct ctc gga ttg cgg cat act ttg ttt aat ccg ctc caa aag ggc ttt Pro Leu Gly Leu Arg His Thr Leu Phe Asn Pro Leu Gln Lys Gly Phe 250 255 260	1301
aaa cgg tcg cat ttt gca gct acg gaa cga ttg gga aac acc aga gac Lys Arg Ser His Phe Ala Ala Thr Glu Arg Leu Gly Asn Thr Arg Asp 265 270 275	1349
ggc acc att tcg ttc cca aac atc aga act tac aca ctt cag ggg gaa Gly Thr Ile Ser Phe Pro Asn Ile Arg Thr Tyr Thr Leu Gln Gly Glu 280 285 290 295	1397
gtc cac gat gaa aaa gca ttc tat tca atg gaa ggc gtt tct ggg cat Val His Asp Glu Lys Ala Phe Tyr Ser Met Glu Gly Val Ser Gly His 300 305 310	1445
gcc gcc ctg ttt tcc acc gtt gac gac gca gca gtg ctc ctt caa gtc Ala Gly Leu Phe Ser Thr Val Asp Asp Ala Ala Val Leu Leu Gln Val 315 320 325	1493
atg ctg aac ggc ggc ggt tac gga aga cag cat cta ttc agc agt tct Met Leu Asn Gly Gly Gly Tyr Gly Arg Gln His Leu Phe Ser Ser Ser 330 335 340	1541
gtc att tca caa ttt aca gag ccg tca aaa aca aat ccc aca tat gga Val Ile Ser Gln Phe Thr Glu Pro Ser Lys Thr Asn Pro Thr Tyr Gly 345 350 355	1589
cta gga tgg cgg ctc aac ggc aat acc gat atg gag tgg atg ttc ggc Leu Gly Trp Arg Leu Asn Gly Asn Thr Asp Met Glu Trp Met Phe Gly 360 365 370 375	1637
aag cac gcc agc agc aaa gca tat ggc cat acc ggc tgg acg gga acg Lys His Ala Ser Ser Lys Ala Tyr Gly His Thr Gly Trp Thr Gly Thr 380 385 390	1685
gtt act atc att gat ccc gtg tat caa atc ggc att gtg ttg tta acc Val Thr Ile Ile Asp Pro Val Tyr Gln Ile Gly Ile Val Leu Leu Thr 395 400 405	1733
aat aaa aag cac tct cct gtt atc aac cct aaa gaa aac ccg aat caa Asn Lys Lys His Ser Pro Val Ile Asn Pro Lys Glu Asn Pro Asn Gln 410 415 420	1781
ttc gaa ggt gat gaa ttt gca acc gga aag tac ggc agc gtc att aca Phe Glu Gly Asp Glu Phe Ala Thr Gly Lys Tyr Gly Ser Val Ile Thr 425 430 435	1829
gct gtt tac gag gcg tta cat cac caa taggaggcga ccctttatat Ala Val Tyr Glu Ala Leu His His Gln 440 445	1876
gaaaagatttt cttcaatgcg cgttgattgc attgctgtta tcgtctctcg ctttgcagcc	1936
ggccgctcgc gaagcagaag caaacacgcg tccggaacaa aacatcaaac aaatggtcag	1996
cagcatgtcg cttgaagaga aaatcgggca aatgctgatg cctgacttta gaaactggaa	2056
gaaaaaaggga gaatcgagcg ccaaaggatt aacagaaatg aatgacgaag ttgctggaat	2116

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cattgaaaaa taccggctcg ggggcgtcat tctttttgct gaaaacgtca caggcacaga 2176
gcagactgta cggttaacgg acggcctgca acaagcgagc cctgacattc cgctctttat 2236
cacgatcgat caggaaggcg ggattgtcac gagactcgaa tcaggcacia acctggcccg 2296
caatatggca gtcggagcat cgagaagcag caaaaacgcc ttcagatcag g 2347

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<211> 448
<212> PRT
<213> Bacillus licheniformis

<400> 24

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1 5 10 15

Leu Pro Ser Thr Ala Gln Thr Ala Ile Gly Asn Glu Thr Lys Gln Arg
20 25 30

Leu Thr Tyr Pro Val Leu Thr Lys Ala Lys Thr Pro Glu Glu Ala Gly
35 40 45

Phe Ser Ser Lys Lys Leu Lys Ala Val Asp Arg Leu Ile Glu Gln Asp
50 55 60

Val Lys Ala Gly Phe Pro Gly Ala Ala Leu Ile Leu Ile Lys Asp Gly
65 70 75 80

Lys Ile Ile Lys Lys Glu Val Tyr Gly Tyr Lys Gln Lys Tyr Asn Gly
85 90 95

Leu Ile Ala Leu Lys His Pro Lys Lys Met Lys Ala Asn Thr Met Phe
100 105 110

Asp Leu Ala Ser Asn Thr Lys Met Tyr Ala Val Asn Phe Ala Leu Gln
115 120 125

His Leu Val Ser Thr Gly Lys Leu Asp Leu Asn Lys Asn Ile Ser Gln
130 135 140

Tyr Leu Pro Asp Phe Lys Asp His Pro Glu Asp Asp Val Lys Gly Lys
145 150 155 160

Asn Arg Leu Arg Val Ile Asp Leu Leu His His Asn Ala Gly Phe Pro
165 170 175

Ala Ser Trp Asn Tyr Tyr Asp Pro Lys Ser Ala Gly His Leu Tyr Ser
180 185 190

Gln Ser Arg Ser Lys Thr Leu Glu Tyr Leu Val Lys Thr Pro Leu Ala
195 200 205

10294.204.ST25.txt

Tyr Glu Pro Gly Thr Lys Gln Ile Tyr Ser Asp Ile Asp Tyr Met Leu
 210 215 220
 Leu Gly Leu Ile Ile Glu Lys Ile Thr Asn Glu Arg Leu Asp Thr Phe
 225 230 235 240
 Val Glu Asn Arg Phe Tyr Arg Pro Leu Gly Leu Arg His Thr Leu Phe
 245 250 255
 Asn Pro Leu Gln Lys Gly Phe Lys Arg Ser His Phe Ala Ala Thr Glu
 260 265 270
 Arg Leu Gly Asn Thr Arg Asp Gly Thr Ile Ser Phe Pro Asn Ile Arg
 275 280 285
 Thr Tyr Thr Leu Gln Gly Glu Val His Asp Glu Lys Ala Phe Tyr Ser
 290 295 300
 Met Glu Gly Val Ser Gly His Ala Gly Leu Phe Ser Thr Val Asp Asp
 305 310 315 320
 Ala Ala Val Leu Leu Gln Val Met Leu Asn Gly Gly Gly Tyr Gly Arg
 325 330 335
 Gln His Leu Phe Ser Ser Ser Val Ile Ser Gln Phe Thr Glu Pro Ser
 340 345 350
 Lys Thr Asn Pro Thr Tyr Gly Leu Gly Trp Arg Leu Asn Gly Asn Thr
 355 360 365
 Asp Met Glu Trp Met Phe Gly Lys His Ala Ser Ser Lys Ala Tyr Gly
 370 375 380
 His Thr Gly Trp Thr Gly Thr Val Thr Ile Ile Asp Pro Val Tyr Gln
 385 390 395 400
 Ile Gly Ile Val Leu Leu Thr Asn Lys Lys His Ser Pro Val Ile Asn
 405 410 415
 Pro Lys Glu Asn Pro Asn Gln Phe Glu Gly Asp Glu Phe Ala Thr Gly
 420 425 430
 Lys Tyr Gly Ser Val Ile Thr Ala Val Tyr Glu Ala Leu His His Gln
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<220>

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 <222> (389)..(3058)

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tgccctgata tgaaacacta gctcgtgctt aaacggctgg ggatttttgc gatccgtccg      180
cctcgaatcg cctcatttaa ttcctcgatc attccgtatg taaaatgccg tcaaaagaca      240
tatgaaaaac tccctctttc tcgttaatcc ttttcgtaaa acgtccattc aataattata      300
gcatgatttg ggacgagtct gaataaattg acttatagag atggatacac caaaagcaac      360
ctttagggca ggaggagtgg acgattca atg aaa tgg cac gag atg gga caa      412
                               Met Lys Trp His Glu Met Gly Gln
                               1                               5

acc gaa ttg tta aat ata aca aaa acg tcc atc gac aaa ggt cta aca      460
Thr Glu Leu Leu Asn Ile Thr Lys Thr Ser Ile Asp Lys Gly Leu Thr
10                               15                               20

gaa aaa gag gcc gga aag cgg ctg gaa aga cac gga aca aac gaa ctt      508
Glu Lys Glu Ala Gly Lys Arg Leu Glu Arg His Gly Thr Asn Glu Leu
25                               30                               35                               40

cag gaa ggg gaa aaa aca tcg gcg gtc gca ttg ttt ttt tct caa ttc      556
Gln Glu Gly Glu Lys Thr Ser Ala Val Ala Leu Phe Phe Ser Gln Phe
45                               50                               55

aaa gat ttc atg gtt ctt gtt ttg ctt gcg gcc acg ttg att tcg ggt      604
Lys Asp Phe Met Val Leu Val Leu Leu Ala Ala Thr Leu Ile Ser Gly
60                               65                               70

ttc ctc ggc gaa tac att gac gcc atc gcg atc atc gcg atc atc ttt      652
Phe Leu Gly Glu Tyr Ile Asp Ala Ile Ala Ile Ile Ala Ile Ile Phe
75                               80                               85

gtt aac ggc att ctc gga ttc ttt cag gag agg cgg gcg gaa agg tcg      700
Val Asn Gly Ile Leu Gly Phe Phe Gln Glu Arg Arg Ala Glu Arg Ser
90                               95                               100

ctc gag gct ttg aaa gaa ctg tca gct cct caa gtg gct gtg ctc cgg      748
Leu Glu Ala Leu Lys Glu Leu Ser Ala Pro Gln Val Ala Val Leu Arg
105                               110                               115

gag ggg aat tgg gtg aaa att cct tcc aaa gag ctt gtc ccg gga gat      796
Glu Gly Asn Trp Val Lys Ile Pro Ser Lys Glu Leu Val Pro Gly Asp
125                               130                               135

gtt gtc cgt ttt gca agc gga gac aga atc ggc gcc gat ctc aga ctt      844
Val Val Arg Phe Ala Ser Gly Asp Arg Ile Gly Ala Asp Leu Arg Leu
140                               145                               150

gtc gag aca aag agc ctt gaa ata gaa gaa tcg gcc ctt aca ggt gaa      892
Val Glu Thr Lys Ser Leu Glu Ile Glu Glu Ser Ala Leu Thr Gly Glu
155                               160                               165

tcg ctc ccc gtg tcc aaa cag gca gat gct ttt cag gcg tca gat gta      940
Ser Leu Pro Val Ser Lys Gln Ala Asp Ala Phe Gln Ala Ser Asp Val
170                               175                               180

tcg ctg ggc gat ctg aag aat atg gct ttc atg gga acg ctt gtc aca      988
Ser Leu Gly Asp Leu Lys Asn Met Ala Phe Met Gly Thr Leu Val Thr
185                               190                               195                               200

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10294.204.ST25.txt																	
agg ggg agc gga atc ggc gtc gtc atc ggt acg ggt atg aac tct gcg	1036																
Arg Gly Ser Gly Ile Gly Val Val Ile Gly Thr Gly Met Asn Ser Ala																	
				205				210					215				
atg ggg aaa atc gcc gat atg ctt gaa tct gcc ggg aat acg gcg acc	1084																
Met Gly Lys Ile Ala Asp Met Leu Glu Ser Ala Gly Asn Thr Ala Thr																	
			220				225					230					
ccg ctg caa aga agg ctt gaa gag ctc ggc aaa att ttg att gtc gcc	1132																
Pro Leu Gln Arg Arg Leu Glu Glu Leu Gly Lys Ile Leu Ile Val Ala																	
		235				240					245						
gct ttg ttc ctg aca ctg ctt gtc gtt gct gcc ggc gtc att cag ggg	1180																
Ala Leu Phe Leu Thr Leu Leu Val Val Ala Ala Gly Val Ile Gln Gly																	
	250				255			260									
cat gat tta tac agc atg ttt tta gcg gga gtt tcc ctt gcc gtc gct	1228																
His Asp Leu Tyr Ser Met Phe Leu Ala Gly Val Ser Leu Ala Val Ala																	
	265				270			275						280			
gcc ata cct gaa ggg ctg cct gcc att gtc acg gtc gct ctg tct ctc	1276																
Ala Ile Pro Glu Gly Leu Pro Ala Ile Val Thr Val Ala Leu Ser Leu																	
			285					290					295				
ggc gtg cag cgg atg atc agg caa aag tgc atc gtc agg aag ctg ccc	1324																
Gly Val Gln Arg Met Ile Arg Gln Lys Ser Ile Val Arg Lys Leu Pro																	
		300					305					310					
gcg gtt gag acg ctc ggc tgc gcg tcc att att tgc tcc gat aaa acc	1372																
Ala Val Glu Thr Leu Gly Cys Ala Ser Ile Ile Cys Ser Asp Lys Thr																	
	315					320					325						
ggg acg atg acg cag aac aaa atg acg gtc acc cat gtc tgg tca ggc	1420																
Gly Thr Met Thr Gln Asn Lys Met Thr Val Thr His Val Trp Ser Gly																	
	330				335					340							
ggg aag ata tgg aac gtg tca ggg atc ggc tat gag cct gaa ggc tct	1468																
Gly Lys Ile Trp Asn Val Ser Gly Ile Gly Tyr Glu Pro Glu Gly Ser																	
	345			350				355						360			
ttc agc atg aac ggg cgc gat gtg caa gca aag cat cat aaa ccg ctc	1516																
Phe Ser Met Asn Gly Arg Asp Val Gln Ala Lys His His Lys Pro Leu																	
			365					370					375				
cag cag gta cta ttg ttc ggc gca tta tgc aat tca tct tcg att atc	1564																
Gln Gln Val Leu Leu Phe Gly Ala Leu Cys Asn Ser Ser Ser Ile Ile																	
		380					385					390					
gaa aaa gac ggg gag ttt cgt ctt gat ggc gat ccc acc gaa ggg gct	1612																
Glu Lys Asp Gly Glu Phe Arg Leu Asp Gly Asp Pro Thr Glu Gly Ala																	
		395				400					405						
ttg ctg acg gcg gct cga aaa gca ggc ttt acg gac aaa tat gtt gat	1660																
Leu Leu Thr Ala Ala Arg Lys Ala Gly Phe Thr Asp Lys Tyr Val Asp																	
	410				415					420							
gaa cat ttt aaa atc atc gag gag ttt ccg ttt gat tca acg cgg aaa	1708																
Glu His Phe Lys Ile Ile Glu Glu Phe Pro Phe Asp Ser Thr Arg Lys																	
	425			430				435						440			
atg atg tct gtc att gtg gaa gac aag agc ggc aag cgc ttt gtc att	1756																
Met Met Ser Val Ile Val Glu Asp Lys Ser Gly Lys Arg Phe Val Ile																	
			445					450					455				
aca aag ggc gcg ccg gat gta ttg atg aag cgt tgc tgc cat acg ctg	1804																
Thr Lys Gly Ala Pro Asp Val Leu Met Lys Arg Ser Ser His Thr Leu																	
		460				465						470					

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aca gaa gaa aag cga gaa atc ttc aca aag gaa agg ctc gct gaa aca Thr Glu Glu Lys Arg Glu Ile Phe Thr Lys Glu Arg Leu Ala Glu Thr 475 480 485	1852
agc gcg gcg ctg gaa act ctt gcg tca cag gcg ctg aga acg att gcc Ser Ala Ala Leu Glu Thr Leu Ala Ser Gln Ala Leu Arg Thr Ile Ala 490 495 500	1900
gtc gcg tat aaa ccg atc aaa gat aca gaa aat ccc ccg ctc gaa aaa Val Ala Tyr Lys Pro Ile Lys Asp Thr Glu Asn Pro Pro Leu Glu Lys 505 510 515 520	1948
gcg gag tca ggc tta act ttc atc ggg ctg tta ggg atg atc gat ccg Ala Glu Ser Gly Leu Thr Phe Ile Gly Leu Leu Gly Met Ile Asp Pro 525 530 535	1996
ccg cgg ccc gaa gtg aaa aca gcg att aaa gaa tgc cgg gaa gcg ggg Pro Arg Pro Glu Val Lys Thr Ala Ile Lys Glu Cys Arg Glu Ala Gly 540 545 550	2044
atc aaa acg gtc atg atc acc ggg gac cat gtg ata acg gcg acg gcg Ile Lys Thr Val Met Ile Thr Gly Asp His Val Ile Thr Ala Thr Ala 555 560 565	2092
att gca aaa gat ctc gga ttg ctg cct ccg cgc gga aag gtc atg gac Ile Ala Lys Asp Leu Gly Leu Pro Pro Arg Gly Lys Val Met Asp 570 575 580	2140
ggc cag atg ctg aac gaa ctc tcg cag gaa gaa ttg gcg gaa att gtt Gly Gln Met Leu Asn Glu Leu Ser Gln Glu Leu Ala Glu Ile Val 585 590 595 600	2188
gac gat gtt tac gta ttt gca agg gtg tcg ccc gaa cat aag ctg aag Asp Asp Val Tyr Val Phe Ala Arg Val Ser Pro Glu His Lys Leu Lys 605 610 615	2236
atc gtg acc gcc tac cag gaa aac ggc cac atc gtc gcc atg acg gga Ile Val Thr Ala Tyr Gln Glu Asn Gly His Ile Val Ala Met Thr Gly 620 625 630	2284
gac gga gtc aat gat gcc cct gcg att aaa cag gcg gat atc ggc ata Asp Gly Val Asn Asp Ala Pro Ala Ile Lys Gln Ala Asp Ile Gly Ile 635 640 645	2332
tcg atg ggg att acg gga acg gat gtc gcc aag gag gcg tcc tca ctc Ser Met Gly Ile Thr Gly Thr Asp Val Ala Lys Glu Ala Ser Ser Leu 650 655 660	2380
atc ctt gtc gat gat aat ttt gca acg att aaa tcg gcc atc aag gaa Ile Leu Val Asp Asp Asn Phe Ala Thr Ile Lys Ser Ala Ile Lys Glu 665 670 675 680	2428
gga cgc aat atc tat gaa aat att aga aag ttc atc aga tac ttg ctc Gly Arg Asn Ile Tyr Glu Asn Ile Arg Lys Phe Ile Arg Tyr Leu Leu 685 690 695	2476
gca tcc aat gtc ggc gaa att ttg gtc atg ctg ttt gca atg ctg ctc Ala Ser Asn Val Gly Glu Ile Leu Val Met Leu Phe Ala Met Leu Leu 700 705 710	2524
gct ctg ccg ctg ccg ctt gtc ccg ata cag att ctg tgg gtc aac ctt Ala Leu Pro Leu Pro Leu Val Pro Ile Gln Ile Leu Trp Val Asn Leu 715 720 725	2572
gta acg gac ggc ctg cct gcc atg gcg ctc ggc atg gat cag cct gag Val Thr Asp Gly Leu Pro Ala Met Ala Leu Gly Met Asp Gln Pro Glu 730 735 740	2620

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gac gat gtg atg cag aga aag ccg cgg agt ccg aaa gaa ggc gtg ttt 2668
 Asp Asp Val Met Gln Arg Lys Pro Arg Ser Pro Lys Glu Gly Val Phe
 745 750 755 760
 gca agg ggg ctc ggc tgg aag gtc gta tcg cgc gga ttc tta atc gga 2716
 Ala Arg Gly Leu Gly Trp Lys Val Val Ser Arg Gly Phe Leu Ile Gly
 765 770 775
 atc gcg aca ctc ggg gcg ttt atg ttc att tat aac cgc aat cca gaa 2764
 Ile Ala Thr Leu Gly Ala Phe Met Phe Ile Tyr Asn Arg Asn Pro Glu
 780 785 790
 gcg ctt gag tat gca cag acg gtt gca ttt gca acg ctc gtc ctt gcg 2812
 Ala Leu Glu Tyr Ala Gln Thr Val Ala Phe Ala Thr Leu Val Leu Ala
 795 800 805
 cag ctg atc cac gtg ttc gac tgc cga agc gag cgg tcc atc ttt gac 2860
 Gln Leu Ile His Val Phe Asp Cys Arg Ser Glu Arg Ser Ile Phe Asp
 810 815 820
 cgc aat ccg ttt gaa aac att tat ttg ctc ggt gca gtg ctg tct tcg 2908
 Arg Asn Pro Phe Glu Asn Ile Tyr Leu Leu Gly Ala Val Leu Ser Ser
 825 830 835 840
 att ctt ttg atg ctt gtc gtt att tat tat ccg ccg ctg cag ccg att 2956
 Ile Leu Leu Met Leu Val Val Ile Tyr Tyr Pro Pro Leu Gln Pro Ile
 845 850 855
 ttt cat acg gtt ccg att tta atg gca gac tgg ctc ctg att gtc gga 3004
 Phe His Thr Val Pro Ile Leu Met Ala Asp Trp Leu Leu Ile Val Gly
 860 865 870
 atg tcg gcg att cca act ttt tta ctg gcc ggg tca ctt tta caa gaa 3052
 Met Ser Ala Ile Pro Thr Phe Leu Leu Ala Gly Ser Leu Leu Gln Glu
 875 880 885
 aaa aat ag 3060
 Lys Asn
 890

<210> 26
 <211> 890
 <212> PRT
 <213> Bacillus licheniformis

<400> 26

Met Lys Trp His Glu Met Gly Gln Thr Glu Leu Leu Asn Ile Thr Lys
 1 5 10 15

Thr Ser Ile Asp Lys Gly Leu Thr Glu Lys Glu Ala Gly Lys Arg Leu
 20 25 30

Glu Arg His Gly Thr Asn Glu Leu Gln Glu Gly Glu Lys Thr Ser Ala
 35 40 45

Val Ala Leu Phe Phe Ser Gln Phe Lys Asp Phe Met Val Leu Val Leu
 50 55 60

Leu Ala Ala Thr Leu Ile Ser Gly Phe Leu Gly Glu Tyr Ile Asp Ala
 65 70 75 80

10294.204.ST25.txt

Ile Ala Ile Ile Ala Ile Ile Phe Val Asn Gly Ile Leu Gly Phe Phe
 85 90 95
 Gln Glu Arg Arg Ala Glu Arg Ser Leu Glu Ala Leu Lys Glu Leu Ser
 100 105 110
 Ala Pro Gln Val Ala Val Leu Arg Glu Gly Asn Trp Val Lys Ile Pro
 115 120 125
 Ser Lys Glu Leu Val Pro Gly Asp Val Val Arg Phe Ala Ser Gly Asp
 130 135 140
 Arg Ile Gly Ala Asp Leu Arg Leu Val Glu Thr Lys Ser Leu Glu Ile
 145 150 155 160
 Glu Glu Ser Ala Leu Thr Gly Glu Ser Leu Pro Val Ser Lys Gln Ala
 165 170 175
 Asp Ala Phe Gln Ala Ser Asp Val Ser Leu Gly Asp Leu Lys Asn Met
 180 185 190
 Ala Phe Met Gly Thr Leu Val Thr Arg Gly Ser Gly Ile Gly Val Val
 195 200 205
 Ile Gly Thr Gly Met Asn Ser Ala Met Gly Lys Ile Ala Asp Met Leu
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 Glu Ser Ala Gly Asn Thr Ala Thr Pro Leu Gln Arg Arg Leu Glu Glu
 225 230 235 240
 Leu Gly Lys Ile Leu Ile Val Ala Ala Leu Phe Leu Thr Leu Leu Val
 245 250 255
 Val Ala Ala Gly Val Ile Gln Gly His Asp Leu Tyr Ser Met Phe Leu
 260 265 270
 Ala Gly Val Ser Leu Ala Val Ala Ala Ile Pro Glu Gly Leu Pro Ala
 275 280 285
 Ile Val Thr Val Ala Leu Ser Leu Gly Val Gln Arg Met Ile Arg Gln
 290 295 300
 Lys Ser Ile Val Arg Lys Leu Pro Ala Val Glu Thr Leu Gly Cys Ala
 305 310 315 320
 Ser Ile Ile Cys Ser Asp Lys Thr Gly Thr Met Thr Gln Asn Lys Met
 325 330 335
 Thr Val Thr His Val Trp Ser Gly Gly Lys Ile Trp Asn Val Ser Gly
 340 345 350

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Ile Gly Tyr Glu Pro Glu Gly Ser Phe Ser Met Asn Gly Arg Asp Val
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Gln Ala Lys His His Lys Pro Leu Gln Gln Val Leu Leu Phe Gly Ala
 370 375 380

Leu Cys Asn Ser Ser Ser Ile Ile Glu Lys Asp Gly Glu Phe Arg Leu
 385 390 395 400

Asp Gly Asp Pro Thr Glu Gly Ala Leu Leu Thr Ala Ala Arg Lys Ala
 405 410 415

Gly Phe Thr Asp Lys Tyr Val Asp Glu His Phe Lys Ile Ile Glu Glu
 420 425 430

Phe Pro Phe Asp Ser Thr Arg Lys Met Met Ser Val Ile Val Glu Asp
 435 440 445

Lys Ser Gly Lys Arg Phe Val Ile Thr Lys Gly Ala Pro Asp Val Leu
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Met Lys Arg Ser Ser His Thr Leu Thr Glu Glu Lys Arg Glu Ile Phe
 465 470 475 480

Thr Lys Glu Arg Leu Ala Glu Thr Ser Ala Ala Leu Glu Thr Leu Ala
 485 490 495

Ser Gln Ala Leu Arg Thr Ile Ala Val Ala Tyr Lys Pro Ile Lys Asp
 500 505 510

Thr Glu Asn Pro Pro Leu Glu Lys Ala Glu Ser Gly Leu Thr Phe Ile
 515 520 525

Gly Leu Leu Gly Met Ile Asp Pro Pro Arg Pro Glu Val Lys Thr Ala
 530 535 540

Ile Lys Glu Cys Arg Glu Ala Gly Ile Lys Thr Val Met Ile Thr Gly
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Asp His Val Ile Thr Ala Thr Ala Ile Ala Lys Asp Leu Gly Leu Leu
 565 570 575

Pro Pro Arg Gly Lys Val Met Asp Gly Gln Met Leu Asn Glu Leu Ser
 580 585 590

Gln Glu Glu Leu Ala Glu Ile Val Asp Asp Val Tyr Val Phe Ala Arg
 595 600 605

Val Ser Pro Glu His Lys Leu Lys Ile Val Thr Ala Tyr Gln Glu Asn
 610 615 620

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Gly His Ile Val Ala Met Thr Gly Asp Gly Val Asn Asp Ala Pro Ala
 625 630 635 640
 Ile Lys Gln Ala Asp Ile Gly Ile Ser Met Gly Ile Thr Gly Thr Asp
 645 650 655
 Val Ala Lys Glu Ala Ser Ser Leu Ile Leu Val Asp Asp Asn Phe Ala
 660 665 670
 Thr Ile Lys Ser Ala Ile Lys Glu Gly Arg Asn Ile Tyr Glu Asn Ile
 675 680 685
 Arg Lys Phe Ile Arg Tyr Leu Leu Ala Ser Asn Val Gly Glu Ile Leu
 690 695 700
 Val Met Leu Phe Ala Met Leu Leu Ala Leu Pro Leu Pro Leu Val Pro
 705 710 715 720
 Ile Gln Ile Leu Trp Val Asn Leu Val Thr Asp Gly Leu Pro Ala Met
 725 730 735
 Ala Leu Gly Met Asp Gln Pro Glu Asp Asp Val Met Gln Arg Lys Pro
 740 745 750
 Arg Ser Pro Lys Glu Gly Val Phe Ala Arg Gly Leu Gly Trp Lys Val
 755 760 765
 Val Ser Arg Gly Phe Leu Ile Gly Ile Ala Thr Leu Gly Ala Phe Met
 770 775 780
 Phe Ile Tyr Asn Arg Asn Pro Glu Ala Leu Glu Tyr Ala Gln Thr Val
 785 790 795 800
 Ala Phe Ala Thr Leu Val Leu Ala Gln Leu Ile His Val Phe Asp Cys
 805 810 815
 Arg Ser Glu Arg Ser Ile Phe Asp Arg Asn Pro Phe Glu Asn Ile Tyr
 820 825 830
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 835 840 845
 Tyr Tyr Pro Pro Leu Gln Pro Ile Phe His Thr Val Pro Ile Leu Met
 850 855 860
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[illegible]

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Ala	Glu	Leu	Ser	Val	Ser	Glu	Arg	Glu	Thr	Gly	Lys	Gly	Ile	Leu	Lys		
			175					180					185				
cag	tta	aga	acg	atc	agg	gat	gaa	gtt	ctt	tca	aaa	act	gaa	aaa	gga		1109
Gln	Leu	Arg	Thr	Ile	Arg	Asp	Glu	Val	Leu	Ser	Lys	Thr	Glu	Lys	Gly		
		190					195					200					
aaa	gag	ctg	tct	tcc	ctt	tac	tat	aaa	gca	gct	cca	ttc	atc	agc	gca		1157
Lys	Glu	Leu	Ser	Ser	Leu	Tyr	Tyr	Lys	Ala	Ala	Pro	Phe	Ile	Ser	Ala		
	205					210					215						
aaa	atg	ctc	ttt	aac	aaa	tcg	atg	aga	gac	agt	gtc	tac	aaa	gac	ctg		1205
Lys	Met	Leu	Phe	Asn	Lys	Ser	Met	Arg	Asp	Ser	Val	Tyr	Lys	Asp	Leu		
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gtg	cag	ctg	aag	ccg	ctg	ttt	gca	gat	gtc	gct	aaa	aac	gga	caa	gtg		1253
Val	Gln	Leu	Lys	Pro	Leu	Phe	Ala	Asp	Val	Ala	Lys	Asn	Gly	Gln	Val		
				240					245					250			
agc	gca	tac	tcg	att	acg	aat	gat	gat	caa	aaa	gcg	atc	agt	cgc	ctg		1301
Ser	Ala	Tyr	Ser	Ile	Thr	Asn	Asp	Asp	Gln	Lys	Ala	Ile	Ser	Arg	Leu		
			255				260						265				
tac	gaa	aca	gct	cg	gcg	tcc	gtt	ccc	gag	ccg	ttg	aaa	aaa	cag	ctg		1349
Tyr	Glu	Thr	Ala	Arg	Ala	Ser	Val	Pro	Glu	Pro	Leu	Lys	Lys	Gln	Leu		
		270					275					280					
gat	caa	gtc	gcg	aaa	gac	atc	ggc	atc	gaa	caa	tta	aca	ggc	agc	aaa		1397
Asp	Gln	Val	Ala	Lys	Asp	Ile	Gly	Ile	Glu	Gln	Leu	Thr	Gly	Ser	Lys		
	285					290					295						
gta	tcg	gct	gtg	ctt	gaa	aaa	gcg	ggg	atg	gcg	aca	gct	tca	tca	agc		1445
Val	Ser	Ala	Val	Leu	Glu	Lys	Ala	Gly	Met	Ala	Thr	Ala	Ser	Ser	315		
300					305			310									
gcg	ccc	gaa	aac	cgt	tac	atc	gta	aaa	ttg	aaa	gaa	ggc	aaa	aaa	ccg		1493
Ala	Pro	Glu	Asn	Arg	Tyr	Ile	Val	Lys	Leu	Lys	Glu	Gly	Lys	Lys	Pro		
				320					325					330			
gga	tct	ttc	aaa	tct	aaa	gcc	caa	tca	tcc	ggc	gtc	cag	gca	tta	gag		1541
Gly	Ser	Phe	Lys	Ser	Lys	Ala	Gln	Ser	Ser	Gly	Val	Gln	Ala	Leu	Glu		
			335				340					345					
ccc	ctc	ggt	aaa	agc	aaa	acg	gca	ttt	aaa	gat	atg	tac	gtt	gtg	gaa		1589
Pro	Leu	Gly	Lys	Ser	Lys	Thr	Ala	Phe	Lys	Asp	Met	Tyr	Val	Val	Glu		
		350					355					360					
atg	aag	gaa	agc	cgt	tct	tcc	gga	ttc	aaa	gcg	gcg	gca	aag	caa	tat		1637
Met	Lys	Glu	Ser	Arg	Ser	Ser	Gly	Phe	Lys	Ala	Ala	Ala	Lys	Gln	Tyr		
	365					370					375						
cag	gcg	gca	gcc	tcc	aag	atc	gcc	aag	atg	cct	gaa	gtg	gaa	ttc	gtc		1685
Gln	Ala	Ala	Ala	Ser	Lys	Ile	Ala	Lys	Met	Pro	Glu	Val	Glu	Phe	Val		
380					385					390					395		
gaa	cag	gtt	cag	caa	tat	gaa	gca	ctg	tca	aga	gac	acc	caa	tat	cca		1733
Glu	Gln	Val	Gln	Gln	Tyr	Glu	Ala	Leu	Ser	Arg	Asp	Thr	Gln	Tyr	Pro		
				400					405					410			
tat	caa	tgg	tcg	ctc	aaa	aat	aac	ggc	aaa	aac	cgt	gct	gcg	aat	gct		1781
Tyr	Gln	Trp	Ser	Leu	Lys	Asn	Asn	Gly	Lys	Asn	Arg	Ala	Ala	Asn	Ala		
			415					420					425				
gac	ata	caa	ttt	gaa	cag	ctt	cag	aag	ctg	atg	aaa	ggc	aaa	aag	ctg		1829

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Asp Ile Gln Phe Glu Gln Leu Gln Lys Leu Met Lys Gly Lys Lys Leu	1877
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aaa gat aca gta atc gcc gtc gtt gac aca ggc gtt gat cat acc ctt	1877
Lys Asp Thr Val Ile Ala Val Val Asp Thr Gly Val Asp His Thr Leu	
445 450 455	
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Ala Asp Leu Ser Gly Ser Val Lys Lys Asp Glu Gly Tyr Asn Tyr Val	
460 465 470 475	
ggc cgc acg gcg gat gcg atg gat gac aat ggc cac ggc aca cac gtg	1973
Gly Arg Thr Ala Asp Ala Met Asp Asp Asn Gly His Gly Thr His Val	
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tca ggc atc att gca gcc gcg caa gac aac cat ttt tcg atg gcg gga	2021
Ser Gly Ile Ile Ala Ala Ala Gln Asp Asn His Phe Ser Met Ala Gly	
495 500 505	
atc aat gct tat gcc aaa att ctg cct gtc aaa gtg ctg gat tct tca	2069
Ile Asn Ala Tyr Ala Lys Ile Leu Pro Val Lys Val Leu Asp Ser Ser	
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Gly Ser Gly Asp Thr Glu Gln Ile Ala Asn Gly Ile Ile Tyr Ala Ala	
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gac cac ggt gca aaa gtc atc aat tta agt ctt ggc ggg cca tac agc	2165
Asp His Gly Ala Lys Val Ile Asn Leu Ser Leu Gly Gly Pro Tyr Ser	
540 545 550 555	
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Arg Val Met Glu Tyr Ala Leu Lys Tyr Ala Ala Ser Lys Asn Val Thr	
560 565 570	
atc gtt gcc gcc acc gga aat gac gga gta tcg gag att tcc tac cct	2261
Ile Val Ala Ala Thr Gly Asn Asp Gly Val Ser Glu Ile Ser Tyr Pro	
575 580 585	
gca tct tcg aaa tat acg ctt tca gtc ggg gcg acc aat aat ctc gat	2309
Ala Ser Ser Lys Tyr Thr Leu Ser Val Gly Ala Thr Asn Asn Leu Asp	
590 595 600	
ctt gtc tcg gac tac tcc aat tat gga aaa ggt ctc gat atg gtg gcg	2357
Leu Val Ser Asp Tyr Ser Asn Tyr Gly Lys Gly Leu Asp Met Val Ala	
605 610 615	
ccg gga acc gat att cca agc ctc gtt ccg gac ggg aat gtc act tat	2405
Pro Gly Thr Asp Ile Pro Ser Leu Val Pro Asp Gly Asn Val Thr Tyr	
620 625 630 635	
atg agc gga aca tcg atg gcg gcg ccg cac gtg gca gct gca gca gga	2453
Met Ser Gly Thr Ser Met Ala Ala Pro His Val Ala Ala Ala Ala Gly	
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ctt ctt ttg tca cag aat ccg tcc ttg aaa cca aag caa atc gca agc	2501
Leu Leu Leu Ser Gln Asn Pro Ser Leu Lys Pro Lys Gln Ile Ala Ser	
655 660 665	
cta ttg acc gag acg aca gca gat gtg gca ttt gaa gag cag gat aat	2549
Leu Leu Thr Glu Thr Thr Ala Asp Val Ala Phe Glu Glu Gln Asp Asn	
670 675 680	
cca aac ccg gat tat gac ctg gat ata gaa ccg gct gca caa att ccc	2597
Pro Asn Pro Asp Tyr Asp Leu Asp Ile Glu Pro Ala Ala Gln Ile Pro	
685 690 695	
gga tat gac ttc gtc tcc ggg tgg gga agg ctg aat gtt ttt cat gca	2645

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Gly	Tyr	Asp	Phe	Val	Ser	Gly	Trp	Gly	Arg	Leu	Asn	Val	Phe	His	Ala			715
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Ala	Ser	Val	Phe	Glu	Leu	Asn	Met	Lys	Val	His	Pro	Val	Leu	Asn	Arg			
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cat	acg	gca	gtg	aca	ggc	aca	gcc	aaa	agc	ggg	gtg	acg	gtc	aaa	atc			2741
His	Thr	Ala	Val	Thr	Gly	Thr	Ala	Lys	Ser	Gly	Val	Thr	Val	Lys	Ile			
			735					740					745					
ttg	cga	ggg	aag	caa	gta	ttg	ggg	acg	ggc	acg	gcc	gga	aaa	tca	ggc			2789
Leu	Arg	Gly	Lys	Gln	Val	Leu	Gly	Thr	Gly	Thr	Ala	Gly	Lys	Ser	Gly			
		750					755					760						
gcg	ttt	tca	gtg	aaa	att	ccg	gcc	cag	aag	gcg	ggg	caa	gtt	ctt	cat			2837
Ala	Phe	Ser	Val	Lys	Ile	Pro	Ala	Gln	Lys	Ala	Gly	Gln	Val	Leu	His			
						770					775							
gtc	gcg	gca	tcg	ggc	cat	cag	gcg	gaa	acc	tcg	ctc	aga	acc	gtc	gtg			2885
Val	Ala	Ala	Ser	Gly	His	Gln	Ala	Glu	Thr	Ser	Leu	Arg	Thr	Val	Val			
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gaa	aaa	gcg	ccg	aaa	aac	ccg	tcc	gtc	aaa	cgc	atc	acg	aac	aaa	gat			2933
Glu	Lys	Ala	Pro	Lys	Asn	Pro	Ser	Val	Lys	Arg	Ile	Thr	Asn	Lys	Asp			
				800					805					810				
act	gcc	gta	acg	ggg	aga	acg	gca	gcc	ggc	tac	acg	atc	aaa	gtg	aaa			2981
Thr	Ala	Val	Thr	Gly	Arg	Thr	Ala	Ala	Gly	Tyr	Thr	Ile	Lys	Val	Lys			
			815					820					825					
aac	gcg	tac	aaa	aaa	gtg	atc	gcg	caa	ggc	ata	gcg	gat	gca	tcc	gtg			3029
Asn	Ala	Tyr	Lys	Lys	Val	Ile	Ala	Gln	Gly	Ile	Ala	Asp	Ala	Ser	Val			
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agc	gtt	aaa	gtg	aaa	atc	aac	aag	caa	aaa	gat	atg	ccg	ttt	tgt	atg			3077
Ser	Val	Lys	Val	Lys	Ile	Asn	Lys	Gln	Lys	Asp	Met	Pro	Phe	Cys	Met			
			845			850					855							
tct	ccg	cat	ctg	ctg	atg	acc	aca	gag	aaa	gcg	gcg	atg	tca	aaa				3122
Ser	Pro	His	Leu	Leu	Met	Thr	Thr	Glu	Lys	Ala	Ala	Met	Ser	Lys				
					865					870								
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 Asp Ser Val Pro Asn Asn Glu Thr Thr Leu Thr Ser Ala Ser Pro Val
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 Glu Ala Ser Phe Gln Ser Asp Asp Glu Val His Trp Tyr Lys Val Asn
 50 55 60
 Pro Ser Asn Gln Glu Ile Ala Asn Tyr Thr His Phe Arg Val Lys Leu
 65 70 75 80
 Lys Ser Asp Ala Glu Leu Asn Ile Ser Val Tyr Ser Ser Leu Glu Asn
 85 90 95
 Ala Thr Gly His Gln Thr Phe Asp Arg Tyr Asn Gly Tyr Ser Tyr Glu
 100 105 110
 Asn Asn Pro Ala Leu Ile Asp Phe Pro Ile Ala Trp Lys Gly Pro Tyr
 115 120 125
 Tyr Ile Lys Val Glu Asn His His Asp Glu Glu Asn Glu Thr Thr Ser
 130 135 140
 Ile Thr Asp Ile Ser Tyr Thr Ile Ser Tyr Glu Gly Val Thr Leu Pro
 145 150 155 160
 Pro Ser Ile Gln Glu Ala Glu Glu Glu Cys Pro Ala Glu Leu Ser Val
 165 170 175
 Ser Glu Arg Glu Thr Gly Lys Gly Ile Leu Lys Gln Leu Arg Thr Ile
 180 185 190
 Arg Asp Glu Val Leu Ser Lys Thr Glu Lys Gly Lys Glu Leu Ser Ser
 195 200 205
 Leu Tyr Tyr Lys Ala Ala Pro Phe Ile Ser Ala Lys Met Leu Phe Asn
 210 215 220
 Lys Ser Met Arg Asp Ser Val Tyr Lys Asp Leu Val Gln Leu Lys Pro
 225 230 235 240
 Leu Phe Ala Asp Val Ala Lys Asn Gly Gln Val Ser Ala Tyr Ser Ile
 245 250 255
 Thr Asn Asp Asp Gln Lys Ala Ile Ser Arg Leu Tyr Glu Thr Ala Arg
 260 265 270

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Ala Ser Val Pro Glu Pro Leu Lys Lys Gln Leu Asp Gln Val Ala Lys
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Asp Ile Gly Ile Glu Gln Leu Thr Gly Ser Lys Val Ser Ala Val Leu
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Glu Lys Ala Gly Met Ala Thr Ala Ser Ser Ser Ala Pro Glu Asn Arg
 305 310 315 320

Tyr Ile Val Lys Leu Lys Glu Gly Lys Lys Pro Gly Ser Phe Lys Ser
 325 330 335

Lys Ala Gln Ser Ser Gly Val Gln Ala Leu Glu Pro Leu Gly Lys Ser
 340 345 350

Lys Thr Ala Phe Lys Asp Met Tyr Val Val Glu Met Lys Glu Ser Arg
 355 360 365

Ser Ser Gly Phe Lys Ala Ala Ala Lys Gln Tyr Gln Ala Ala Ala Ser
 370 375 380

Lys Ile Ala Lys Met Pro Glu Val Glu Phe Val Glu Gln Val Gln Gln
 385 390 395 400

Tyr Glu Ala Leu Ser Arg Asp Thr Gln Tyr Pro Tyr Gln Trp Ser Leu
 405 410 415

Lys Asn Asn Gly Lys Asn Arg Ala Ala Asn Ala Asp Ile Gln Phe Glu
 420 425 430

Gln Leu Gln Lys Leu Met Lys Gly Lys Lys Leu Lys Asp Thr Val Ile
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Ala Val Val Asp Thr Gly Val Asp His Thr Leu Ala Asp Leu Ser Gly
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Ser Val Lys Lys Asp Glu Gly Tyr Asn Tyr Val Gly Arg Thr Ala Asp
 465 470 475 480

Ala Met Asp Asp Asn Gly His Gly Thr His Val Ser Gly Ile Ile Ala
 485 490 495

Ala Ala Gln Asp Asn His Phe Ser Met Ala Gly Ile Asn Ala Tyr Ala
 500 505 510

Lys Ile Leu Pro Val Lys Val Leu Asp Ser Ser Gly Ser Gly Asp Thr
 515 520 525

Glu Gln Ile Ala Asn Gly Ile Ile Tyr Ala Ala Asp His Gly Ala Lys
 530 535 540

10294.204.ST25.txt

Val Ile Asn Leu Ser Leu Gly Gly Pro Tyr Ser Arg Val Met Glu Tyr
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Ala Leu Lys Tyr Ala Ala Ser Lys Asn Val Thr Ile Val Ala Ala Thr
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 580 585 590

Thr Leu Ser Val Gly Ala Thr Asn Asn Leu Asp Leu Val Ser Asp Tyr
 595 600 605

Ser Asn Tyr Gly Lys Gly Leu Asp Met Val Ala Pro Gly Thr Asp Ile
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Pro Ser Leu Val Pro Asp Gly Asn Val Thr Tyr Met Ser Gly Thr Ser
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Met Ala Ala Pro His Val Ala Ala Ala Ala Gly Leu Leu Leu Ser Gln
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Asn Pro Ser Leu Lys Pro Lys Gln Ile Ala Ser Leu Leu Thr Glu Thr
 660 665 670

Thr Ala Asp Val Ala Phe Glu Glu Gln Asp Asn Pro Asn Pro Asp Tyr
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Asp Leu Asp Ile Glu Pro Ala Ala Gln Ile Pro Gly Tyr Asp Phe Val
 690 695 700

Ser Gly Trp Gly Arg Leu Asn Val Phe His Ala Ala Ser Val Phe Glu
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Leu Asn Met Lys Val His Pro Val Leu Asn Arg His Thr Ala Val Thr
 725 730 735

Gly Thr Ala Lys Ser Gly Val Thr Val Lys Ile Leu Arg Gly Lys Gln
 740 745 750

Val Leu Gly Thr Gly Thr Ala Gly Lys Ser Gly Ala Phe Ser Val Lys
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Ile Pro Ala Gln Lys Ala Gly Gln Val Leu His Val Ala Ala Ser Gly
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His Gln Ala Glu Thr Ser Leu Arg Thr Val Val Glu Lys Ala Pro Lys
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Asn Pro Ser Val Lys Arg Ile Thr Asn Lys Asp Thr Ala Val Thr Gly
 805 810 815

10294.204.ST25.txt

Arg Thr Ala Ala Gly Tyr Thr Ile Lys Val Lys Asn Ala Tyr Lys Lys
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Val Ile Ala Gln Gly Ile Ala Asp Ala Ser Val Ser Val Lys Val Lys
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 cctttcattt cccaacctt aaatcccctt gaactacctt tatcttaaat aatgaatgag 420
 tgttcagtca atatattttc ataaatgcag gaaaataggg ggacactatt ctttacacga 480
 aaaaagggga gtg tct tca ttg gtg ccg ctt atg att atg gta tgt ttt ctc 531
 Val Ser Ser Leu Val Pro Leu Met Ile Met Val Cys Phe Leu
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 atc ctg ctt ctt gcg ctc gat ttc cat ttt ggc cgc aaa gcc ttt gag 579
 Ile Leu Leu Leu Ala Leu Asp Phe His Phe Gly Arg Lys Ala Phe Glu
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 aag aaa gcc tac gag ccc gtt ttt tca gag aag aaa agc gat att gaa 627
 Lys Lys Ala Tyr Glu Pro Val Phe Ser Glu Lys Lys Ser Asp Ile Glu
 35 40 45
 ctg att cat aat gga gaa gac ttg tgt gag cgg ctg ctg gat gac atc 675
 Leu Ile His Asn Gly Glu Asp Leu Cys Glu Arg Leu Leu Asp Asp Ile
 50 55 60
 cgc cag gcc gaa tcg tcg gtg cat gtc atg ttt tat att gtg aag aac 723
 Arg Gln Ala Glu Ser Ser Val His Val Met Phe Tyr Ile Val Lys Asn
 65 70 75
 gat gac atc agc ctt gaa ttt ttg aag gtg ctg aag gat aaa gcg aaa 771
 Asp Asp Ile Ser Leu Glu Phe Leu Lys Val Leu Lys Asp Lys Ala Lys
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10294.204.ST25.txt

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gtg aag aaa aaa acg ctc tcc ggc ctg aaa caa agc ggt gtg cac gtt	867
Val Lys Lys Lys Thr Leu Ser Gly Leu Lys Gln Ser Gly Val His Val	
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Phe Phe Ala Asn Lys Pro Gly Phe Pro Tyr Phe Phe Tyr Arg Leu Asn	
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Ala Arg Asn His Arg Lys Ile Ala Val Ile Asp Gly Lys Ile Gly Tyr	
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Val Gly Gly Phe Asn Ile Ala Lys Glu Tyr Leu Gly Lys Lys Ala Glu	
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Phe Gly Pro Trp Lys Asp Tyr His Leu Arg Met Thr Gly Glu Gly Val	
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gcc gac ttg cag cac att ttt ata tcg gac ttc aaa aga gaa gcg ccg	1107
Ala Asp Leu Gln His Ile Phe Ile Ser Asp Phe Lys Arg Glu Ala Pro	
195 200 205	
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Gln Ala Lys Pro Ala Asn Ser Val Phe Pro Pro Leu Gln Gln Gly Ala	
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Val Thr His Thr Thr His Ala Thr Lys Gly Phe Ser Leu Glu Glu Lys	
225 230 235	
tac att tca ttt atc gaa cag gca aaa gaa aga atc atg att tgc acg	1251
Tyr Ile Ser Phe Ile Glu Gln Ala Lys Glu Arg Ile Met Ile Cys Thr	
240 245 250	
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Pro Tyr Tyr Ile Pro Ser Pro Ala Leu Gln Gln Ala Val Leu Ser Ala	
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Arg Glu Arg Gly Val Ile Val Ser Val Leu Val Pro Met Lys Pro Asp	
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Lys Ala Gly Cys Tyr Ile Tyr Arg Tyr Tyr Arg Gly Phe Tyr His Ala	
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Lys Ala Leu Ile Val Asp Asp Arg His Val Met Ile Gly Thr Ser Asn	
320 325 330	
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Phe Asp Asn Arg Ser Leu Phe Leu Asn Asp Glu Val Asn Val Val Ile	
335 340 345 350	
cat gat aaa gac tgg aca aag caa ttc ttc gac gtc gtc aag gaa agc	1587
His Asp Lys Asp Trp Thr Lys Gln Phe Phe Asp Val Val Lys Glu Ser	
355 360 365	

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 Ile Glu His Ala Glu Leu Leu Thr Lys Glu Arg Tyr Ala Lys Arg Pro
 370 375 380

gtg atg cag cgg ccc gtc gaa tgg ctg gcg aaa tcg att tca ttc ttt 1683
 Val Met Gln Arg Pro Val Glu Trp Leu Ala Lys Ser Ile Ser Phe Phe
 385 390 395

tta taaaacgtac gtttatcctg catgacatgc gggtaacatt tcaccaaagt 1736
 Leu

gatgattaca tacggagggg atgtacgatg aaccaagcag agtcgattaa actccgcgcc 1796
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 20 25 30

Ala Tyr Glu Pro Val Phe Ser Glu Lys Lys Ser Asp Ile Glu Leu Ile
 35 40 45

His Asn Gly Glu Asp Leu Cys Glu Arg Leu Leu Asp Asp Ile Arg Gln
 50 55 60

Ala Glu Ser Ser Val His Val Met Phe Tyr Ile Val Lys Asn Asp Asp
 65 70 75 80

Ile Ser Leu Glu Phe Leu Lys Val Leu Lys Asp Lys Ala Lys Ser Gly
 85 90 95

Val Cys Val Arg Leu Leu Ile Asp Arg Ile Gly Ala Met Lys Val Lys
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Lys Lys Thr Leu Ser Gly Leu Lys Gln Ser Gly Val His Val Phe Phe
 115 120 125

10294.204.ST25.txt

Ala Asn Lys Pro Gly Phe Pro Tyr Phe Phe Tyr Arg Leu Asn Ala Arg
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 145 150 155 160
 Gly Phe Asn Ile Ala Lys Glu Tyr Leu Gly Lys Lys Ala Glu Phe Gly
 165 170 175
 Pro Trp Lys Asp Tyr His Leu Arg Met Thr Gly Glu Gly Val Ala Asp
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 Leu Gln His Ile Phe Ile Ser Asp Phe Lys Arg Glu Ala Pro Gln Ala
 195 200 205
 Lys Pro Ala Asn Ser Val Phe Pro Pro Leu Gln Gln Gly Ala Val Thr
 210 215 220
 His Thr Thr His Ala Thr Lys Gly Phe Ser Leu Glu Glu Lys Tyr Ile
 225 230 235 240
 Ser Phe Ile Glu Gln Ala Lys Glu Arg Ile Met Ile Cys Thr Pro Tyr
 245 250 255
 Tyr Ile Pro Ser Pro Ala Leu Gln Gln Ala Val Leu Ser Ala Arg Glu
 260 265 270
 Arg Gly Val Ile Val Ser Val Leu Val Pro Met Lys Pro Asp His Pro
 275 280 285
 Leu Val Lys Glu Ala Ala Tyr Thr His Phe Pro Ala Leu Leu Lys Ala
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 Gly Cys Tyr Ile Tyr Arg Tyr Tyr Arg Gly Phe Tyr His Ala Lys Ala
 305 310 315 320
 Leu Ile Val Asp Asp Arg His Val Met Ile Gly Thr Ser Asn Phe Asp
 325 330 335
 Asn Arg Ser Leu Phe Leu Asn Asp Glu Val Asn Val Val Ile His Asp
 340 345 350
 Lys Asp Trp Thr Lys Gln Phe Phe Asp Val Val Lys Glu Ser Ile Glu
 355 360 365
 His Ala Glu Leu Leu Thr Lys Glu Arg Tyr Ala Lys Arg Pro Val Met
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10294.204.ST25.txt

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 aag gaa ttg tgg aca ttg atc gaa cta ttt agt gat tat gtg ctc cat 168
 Glu Leu Trp Thr Leu Ile Glu Leu Phe Ser Asp Tyr Val Leu His
 1 5 10 15
 ttt gaa cgt tat ttt gtt tta agc aga cag agc atg ctt gtc att cag 216
 Phe Glu Arg Tyr Phe Val Leu Ser Arg Gln Ser Met Leu Val Ile Gln
 20 25 30
 tgg tgt gtg aca ggc ctt gtc ctt ttg tat gcc gtg tca ttt cat cca 264
 Trp Cys Val Thr Gly Leu Val Leu Tyr Ala Val Ser Phe His Pro
 35 40 45
 aaa gtg tgc agg cgg cgc ctc ttt ttt tat gca ggc atc gtt ctc agg 312
 Lys Val Cys Arg Arg Arg Leu Phe Phe Tyr Ala Gly Ile Val Leu Arg
 50 55 60
 ctg ata ctg gtt ggc gcc ctt tcg ttt gaa ttg gct cac caa atg aaa 360
 Leu Ile Leu Val Gly Ala Leu Ser Phe Glu Leu Ala His Gln Met Lys
 65 70 75
 gcc gct gag ttt tca aac ctg tac ata gac gaa caa gat gcg ctt ctg 408
 Ala Ala Glu Phe Ser Asn Leu Tyr Ile Asp Glu Gln Asp Ala Leu Leu
 80 85 90 95
 cct ttt atg cag ttt ttg ctg ttc ggc tat att ttg ctt gtc tct ttt 456
 Pro Phe Met Gln Phe Leu Leu Phe Gly Tyr Ile Leu Leu Val Ser Phe
 100 105 110
 cat tat atg atg aca ctc gcg gaa aaa ggg ggc aag ggg ctg ttt ttt 504
 His Tyr Met Met Thr Leu Ala Glu Lys Gly Gly Lys Gly Leu Phe Phe
 115 120 125
 gca ttt gac att gcg gtg atg gcg atg ccg ctt ttc caa tcg ctg ttc 552
 Ala Phe Asp Ile Ala Val Met Ala Met Pro Leu Phe Gln Ser Leu Phe
 130 135 140
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 Ser Phe Ala Ala Tyr Leu Lys Glu Phe Gly Ala Glu Glu Leu Glu Glu
 145 150 155
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 Leu Pro Leu Val Leu Leu Leu Ile Val Gly Ile Pro Gly Leu Met Ile
 160 165 170 175
 tgc ttg ttt ttt cag ctt tat tgg aaa aga aac cgt tac gtt ctc ctt 696
 Cys Leu Phe Phe Gln Leu Tyr Trp Lys Arg Asn Arg Tyr Val Leu Leu
 180 185 190
 ttg att ttt tat att gtg acg atc ggc ggt ttc ttc atc aaa aag ctt 744
 Leu Ile Phe Tyr Ile Val Thr Ile Gly Gly Phe Phe Ile Lys Lys Leu
 195 200 205
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10294.204.ST25.txt

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Val	Lys	Arg	Val	Leu	Ala	Ala	Gly	Thr	Ala	Val	Phe	Phe	Thr	Leu	His		
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ctc	aat	cct	ttt	tac	aat	ttg	gcg	gat	gcc	gct	ttt	aca	atc	tca	cac		936
Leu	Asn	Pro	Phe	Tyr	Asn	Leu	Ala	Asp	Ala	Ala	Phe	Thr	Ile	Ser	His		
				260					265					270			
ccg	gag	gtt	tca	gac	gtg	gtt	gat	gcc	aat	ttt	cgg	cct	gtt	tcg	gtt		984
Pro	Glu	Val	Ser	Asp	Val	Val	Asp	Ala	Asn	Phe	Arg	Pro	Val	Ser	Val		
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Lys	Glu	Ala	Lys	Gln	Thr	Val	Ser	Ser	Phe	Phe	Pro	Thr	Glu	Ser	Phe		
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Ile	Tyr	Leu	Ser	Ala	Thr	Asn	Gln	Asp	Phe	His	Asn	Val	Tyr	His	Phe		
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Lys	Thr	Lys	Asp	Tyr	Asp	Ala	Asp	Val	Asp	Gly	Trp	Thr	Gly	Met	Ile		
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acc	aat	tat	cac	aat	caa	aaa	aag	cct	agc	ggg	aat	atc	ctg	tcc	ggt		1176
Thr	Asn	Tyr	His	Asn	Gln	Lys	Lys	Pro	Ser	Gly	Asn	Ile	Leu	Ser	Gly		
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Gln	Ala	Tyr	Ile	Lys	Arg	Ser	Lys	Gln	Phe	Leu	Arg	Glu	His	Gly	Arg		
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Ala	Thr	Val	Glu	Phe	Tyr	Arg	Glu	Gly	Glu	Asp	Pro	Glu	Leu	Ser	Thr		
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atg	tgg	ttt	act	tgg	cgg	aag	gag	act	ctg	atg	gga	ttc	cat	gag	gac		1368
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gcg	tct	gtt	tac	agc	tta	gaa	agc	gtg	aac	caa	gcc	cgc	gtt	tct	ggt		1416
Ala	Ser	Val	Tyr	Ser	Leu	Glu	Ser	Val	Asn	Gln	Ala	Arg	Val	Ser	Gly		
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gag	gat	atc	gag	cgg	gga	gtt	gaa	gcc	gtc	tat	cgt	aag	ctg	ggc	ata		1464
Glu	Asp	Ile	Glu	Arg	Gly	Val	Glu	Ala	Val	Tyr	Arg	Lys	Leu	Gly	Ile		
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ccc	gtc	tca	tct	tat	cgg	ctg	aca	gat	att	gat	tta	tta	ttc	cca	ttc		1512
Pro	Val	Ser	Ser	Tyr	Arg	Leu	Thr	Asp	Ile	Asp	Leu	Leu	Phe	Pro	Phe		
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agc	ctc	aac	tcg	gca	tcc	atc	aac	ata	aag	aca	agt	gac	gga	atg	ggg		1560
Ser	Leu	Asn	Ser	Ala	Ser	Ile	Asn	Ile	Lys	Thr	Ser	Asp	Gly	Met	Gly		
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10294.204.ST25.txt

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				500				505						510		
ctt	tca	tta	ttt	gat	caa	gac	att	tcc	aat	ctg	aaa	agg	gtg	gag	tta	1704
Leu	Ser	Leu	Phe	Asp	Gln	Asp	Ile	Ser	Asn	Leu	Lys	Arg	Val	Glu	Leu	
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gaa	aag	gat	ctg	ata	gaa	ttt	cag	aaa	aaa	gaa	agc	gat	gct	gtg	tta	1752
Glu	Lys	Asp	Leu	Ile	Glu	Phe	Gln	Lys	Lys	Glu	Ser	Asp	Ala	Val	Leu	
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Asn	Thr	Val	Trp	Thr	Met	Thr	Lys	His	Glu	Glu	Gly	Ala	Tyr	Leu	Thr	
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gtg	aga	aaa	aac	ttt	caa	aaa	gca	gat	gaa	aaa	ccc	ccc	tac	acg	tat	1848
Val	Arg	Lys	Asn	Phe	Gln	Lys	Ala	Asp	Glu	Lys	Pro	Pro	Tyr	Thr	Tyr	
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aaa	cat	ttt	gat	gac	aaa	tgaagaaaaa	aaagcgggtgt	ttatcgattt								2088
Lys	His	Phe	Asp	Asp	Lys											
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gaaaaaaagc	ttggaaggca	gggagggtta	acaatatgaa	atgccatctt	gtaagagatt											2868

10294.204.ST25.txt

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2908

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Cys Val Thr Gly Leu Val Leu Leu Tyr Ala Val Ser Phe His Pro Lys
 35 40 45

Val Cys Arg Arg Arg Leu Phe Phe Tyr Ala Gly Ile Val Leu Arg Leu
 50 55 60

Ile Leu Val Gly Ala Leu Ser Phe Glu Leu Ala His Gln Met Lys Ala
 65 70 75 80

Ala Glu Phe Ser Asn Leu Tyr Ile Asp Glu Gln Asp Ala Leu Leu Pro
 85 90 95

Phe Met Gln Phe Leu Leu Phe Gly Tyr Ile Leu Leu Val Ser Phe His
 100 105 110

Tyr Met Met Thr Leu Ala Glu Lys Gly Gly Lys Gly Leu Phe Phe Ala
 115 120 125

Phe Asp Ile Ala Val Met Ala Met Pro Leu Phe Gln Ser Leu Phe Ser
 130 135 140

Phe Ala Ala Tyr Leu Lys Glu Phe Gly Ala Glu Glu Leu Glu Glu Leu
 145 150 155 160

Pro Leu Val Leu Leu Leu Ile Val Gly Ile Pro Gly Leu Met Ile Cys
 165 170 175

Leu Phe Phe Gln Leu Tyr Trp Lys Arg Asn Arg Tyr Val Leu Leu Leu
 180 185 190

Ile Phe Tyr Ile Val Thr Ile Gly Gly Phe Phe Ile Lys Lys Leu Gly
 195 200 205

Tyr Glu Phe Phe Pro Leu Asn Val Phe Leu Thr Met Ile Gly Phe Leu
 210 215 220

Met Thr Tyr His Leu Leu Asn Asp Ser Arg Lys Pro Leu Leu Met Val
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225 230 235 240

Lys Arg Val Leu Ala Ala Gly Thr Ala Val Phe Phe Thr Leu His Leu
 245 250 255

Asn Pro Phe Tyr Asn Leu Ala Asp Ala Ala Phe Thr Ile Ser His Pro
 260 265 270

Glu Val Ser Asp Val Val Asp Ala Asn Phe Arg Pro Val Ser Val Lys
 275 280 285

Glu Ala Lys Gln Thr Val Ser Ser Phe Phe Pro Thr Glu Ser Phe Ile
 290 295 300

Tyr Leu Ser Ala Thr Asn Gln Asp Phe His Asn Val Tyr His Phe Lys
305 310 315 320

Thr Lys Asp Tyr Asp Ala Asp Val Asp Gly Trp Thr Gly Met Ile Thr
 325 330 335

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 340 345 350

Ala Tyr Ile Lys Arg Ser Lys Gln Phe Leu Arg Glu His Gly Arg Glu
 355 360 365

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370 375 380

Thr Val Glu Phe Tyr Arg Glu Gly Glu Asp Pro Glu Leu Ser Thr Met
385 390 395 400

Trp Phe Thr Trp Arg Lys Glu Thr Leu Met Gly Phe His Glu Asp Ala
 405 410 415

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Asp Ile Glu Arg Gly Val Glu Ala Val Tyr Arg Lys Leu Gly Ile Pro
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Val Ser Ser Tyr Arg Leu Thr Asp Ile Asp Leu Leu Phe Pro Phe Ser
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Leu Asn Ser Ala Ser Ile Asn Ile Lys Thr Ser Asp Gly Met Gly Met
465 470 475 480

Glu Phe His Pro Val Thr Gly Ala Leu Thr Ala Ile Ser Ile Lys Ser
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Glu Ser Ala Leu Pro Tyr Arg Gly Gln Glu Leu Glu Lys Arg Leu Leu

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500

505

510

Ser Leu Phe Asp Gln Asp Ile Ser Asn Leu Lys Arg Val Glu Leu Glu
 515 520 525

Lys Asp Leu Ile Glu Phe Gln Lys Lys Glu Ser Asp Ala Val Leu Asn
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Thr Val Trp Thr Met Thr Lys His Glu Glu Gly Ala Tyr Leu Thr Val
 545 550 555 560

Arg Lys Asn Phe Gln Lys Ala Asp Glu Lys Pro Pro Tyr Thr Tyr Ala
 565 570 575

Asp Gly Glu Lys Ala Phe Gln Lys Val Ser Glu Arg Tyr Gln Lys Gly
 580 585 590

Leu Val Tyr His Lys Arg Thr Lys Leu Val Ile Val Ser Asp Gly Asp
 595 600 605

Gln Lys Ser Arg Tyr Ala Trp Leu Val Ile Ile Gln Pro Phe Gly Ser
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His Phe Asp Asp Lys
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 aaacagctac tgcacgagct ttatgaatat gctgtcagct ggtctgaggc ttttaattgtt 300
 caagctgctt atgaaccgct ctattatgcc tgcgaataact tcatccaaag ctggtggaag 360
 gaaggcttca gccagcggga aagacgcttt aagcttcggc tcagataaaa caaagtttta 420
 tgaaaaagtg aggccaagct taatcatatt tcctttcctt gtcccatatc ttgtagtaag 480
 gacgagcggg agggaaaggg atg aag aaa aaa ata aaa tgg ctc ggg ttt tta 533
 Met Lys Lys Lys Ile Lys Trp Leu Gly Phe Leu

10294.204.ST25.txt

1	5	10	
ctc ggc ttt gtc gtt tta tta tgt tta ttt caa tat caa ttc aac aat Leu Gly Phe Val Val Leu Leu Cys Leu Phe Gln Tyr Gln Phe Asn Asn 15 20 25			581
gat gat tct tgg cgg tca tgg aat ctt ccg ctg agc ggc aaa atc att Asp Asp Ser Trp Arg Ser Trp Asn Leu Pro Leu Ser Gly Lys Ile Ile 30 35 40			629
tat att gat cct gga cac ggg ggc gcc gat gga ggg gca tca agc ggt Tyr Ile Asp Pro Gly His Gly Gly Ala Asp Gly Gly Ala Ser Ser Gly 45 50 55			677
gaa ctc ctt gaa aaa gac gtg gct ctt gaa gta tcc cta aga atc agg Glu Leu Leu Glu Lys Asp Val Ala Leu Glu Val Ser Leu Arg Ile Arg 60 65 70 75			725
gac tat ctc cag gag cag ggc gcc ttg gtg atg ctg acg cgg gag gac Asp Tyr Leu Gln Glu Gln Gly Ala Leu Val Met Leu Thr Arg Glu Asp 80 85 90			773
gat cat gat ctc gct cct gaa gaa acg agg gga ctc agc aga aga aaa Asp His Asp Leu Ala Pro Glu Glu Thr Arg Gly Leu Ser Arg Arg Lys 95 100 105			821
gct gaa gac ttg cgg aag agg gtc gat atg atc aac aat tct gaa gcc Ala Glu Asp Leu Arg Lys Arg Val Asp Met Ile Asn Asn Ser Glu Ala 110 115 120			869
gat ctt tac ctc agc atc cat ttg aat gcg att cct tcc gcg cga tgg Asp Leu Tyr Leu Ser Ile His Leu Asn Ala Ile Pro Ser Ala Arg Trp 125 130 135			917
agc ggt gcg caa agc ttc tat tac ggg caa tat gaa gag aat gaa cgg Ser Gly Ala Gln Ser Phe Tyr Tyr Gly Gln Tyr Glu Glu Asn Glu Arg 140 145 150 155			965
gcc gcc aag ttt att cag gat gaa tta aga cat aat ctt gaa aac acg Ala Ala Lys Phe Ile Gln Asp Glu Leu Arg His Asn Leu Glu Asn Thr 160 165 170			1013
acg cgg aag gca aag cgg ata cac gga att tat ttg atg caa aat gtt Thr Arg Lys Ala Lys Arg Ile His Gly Ile Tyr Leu Met Gln Asn Val 175 180 185			1061
aaa aag ccc ggg gcc ctt gtc gaa atc ggg ttt ttg tct aac ccg gaa Lys Lys Pro Gly Ala Leu Val Glu Ile Gly Phe Leu Ser Asn Pro Glu 190 195 200			1109
gag gca aaa cag ctg gcc aag ccc aaa tat cag gac aaa atc gca gca Glu Ala Lys Gln Leu Ala Lys Pro Lys Tyr Gln Asp Lys Ile Ala Ala 205 210 215			1157
tcc gtt tat aaa ggc gta ttg cgc tac ttt aca gaa gac aga gac cct Ser Val Tyr Lys Gly Val Leu Arg Tyr Phe Thr Glu Asp Arg Asp Pro 220 225 230 235			1205
cct gaa taagagggtt tctttttgtg tcaaagacac tataaggaaa gatatgctat Pro Glu			1261
acttatttttg taaacgaata caacaaaggg tgagatcaat gttgcgagaa gacgatgtaa			1321
aaaagatagt cggcgatttg gacgagccat ttcttcacaa gccgctcaga gagctggatg			1381
ccgtaaaaga aattaaaata aaacccgaaa aacggcacgt cagcgtaaag gtggcgctcg			1441

10294.204.ST25.txt

caaaaacggg atctgccgaa caaatgcagc ttcagcagga aatcgtcata cggttgaaag 1501
aagccggtgc agagacggtc ggcctgcgtt ttgaggagct gcccgaagaa gtcgtaatga 1561
gttatcaaga gtctgccaaa gggcaggatc aatctctgct gaatagtga aaacagcctg 1621
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tggctgtgtc cctggcgcgga atcggaaga a 1712

<210> 34
<211> 237
<212> PRT
<213> Bacillus licheniformis

<400> 34

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Leu Leu Cys Leu Phe Gln Tyr Gln Phe Asn Asn Asp Asp Ser Trp Arg
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Ser Trp Asn Leu Pro Leu Ser Gly Lys Ile Ile Tyr Ile Asp Pro Gly
35 40 45
His Gly Gly Ala Asp Gly Gly Ala Ser Ser Gly Glu Leu Leu Glu Lys
50 55 60
Asp Val Ala Leu Glu Val Ser Leu Arg Ile Arg Asp Tyr Leu Gln Glu
65 70 75 80
Gln Gly Ala Leu Val Met Leu Thr Arg Glu Asp Asp His Asp Leu Ala
85 90 95
Pro Glu Glu Thr Arg Gly Leu Ser Arg Arg Lys Ala Glu Asp Leu Arg
100 105 110
Lys Arg Val Asp Met Ile Asn Asn Ser Glu Ala Asp Leu Tyr Leu Ser
115 120 125
Ile His Leu Asn Ala Ile Pro Ser Ala Arg Trp Ser Gly Ala Gln Ser
130 135 140
Phe Tyr Tyr Gly Gln Tyr Glu Glu Asn Glu Arg Ala Ala Lys Phe Ile
145 150 155 160
Gln Asp Glu Leu Arg His Asn Leu Glu Asn Thr Thr Arg Lys Ala Lys
165 170 175
Arg Ile His Gly Ile Tyr Leu Met Gln Asn Val Lys Lys Pro Gly Ala
180 185 190
Leu Val Glu Ile Gly Phe Leu Ser Asn Pro Glu Glu Ala Lys Gln Leu
195 200 205

—

Ala Lys Pro Lys Tyr Gln Asp Lys Ile Ala Ala Ser Val Tyr Lys Gly
210 215 220

Val Leu Arg Tyr Phe Thr Glu Asp Arg Asp Pro Pro Glu
225 230 235

<210> 35
<211> 1988
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(1487)

[illegible]

10294.204.ST25.txt

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aaa Lys 140	gct Ala 140	tct Ser 140	aca Thr 140	tat Tyr 145	atc Ile 145	ggc Gly 145	aca Thr 145	aat Asn 150	aat Asn 150	atg Met 150	gaa Glu 150	gcg Ala 150	ggt Gly 150	gct Ala 155	gtg Val 155	965
gcc Ala 160	gca Ala 160	agg Arg 160	cga Arg 160	atg Met 160	gcc Ala 160	gaa Glu 165	ttt Phe 165	ttg Leu 165	aat Asn 165	gga Gly 165	aag Lys 165	gga Gly 170	gaa Glu 170	acc Thr 170	gcg Ala 170	1013
gtc Val 175	att Ile 175	acc Thr 175	cag Gln 175	ccg Pro 175	cag Gln 180	cag Gln 180	tac Tyr 180	aat Asn 180	cat His 180	cag Gln 185	gaa Glu 185	agg Arg 185	acg Thr 185	aag Lys 185	ggc Gly 185	1061
ttt Phe 190	gaa Glu 190	caa Gln 190	acg Thr 190	atc Ile 195	aag Lys 195	caa Gln 195	aaa Lys 195	tac Tyr 195	ccg Pro 200	aac Asn 200	atg Met 200	aag Lys 200	gtt Val 200	gcc Ala 200	gcg Ala 200	1109
gtt Val 205	ttg Leu 205	gac Asp 205	gga Gly 205	aaa Lys 210	ggg Gly 210	gat Asp 210	gag Glu 210	ctg Leu 210	acg Thr 215	tcg Ser 215	aaa Lys 215	aaa Lys 215	gaa Glu 215	gcg Ala 215	gcg Ala 215	1157
aag Lys 220	att Ile 220	ttg Leu 220	gag Glu 225	gaa Glu 225	aat Asn 225	ccg Pro 225	tcc Ser 225	atc Ile 230	aaa Lys 230	gga Gly 230	att Ile 230	ttc Phe 230	acg Thr 235	act Thr 235	gaa Glu 235	1205
gcc Ala 240	aat Asn 240	gga Gly 240	gcg Ala 240	agc Ser 240	ggc Gly 245	gtg Val 245	gcc Ala 245	cgt Arg 245	gct Ala 245	gtg Val 245	aag Lys 250	gag Glu 250	gcg Ala 250	gga Gly 250	ctt Leu 250	1253
gaa Glu 255	ggg Gly 255	gaa Glu 255	gta Val 255	tgt Cys 255	atc Ile 260	atc Ile 260	ggc Gly 260	ttt Phe 260	gat Asp 260	aaa Lys 265	gac Asp 265	aag Lys 265	aaa Lys 265	acg Thr 265	ctg Leu 265	1301
gac Asp 270	ggc Gly 270	atc Ile 270	aaa Lys 275	aac Asn 275	gga Gly 275	tcg Ser 275	att Ile 275	tcc Ser 280	gcg Ala 280	aca Thr 280	atg Met 280	agc Ser 280	cag Gln 280	gac Asp 280	aca Thr 280	1349
tgg Trp 285	caa Gln 285	atg Met 285	ggc Gly 290	tat Tyr 290	tgg Trp 290	tcg Ser 290	ctg Leu 290	cac His 295	atg Met 295	ctg Leu 295	ttt Phe 295	ttc Phe 295	tca Ser 295	aat Asn 295	cac His 295	1397
cat His 300	ctg Leu 300	aag Lys 300	cat His 305	gaa Glu 305	cgc Arg 305	ccg Pro 310	ctt Leu 310	ccg Pro 310	gcc Ala 310	gca Ala 310	atc Ile 315	gac Asp 315	aca Thr 315	ggc Gly 315	att Ile 315	1445
acc Thr 320	atc Ile 320	ata Ile 320	acg Thr 320	aaa Lys 320	gaa Glu 325	aat Asn 325	gtg Val 325	gca Ala 325	gcc Ala 325	tat Tyr 325	tat Tyr 325	gcg Ala 325	aat Asn 325			1487
gattaaacgt ttgatcaata atgcgccgat ccgtcataag ctgatcagcc ttctcttggt																1547
aatcagcatg ctgccgacga tcggcctggg cattttatcg ggatgggccg ttgaaaatat																1607
tattgaaaaa caggtgatcg accaaacact gcagctgacg ggcgaagtga acaagacggc																1667
tgaagtgtat gtcagccaca tgcagaacct gacatattta atatcaatga atgaagaaat																1727
ggaagcgttt tttagtcata aaaaggagga tggagaggcg gattataagc gaaggacggt																1787
tttgcagggc ctgacttctt tatattccga agcagcgggt attctcgttg tcaatgataa																1847
gggtgagatg atcagcaatg agatgtatga acgcacgccg acagatttga caaaagaacc																1907
atggtatcag gcggctctcg acaatgaagg gattttcaag atgatcggga agcctgtcaa																1967

10294.204.ST25.txt

1988

ccggaatatc agaagccatg t

<210> 36
 <211> 329
 <212> PRT
 <213> Bacillus licheniformis

<400> 36

Met Lys Lys Leu Leu Val Val Tyr Ala Val Met Leu Cys Leu Phe Phe
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Leu Tyr Val Tyr Asp Tyr Ser Arg Gly Asp Lys Ala Gly Ser Ala Glu
 20 25 30

Glu Ser Arg Arg Pro Ala Ala Ala Gly Ser Leu Ser Glu Lys Tyr Val
 35 40 45

Met Val Thr Phe Gln Ser Gly Ile Glu Tyr Trp Lys Ser Gly Leu Lys
 50 55 60

Gly Phe Glu Asp Ala Ala Gln Leu Phe Asn Val Ser Val Glu Tyr Arg
 65 70 75 80

Gly Ala Ala His Tyr Asp Val His Glu Gln Thr Thr Val Leu Glu Gln
 85 90 95

Val Ile Ala Lys Lys Pro Ala Gly Ile Ala Val Ser Ala Ile Asn Pro
 100 105 110

Lys Ala Leu Asn Pro Val Ile Asp Lys Ala His Glu Gln Gly Ile Pro
 115 120 125

Ile Val Leu Phe Asp Ser Asp Ala Pro Leu Ser Lys Ala Ser Thr Tyr
 130 135 140

Ile Gly Thr Asn Asn Met Glu Ala Gly Ala Val Ala Ala Arg Arg Met
 145 150 155 160

Ala Glu Phe Leu Asn Gly Lys Gly Glu Thr Ala Val Ile Thr Gln Pro
 165 170 175

Gln Gln Tyr Asn His Gln Glu Arg Thr Lys Gly Phe Glu Gln Thr Ile
 180 185 190

Lys Gln Lys Tyr Pro Asn Met Lys Val Ala Ala Val Leu Asp Gly Lys
 195 200 205

Gly Asp Glu Leu Thr Ser Lys Lys Glu Ala Ala Lys Ile Leu Glu Glu
 210 215 220

Asn Pro Ser Ile Lys Gly Ile Phe Thr Thr Glu Ala Asn Gly Ala Ser
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10294.204.ST25.txt

225

230

235

240

Gly Val Ala Arg Ala Val Lys Glu Ala Gly Leu Glu Gly Glu Val Cys
 245 250 255

Ile Ile Gly Phe Asp Lys Asp Lys Lys Thr Leu Asp Gly Ile Lys Asn
 260 265 270

Gly Ser Ile Ser Ala Thr Met Ser Gln Asp Thr Trp Gln Met Gly Tyr
 275 280 285

Trp Ser Leu His Met Leu Phe Phe Ser Asn His His Leu Lys His Glu
 290 295 300

Arg Pro Leu Pro Ala Ala Ile Asp Thr Gly Ile Thr Ile Ile Thr Lys
 305 310 315 320

Glu Asn Val Ala Ala Tyr Tyr Ala Asn
 325

<210> 37
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 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(2282)

<400> 37
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 gaaaattccc aaaatataaa caaaacatta ataaaatcaa gccatttgat taacaaattt 420
 acgatacgat catatagaac ttgatgattg ggaaaagcat tttgagagaa gattaagagc 480
 aaggagagata tgatgtgaga atg aaa cga tta agg atg agg aag cat tta ctg 533
 Met Lys Arg Leu Arg Met Arg Lys His Leu Leu
 1 5 10
 ata gct gtc tgt act ttg gca ctt ctt cta agt tcc ccg att gta agc 581
 Ile Ala Val Cys Thr Leu Ala Leu Leu Leu Ser Ser Pro Ile Val Ser
 15 20 25
 gat gcg agc ccg gca act aaa cca aca act gca gat tcg ccg caa tct 629
 Asp Ala Ser Pro Ala Thr Lys Pro Thr Thr Ala Asp Ser Pro Gln Ser
 30 35 40
 tcc gga ttt ttc gta gac cat tac aaa aat aat atc tct gcc aat acg 677
 Ser Gly Phe Phe Val Asp His Tyr Lys Asn Asn Ile Ser Ala Asn Thr

10294.204.ST25.txt

45	50	55	
acg gcg gaa tcc aat cct gtc atc ggc ctg ctt tcc gaa ttt aat aaa			725
Thr Ala Glu Ser Asn Pro Val Ile Gly Leu Leu Ser Glu Phe Asn Lys			
60	65	70	75
ctt tgg act ccc gga aag aca tgg aat acc ggt act aaa ctg aac agc			773
Leu Trp Thr Pro Gly Lys Thr Trp Asn Thr Gly Thr Lys Leu Asn Ser			
80	85	90	
agg gtg ctg gat gcc aac att caa aaa gtc gtg gat att gct gaa cgc			821
Arg Val Leu Asp Ala Asn Ile Gln Lys Val Val Asp Ile Ala Glu Arg			
95	100	105	
cgc acg atg ctt gag gaa aat gct gcc tat ttt gat gat cgg cgg agc			869
Arg Thr Met Leu Glu Glu Asn Ala Tyr Phe Asp Asp Arg Arg Ser			
110	115	120	
cag agc tac agt ata att gac ggc ctc ggc aag ctt gcc ggc gtc tat			917
Gln Ser Tyr Ser Ile Ile Asp Gly Leu Gly Lys Leu Ala Gly Val Tyr			
125	130	135	
cga atg aac gcg gga gcg acg aca acg atc acc agc att ccg gca gat			965
Arg Met Asn Ala Gly Ala Thr Thr Thr Ile Thr Ser Ile Pro Ala Asp			
140	145	150	155
gcc tcg att aga aaa tac aat gat gaa gga acc aat tcg ggc agc acc			1013
Ala Ser Ile Arg Lys Tyr Asn Asp Glu Gly Thr Asn Ser Gly Ser Thr			
160	165	170	
agc tct gaa ctt gga aat gtc gta agt ttg gtc aat act tta cgc ggc			1061
Ser Ser Glu Leu Gly Asn Val Val Ser Leu Val Asn Thr Leu Arg Gly			
175	180	185	
aac tat tct tca tcg aat ccg gct aaa agc tat ttc aac tat ccc cgc			1109
Asn Tyr Ser Ser Ser Asn Pro Ala Lys Ser Tyr Phe Asn Tyr Pro Arg			
190	195	200	
ccg ttt cgc tgg aaa gac aat tcg atc att gtt cca acg ctt atc ccc			1157
Pro Phe Arg Trp Lys Asp Asn Ser Ile Ile Val Pro Thr Leu Ile Pro			
205	210	215	
gtc atc aat cct gat ccg aac aaa gac gga ggt ttt cca agc gga cac			1205
Val Ile Asn Pro Asp Pro Asn Lys Asp Gly Gly Phe Pro Ser Gly His			
220	225	230	235
acg aac gcc gca tat ctc agc gct ttt gct atg gcc tat gcg ata ccg			1253
Thr Asn Ala Ala Tyr Leu Ser Ala Phe Ala Met Ala Tyr Ala Ile Pro			
240	245	250	
gag cgt tat cag gag ctg ctg act cgc gct tca gaa ctc ggt cat aac			1301
Glu Arg Tyr Gln Glu Leu Leu Thr Arg Ala Ser Glu Leu Gly His Asn			
255	260	265	
cgg att gtt gcc ggt atg cat tcc ccg ctg gac gtc atg ggg gga cga			1349
Arg Ile Val Ala Gly Met His Ser Pro Leu Asp Val Met Gly Gly Arg			
270	275	280	
gta atg gca aca gct ttg tct gca gca atc ctg tct gac ccc gca aat			1397
Val Met Ala Thr Ala Leu Ser Ala Ala Ile Leu Ser Asp Pro Ala Asn			
285	290	295	
gaa aga ttg aag aaa acg gct ttt gat gaa gcc cgc cgt aaa tta tta			1445
Glu Arg Leu Lys Lys Thr Ala Phe Asp Glu Ala Arg Arg Lys Leu Leu			
300	305	310	315
acg caa acc ggt aca gct gaa gac aga tac agc gat tat gag aag aat			1493
Thr Gln Thr Gly Thr Ala Glu Asp Arg Tyr Ser Asp Tyr Glu Lys Asn			

10294.204.ST25.txt

320	325	330	
aaa aaa caa tat acg gaa cga ttg aca tat gga ttt cga caa atg aac Lys Lys Gln Tyr Thr Glu Arg Leu Thr Tyr Gly Phe Arg Gln Met Asn 335 340 345			1541
aaa acc gcc aaa cca atg gca gtt cca aag gga gcc gaa gtc ctg ctg Lys Thr Ala Lys Pro Met Ala Val Pro Lys Gly Ala Glu Val Leu Leu 350 355 360			1589
gaa aca cgt ttt cct tac ctt gac aaa aag cag cgc cgt tcg gtt tta Glu Thr Arg Phe Pro Tyr Leu Asp Lys Lys Gln Arg Arg Ser Val Leu 365 370 375			1637
gcc act acc ggt ctt ccg gcc ggc tac cct gtt ctt gat gat cga gaa Ala Thr Thr Gly Leu Pro Ala Gly Tyr Pro Val Leu Asp Asp Arg Glu 380 385 390 395			1685
gga tgg gga agg ctt aat ctc ttt tcc gcg gca gat ggg tat ggg gct Gly Trp Gly Arg Leu Asn Leu Phe Ser Ala Ala Asp Gly Tyr Gly Ala 400 405 410			1733
ttt acc aaa aat gtt acc gtg acc atg gat tcc gca aaa ggc ggc ttc Phe Thr Lys Asn Val Thr Val Thr Met Asp Ser Ala Lys Gly Gly Phe 415 420 425			1781
cat aca gcc gat cgc tgg cgc aac gac atc tcc ggc acc gga aag ctg His Thr Ala Asp Arg Trp Arg Asn Asp Ile Ser Gly Thr Gly Lys Leu 430 435 440			1829
acc aaa aaa ggg aca ggc gct ttg aag ctg gaa ggg gat aat aca tat Thr Lys Lys Gly Thr Gly Ala Leu Lys Leu Glu Gly Asp Asn Thr Tyr 445 450 455			1877
tcc ggc ggt aca cgg att gat caa gga aca ctt gag ggc ggt tcg gag Ser Gly Gly Thr Arg Ile Asp Gln Gly Thr Leu Glu Gly Gly Ser Glu 460 465 470 475			1925
aca gct ttc ggg aga ggt gat gtt gca cta aac gga ggc atc ctt aag Thr Ala Phe Gly Arg Gly Asp Val Ala Leu Asn Gly Gly Ile Leu Lys 480 485 490			1973
gaa gat gcg ccg gga aaa ctg atc atc gaa gga gac tac aaa caa tct Glu Asp Ala Pro Gly Lys Leu Ile Ile Glu Gly Asp Tyr Lys Gln Ser 495 500 505			2021
gct aaa gga ata ctt gaa ctt cag ctc agc ggc aaa aaa gat cag ttg Ala Lys Gly Ile Leu Glu Leu Gln Leu Ser Gly Lys Lys Asp Gln Leu 510 515 520			2069
aaa att aag gga aaa gca aga ttg aaa ggg aca ttg cgt ctc aat ttt Lys Ile Lys Gly Lys Ala Arg Leu Lys Gly Thr Leu Arg Leu Asn Phe 525 530 535			2117
acg gac aat tac gta ccg gct gac gga tcg gcg atc ata acc ttc cgc Thr Asp Asn Tyr Val Pro Ala Asp Gly Ser Ala Ile Ile Thr Phe Arg 540 545 550 555			2165
aag cgt cat gga tca ttt tct tcc gtc gag acc agt gga ttg cca agc Lys Arg His Gly Ser Phe Ser Ser Val Glu Thr Ser Gly Leu Pro Ser 560 565 570			2213
aag tat aaa gtg aag atc atc tat aaa tcc aac agt att cag ttg aaa Lys Tyr Lys Val Lys Ile Ile Tyr Lys Ser Asn Ser Ile Gln Leu Lys 575 580 585			2261
gtt gag caa aag ggg aga agc tgatctgcaa gaggattcac tcaaaagctg Val Glu Gln Lys Gly Arg Ser			2312

10294.204.ST25.txt

590

caagctggcg catactgccg ccagcttgct tttagttttg atgaaatcac agccagaatg 2372
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 gatcggggac cctttaaatg cggatgcata gggactgcat acaaatgcag ccagtctgcc 2492
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 gattgttaat ttgataagc tttttgacaa tgataatagc attgattttg tcatacaata 2732
 ctgaggcatc tggcctgaag gcatcatcgc ttcttcactt gcgataaaga tga 2785

<210> 38
 <211> 594
 <212> PRT
 <213> Bacillus licheniformis

<400> 38

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 20 25 30
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 35 40 45
 Asp His Tyr Lys Asn Asn Ile Ser Ala Asn Thr Thr Ala Glu Ser Asn
 50 55 60
 Pro Val Ile Gly Leu Leu Ser Glu Phe Asn Lys Leu Trp Thr Pro Gly
 65 70 75 80
 Lys Thr Trp Asn Thr Gly Thr Lys Leu Asn Ser Arg Val Leu Asp Ala
 85 90 95
 Asn Ile Gln Lys Val Val Asp Ile Ala Glu Arg Arg Thr Met Leu Glu
 100 105 110
 Glu Asn Ala Ala Tyr Phe Asp Asp Arg Arg Ser Gln Ser Tyr Ser Ile
 115 120 125
 Ile Asp Gly Leu Gly Lys Leu Ala Gly Val Tyr Arg Met Asn Ala Gly
 130 135 140
 Ala Thr Thr Thr Ile Thr Ser Ile Pro Ala Asp Ala Ser Ile Arg Lys
 145 150 155 160
 Tyr Asn Asp Glu Gly Thr Asn Ser Gly Ser Thr Ser Ser Glu Leu Gly
 165 170 175

10294.204.ST25.txt

Asn Val Val Ser Leu Val Asn Thr Leu Arg Gly Asn Tyr Ser Ser Ser
 180 185 190

Asn Pro Ala Lys Ser Tyr Phe Asn Tyr Pro Arg Pro Phe Arg Trp Lys
 195 200 205

Asp Asn Ser Ile Ile Val Pro Thr Leu Ile Pro Val Ile Asn Pro Asp
 210 215 220

Pro Asn Lys Asp Gly Gly Phe Pro Ser Gly His Thr Asn Ala Ala Tyr
 225 230 235 240

Leu Ser Ala Phe Ala Met Ala Tyr Ala Ile Pro Glu Arg Tyr Gln Glu
 245 250 255

Leu Leu Thr Arg Ala Ser Glu Leu Gly His Asn Arg Ile Val Ala Gly
 260 265 270

Met His Ser Pro Leu Asp Val Met Gly Gly Arg Val Met Ala Thr Ala
 275 280 285

Leu Ser Ala Ala Ile Leu Ser Asp Pro Ala Asn Glu Arg Leu Lys Lys
 290 295 300

Thr Ala Phe Asp Glu Ala Arg Arg Lys Leu Leu Thr Gln Thr Gly Thr
 305 310 315 320

Ala Glu Asp Arg Tyr Ser Asp Tyr Glu Lys Asn Lys Lys Gln Tyr Thr
 325 330 335

Glu Arg Leu Thr Tyr Gly Phe Arg Gln Met Asn Lys Thr Ala Lys Pro
 340 345 350

Met Ala Val Pro Lys Gly Ala Glu Val Leu Leu Glu Thr Arg Phe Pro
 355 360 365

Tyr Leu Asp Lys Lys Gln Arg Arg Ser Val Leu Ala Thr Thr Gly Leu
 370 375 380

Pro Ala Gly Tyr Pro Val Leu Asp Asp Arg Glu Gly Trp Gly Arg Leu
 385 390 395 400

Asn Leu Phe Ser Ala Ala Asp Gly Tyr Gly Ala Phe Thr Lys Asn Val
 405 410 415

Thr Val Thr Met Asp Ser Ala Lys Gly Gly Phe His Thr Ala Asp Arg
 420 425 430

Trp Arg Asn Asp Ile Ser Gly Thr Gly Lys Leu Thr Lys Lys Gly Thr
 435 440 445

10294.204.ST25.txt

Gly Ala Leu Lys Leu Glu Gly Asp Asn Thr Tyr Ser Gly Gly Thr Arg
 450 455 460

Ile Asp Gln Gly Thr Leu Glu Gly Gly Ser Glu Thr Ala Phe Gly Arg
 465 470 475 480

Gly Asp Val Ala Leu Asn Gly Gly Ile Leu Lys Glu Asp Ala Pro Gly
 485 490 495

Lys Leu Ile Ile Glu Gly Asp Tyr Lys Gln Ser Ala Lys Gly Ile Leu
 500 505 510

Glu Leu Gln Leu Ser Gly Lys Lys Asp Gln Leu Lys Ile Lys Gly Lys
 515 520 525

Ala Arg Leu Lys Gly Thr Leu Arg Leu Asn Phe Thr Asp Asn Tyr Val
 530 535 540

Pro Ala Asp Gly Ser Ala Ile Ile Thr Phe Arg Lys Arg His Gly Ser
 545 550 555 560

Phe Ser Ser Val Glu Thr Ser Gly Leu Pro Ser Lys Tyr Lys Val Lys
 565 570 575

Ile Ile Tyr Lys Ser Asn Ser Ile Gln Leu Lys Val Glu Gln Lys Gly
 580 585 590

Arg Ser

<210> 39
 <211> 2009
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1526)

<400> 39
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 actttgttaa agaaaaatca aatggctatg ttctatcaaa cggaactt tcttaaaaaa 180
 cagcgattat ttccgtgacg acgactcaat taagatcgat gctgggcggc atgaatatga 240
 agagcacgta tgcttctgta tccagcaata cgaacgcttt tactctcagc ggtaaaggat 300
 tcggacacgg catcggcatg agtcagtacg gatcaaatgc cagagctgct gccgggcacg 360
 attacaagaa gattttaagt ttctactatc caaatacgac tctatcaagc tattaataga 420
 gtttgaacag gaagcagcag tgcctcctct gttcatgttc atgggaaaac ataacattta 480

10294.204.ST25.txt

catttttggga gggtattttt ttg aag gtc ttt ctt aaa gct gta cct atg ttg 533
 Leu Lys Val Phe Leu Lys Ala Val Pro Met Leu
 1 5 10

tcg tta cgg ttc ttt ttg ttt gtg cct aat gta ttt gcg gcc aac tct 581
 Ser Leu Arg Phe Phe Leu Phe Val Pro Asn Val Phe Ala Ala Asn Ser
 15 20 25

gtc aca aga ttg gac ggt gca aac cga tat gag gtt gcg gtg aac gtt 629
 Val Thr Arg Leu Asp Gly Ala Asn Arg Tyr Glu Val Ala Val Asn Val
 30 35 40

tcc aag cag ggg tgg aca agt gca agc act gtg att gtt gca aat gga 677
 Ser Lys Gln Gly Trp Thr Ser Ala Ser Thr Val Ile Val Ala Asn Gly
 45 50 55

aag gca tat gca gac gtc ctt tca gcg act cca ttt gcc tat cga aac 725
 Lys Ala Tyr Ala Asp Val Leu Ser Ala Thr Pro Phe Ala Tyr Arg Asn
 60 65 70 75

aac gcg cct gtt cta tta acg gaa gcg tct aaa ctg cca acg gcc act 773
 Asn Ala Pro Val Leu Leu Thr Glu Ala Ser Lys Leu Pro Thr Ala Thr
 80 85 90

aaa aac cga atc agt caa tta aaa cct agc aaa gtg atc gta atc ggc 821
 Lys Asn Arg Ile Ser Gln Leu Lys Pro Ser Lys Val Ile Val Ile Gly
 95 100 105

gga acc gtc agc gtt caa aac ggt gtc gta agc gag atc aaa aag ctt 869
 Gly Thr Val Ser Val Gln Asn Gly Val Val Ser Glu Ile Lys Lys Leu
 110 115 120

ggt gtg tca tct gtc gaa cgc atc ggc gga gcg aat cgc tac gag gtt 917
 Gly Val Ser Ser Val Glu Arg Ile Gly Gly Ala Asn Arg Tyr Glu Val
 125 130 135

gcg gcg aat att gcg aat aag ctg ccg agc aat tcg aaa gct gtc atc 965
 Ala Ala Asn Ile Ala Asn Lys Leu Pro Ser Asn Ser Lys Ala Val Ile
 140 145 150 155

gca aac ggg acg gcc tat gct gac agc ctt gcg atc ggc gca tat gcc 1013
 Ala Asn Gly Thr Ala Tyr Ala Asp Ser Leu Ala Ile Gly Ala Tyr Ala
 160 165 170

gcg aga aac ggc atc ccg att ctt tta aca tcg tcg aat tcc ata ccg 1061
 Ala Arg Asn Gly Ile Pro Ile Leu Leu Thr Ser Ser Asn Ser Ile Pro
 175 180 185

aca gcg aca aaa aat gcg atg aag agc aaa gga aca aca tcg acc att 1109
 Thr Ala Thr Lys Asn Ala Met Lys Ser Lys Gly Thr Thr Ser Thr Ile
 190 195 200

gtc gta ggc ggt gaa gtc agc atc tcc agc agc gtt tac aaa cag ctt 1157
 Val Val Gly Gly Glu Val Ser Ile Ser Ser Ser Val Tyr Lys Gln Leu
 205 210 215

gct tct ccg acg cgg atc ggc ggc agc aac cgc tat gaa gtc gcg gcc 1205
 Ala Ser Pro Thr Arg Ile Gly Gly Ser Asn Arg Tyr Glu Val Ala Ala
 220 225 230 235

aat gtc gtc aag aaa tat tat tct tct gcc aag aat gca atc atc agc 1253
 Asn Val Val Lys Lys Tyr Tyr Ser Ser Ala Lys Asn Ala Ile Ile Ser
 240 245 250

aac ggc tat gcg tat gcc gac gga tta aca gga tct gtt ctg gcg gct 1301
 Asn Gly Tyr Ala Tyr Ala Asp Gly Leu Thr Gly Ser Val Leu Ala Ala
 255 260 265

10294.204.ST25.txt

aag caa aac cgt ccg atg atg ttc acg aat gca tca tct ttg ccg aca 1349
Lys Gln Asn Arg Pro Met Met Phe Thr Asn Ala Ser Ser Leu Pro Thr
275 280
ccg aca aga gaa gtg atc ggt tcc aaa aac atg acg acg ttt act gtg 1397
Pro Thr Arg Glu Val Ile Gly Ser Lys Asn Met Thr Thr Phe Thr Val
285 290 295
ctt ggc gga acg gtt tct ctt caa tcc aat gtc gtg tca cag ctg aag 1445
Leu Gly Gly Thr Val Ser Leu Gln Ser Asn Val Val Ser Gln Leu Lys
300 305 310 315
aat ccg atc gtc ggc aaa aaa atc ttc att gat gca ggg cac gga ggt 1493
Asn Pro Ile Val Gly Lys Lys Ile Phe Ile Asp Ala Gly His Gly Gly
320 325 330
aca gac agc ggt gcc cgt cgg caa cgg ttt ata tgagaaaagc gtgaaccttg 1546
Thr Asp Ser Gly Ala Arg Arg Gln Arg Phe Ile
335 340
atgttgcaaaa attaatatt acgaaactat caaacggcgg tgctctgcca attatggcga 1606
gaacgaacga cacttacctg acgctcgac agcgctgtc aaaagcgag tcaaatactg 1666
cggatttggt tgctcagcatc catgcaaact cggcaacgcc agctgcttcc ggaacagaaa 1726
cctactatta tacaacatat gaactctgcca acagcaaacg gctggcaacc gagattcaaa 1786
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tcacagggga atcaaaaatg ccaagctgcc ttgttgaact tgcgtttatc agcaatgtaa 1906
gcgatgcgac aaaactcaaa agctcgactt acaaagaaaa aggcgctaaa gcgatttacg 1966
acggaatcgt tgcttactat taaaatataa acagaaaact cgt 2009

<210> 40
<211> 342
<212> PRT
<213> Bacillus licheniformis

<400> 40

Leu Lys Val Phe Leu Lys Ala Val Pro Met Leu Ser Leu Arg Phe Phe
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Leu Phe Val Pro Asn Val Phe Ala Ala Asn Ser Val Thr Arg Leu Asp
20 25 30

Gly Ala Asn Arg Tyr Glu Val Ala Val Asn Val Ser Lys Gln Gly Trp
35 40 45

Thr Ser Ala Ser Thr Val Ile Val Ala Asn Gly Lys Ala Tyr Ala Asp
50 55 60

Val Leu Ser Ala Thr Pro Phe Ala Tyr Arg Asn Asn Ala Pro Val Leu
65 70 75 80

Leu Thr Glu Ala Ser Lys Leu Pro Thr Ala Thr Lys Asn Arg Ile Ser
85 90 95

10294.204.ST25.txt

Gln Leu Lys Pro Ser Lys Val Ile Val Ile Gly Gly Thr Val Ser Val
 100 105 110
 Gln Asn Gly Val Val Ser Glu Ile Lys Lys Leu Gly Val Ser Ser Val
 115 120 125
 Glu Arg Ile Gly Gly Ala Asn Arg Tyr Glu Val Ala Ala Asn Ile Ala
 130 135 140
 Asn Lys Leu Pro Ser Asn Ser Lys Ala Val Ile Ala Asn Gly Thr Ala
 145 150 155 160
 Tyr Ala Asp Ser Leu Ala Ile Gly Ala Tyr Ala Ala Arg Asn Gly Ile
 165 170 175
 Pro Ile Leu Leu Thr Ser Ser Asn Ser Ile Pro Thr Ala Thr Lys Asn
 180 185 190
 Ala Met Lys Ser Lys Gly Thr Thr Ser Thr Ile Val Val Gly Gly Glu
 195 200 205
 Val Ser Ile Ser Ser Ser Val Tyr Lys Gln Leu Ala Ser Pro Thr Arg
 210 215 220
 Ile Gly Gly Ser Asn Arg Tyr Glu Val Ala Ala Asn Val Val Lys Lys
 225 230 235 240
 Tyr Tyr Ser Ser Ala Lys Asn Ala Ile Ile Ser Asn Gly Tyr Ala Tyr
 245 250 255
 Ala Asp Gly Leu Thr Gly Ser Val Leu Ala Ala Lys Gln Asn Arg Pro
 260 265 270
 Met Met Phe Thr Asn Ala Ser Ser Leu Pro Thr Pro Thr Arg Glu Val
 275 280 285
 Ile Gly Ser Lys Asn Met Thr Thr Phe Thr Val Leu Gly Gly Thr Val
 290 295 300
 Ser Leu Gln Ser Asn Val Val Ser Gln Leu Lys Asn Pro Ile Val Gly
 305 310 315 320
 Lys Lys Ile Phe Ile Asp Ala Gly His Gly Gly Thr Asp Ser Gly Ala
 325 330 335
 Arg Arg Gln Arg Phe Ile
 340

<210> 41
 <211> 2044
 <212> DNA

10294.204.ST25.txt

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (469)..(1566)

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ggcagcatca ccgaaatcgt cacggcgatt caaaccgaaa catcttccat ggccggtgat 120
ttaaaaaccg gtttttcaga agttcataaa ggaaaaaacc agattgagac ttccggccga 180
tacttttcag agattaaaaa taaagtgcag gatatggctg gccgtgtatc ggacatttcg 240
gaggcattat cgcatttcag acgttcaagc gaggagatta acggctcggg cgagcatatc 300
gcggcgattt ccgaagaaag cgcggccggg tctgaagaaa ttccagcgtc cgtacatgag 360
caaagcggct cgattgaaaa gatggacgaa agcgcaaggc ttctgggaga gatggttgaa 420
cggatgaatg tgatgatcaa acggtttaag ctctgatgcc gatacaga atg ggg ggt 477
                                     Met Gly Gly
                                     1

ttt aat gtt gtc gat ata tgt gaa aag agg gct gtt ggc act tgc gct 525
Phe Asn Val Val Asp Ile Cys Glu Lys Arg Ala Val Gly Thr Cys Ala
      5                10                15

ggt cag tct cct cac agc tgt tgc cgg gtg ctc att caa ttc tgc tta 573
Val Gln Ser Pro His Ser Cys Cys Arg Val Leu Ile Gln Phe Cys Leu
      20                25                30                35

aaa aag cgc caa ccg tta aga aaa agt aaa gct gat tgc cga ctc cga 621
Lys Lys Arg Gln Pro Leu Arg Lys Ser Lys Ala Asp Cys Arg Leu Arg
                        40                45                50

caa att gta cgt cgg ttt tgc cat cga tac gct gaa gga aga acg ctg 669
Gln Ile Val Arg Arg Phe Cys His Arg Tyr Ala Glu Gly Arg Thr Leu
                        55                60                65

gta caa aga tca aga agc gtt cga gaa aga agt tca aaa cct cgg ggg 717
Val Gln Arg Ser Arg Ser Val Arg Glu Arg Ser Ser Lys Pro Arg Gly
      70                75                80

gga agt caa gac gct tgc cgc tca cgg aaa tca aga agt tca gat tca 765
Gly Ser Gln Asp Ala Cys Arg Ser Arg Lys Ser Arg Ser Ser Asp Ser
      85                90                95

gca ggc cga gct ctt gat cag cga agg cgt cga cgt gct tgt tgt tgt 813
Ala Gly Arg Ala Leu Asp Gln Arg Arg Arg Arg Arg Ala Cys Cys Cys
     100                105                110                115

acc ggc aga tgc gga tgc cgc ggc gga gat cgt gaa aaa ggc gca cag 861
Thr Gly Arg Cys Gly Cys Arg Gly Gly Asp Arg Glu Lys Gly Ala Gln
                        120                125                130

cgc cgg tgt aaa agt gat ttc gta tta ccg gct gat tcg aaa cgc gga 909
Arg Arg Cys Lys Ser Asp Phe Val Leu Pro Ala Asp Ser Lys Arg Gly
                        135                140                145

tgt tta tta tta cgt ttc att tta tca cga aaa ggt cgg gga act gca 957
Cys Leu Leu Leu Arg Phe Ile Leu Ser Arg Lys Gly Arg Gly Thr Ala
      150                155                160

ggc gga agc gat tgt aaa aaa agc gaa gaa agg aaa ctt cgt ata tat 1005
Gly Gly Ser Asp Cys Lys Lys Ser Glu Glu Arg Lys Leu Arg Ile Tyr

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10294.204.ST25.txt

165	170	175	
cgg cgg atc gtc tct tta caa caa tgc ggt ctt att ccg gaa cgg cgc Arg Arg Ile Val Ser Leu Gln Gln Cys Gly Leu Ile Pro Glu Arg Arg 180 185 190			1053
cat gaa agt gct cga acc gtt gaa gcg gca ggg tca agt caa gct cgt His Glu Ser Ala Arg Thr Val Glu Ala Gly Ser Ser Gln Ala Arg 200 205 210			1101
gct tta cga ata tac gaa aga ctg gct acc aga aga agc gaa aaa gaa Ala Leu Arg Ile Tyr Glu Arg Leu Ala Thr Arg Arg Ser Glu Lys Glu 215 220 225			1149
cat gaa aaa agc att gaa caa gac gag aga tat cga cgc cgt gat cgc His Glu Lys Ser Ile Glu Gln Asp Gly Arg Tyr Arg Arg Arg Asp Arg 230 235 240			1197
cgc caa tta cgg tac ggc tgg cgg ggt gat cga ggc gct tca gga ggc Arg Gln Leu Arg Tyr Gly Trp Arg Gly Asp Arg Gly Ala Ser Gly Gly 245 250 255			1245
ggg cct ggc cgg gaa aat tcc ggt gtc cgg aca gga cgc gga aat tca Gly Pro Gly Arg Glu Asn Ser Gly Val Arg Thr Gly Arg Gly Asn Ser 260 265 270 275			1293
agg cgt ccg acg aat tgt gaa cgg tac gca gac gat gac cgt tta caa Arg Arg Pro Thr Asn Cys Glu Arg Tyr Ala Asp Asp Asp Arg Leu Gln 280 285 290			1341
acc gat tcc cgc gct tgc caa aaa aag cgc tta aat ggc tgt tca agc Thr Asp Ser Arg Ala Cys Gln Lys Lys Arg Leu Asn Gly Cys Ser Ser 295 300 305			1389
ggc gaa agg cga agc gat tca aac cga tac aac cgt cga aaa cgg caa Gly Glu Arg Arg Ser Asp Ser Asn Arg Tyr Asn Arg Arg Lys Arg Gln 310 315 320			1437
agc caa agt acc ggc gat ttt act tta gcc gta tgc cgt tac gaa agg Ser Gln Ser Thr Gly Asp Phe Thr Leu Ala Val Cys Arg Tyr Glu Arg 325 330 335			1485
caa tat caa tta gac tgt gat caa aga cgg cca tct gtc caa aaa aga Gln Tyr Gln Leu Asp Cys Asp Gln Arg Arg Pro Ser Val Gln Lys Arg 340 345 350 355			1533
tat tca tca ata aaa cga agt cag cca tcc gct acaggatggc tgactttgtt Tyr Ser Ser Ile Lys Arg Ser Gln Pro Ser Ala 360 365			1586
aaatttccac tttcacatcg gcgcttttct taagcttttc gacctgctgt ccgagttttt			1646
cctgtctttt ttgctgtttg agcatatcctt ggatttgctg tttgacatcg tcaaacgcag			1706
gtgtgttttt ctgtccgctg tcttttttgct gtgcggcaaa ttgatcataa tagtctttga			1766
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tgctgtcggc aatgtcgctt ttcagcggtg tcatgtttaa gcctgctttt ttgaccgctt			1886
cctcaaaatc ttgctcgttt ttatactgct ttttgctttc gtccagctgt ttttcaattt			1946
ctttctcaga tgctttgtag ctttttttggt ccgcttcctg cgtaattaat gcctgtccga			2006
tcaggctgtc gatcgctgc tttttgattt gctgcgcc			2044

10294.204.ST25.txt

<211> 366

<212> PRT

<213> Bacillus licheniformis

<400> 42

Met Gly Gly Phe Asn Val Val Asp Ile Cys Glu Lys Arg Ala Val Gly
 1 5 10 15

Thr Cys Ala Val Gln Ser Pro His Ser Cys Cys Arg Val Leu Ile Gln
 20 25 30

Phe Cys Leu Lys Lys Arg Gln Pro Leu Arg Lys Ser Lys Ala Asp Cys
 35 40 45

Arg Leu Arg Gln Ile Val Arg Arg Phe Cys His Arg Tyr Ala Glu Gly
 50 55 60

Arg Thr Leu Val Gln Arg Ser Arg Ser Val Arg Glu Arg Ser Ser Lys
 65 70 75 80

Pro Arg Gly Gly Ser Gln Asp Ala Cys Arg Ser Arg Lys Ser Arg Ser
 85 90 95

Ser Asp Ser Ala Gly Arg Ala Leu Asp Gln Arg Arg Arg Arg Arg Ala
 100 105 110

Cys Cys Cys Thr Gly Arg Cys Gly Cys Arg Gly Gly Asp Arg Glu Lys
 115 120 125

Gly Ala Gln Arg Arg Cys Lys Ser Asp Phe Val Leu Pro Ala Asp Ser
 130 135 140

Lys Arg Gly Cys Leu Leu Leu Arg Phe Ile Leu Ser Arg Lys Gly Arg
 145 150 155 160

Gly Thr Ala Gly Gly Ser Asp Cys Lys Lys Ser Glu Glu Arg Lys Leu
 165 170 175

Arg Ile Tyr Arg Arg Ile Val Ser Leu Gln Gln Cys Gly Leu Ile Pro
 180 185 190

Glu Arg Arg His Glu Ser Ala Arg Thr Val Glu Ala Ala Gly Ser Ser
 195 200 205

Gln Ala Arg Ala Leu Arg Ile Tyr Glu Arg Leu Ala Thr Arg Arg Ser
 210 215 220

Glu Lys Glu His Glu Lys Ser Ile Glu Gln Asp Glu Arg Tyr Arg Arg
 225 230 235 240

Arg Asp Arg Arg Gln Leu Arg Tyr Gly Trp Arg Gly Asp Arg Gly Ala
 245 250 255

10294.204.ST25.txt

Ser Gly Gly Gly Pro Gly Arg Glu Asn Ser Gly Val Arg Thr Gly Arg
260 265 270

Gly Asn Ser Arg Arg Pro Thr Asn Cys Glu Arg Tyr Ala Asp Asp Asp
275 280 285

Arg Leu Gln Thr Asp Ser Arg Ala Cys Gln Lys Lys Arg Leu Asn Gly
290 295 300

Cys Ser Ser Gly Glu Arg Arg Ser Asp Ser Asn Arg Tyr Asn Arg Arg
305 310 315 320

Lys Arg Gln Ser Gln Ser Thr Gly Asp Phe Thr Leu Ala Val Cys Arg
325 330 335

Tyr Glu Arg Gln Tyr Gln Leu Asp Cys Asp Gln Arg Arg Pro Ser Val
340 345 350

Gln Lys Arg Tyr Ser Ser Ile Lys Arg Ser Gln Pro Ser Ala
355 360 365

<210> 43
<211> 1690
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (480)..(1208)

<400> 43
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cccgaggcg acattgctga tcctcggtgt ggcaagggag ttgtccgcca atgtcagtgc 180
atcgattccg gctgatttta gctcctctgc ggcgtgcaaa aattttctcaa agtttaattg 240
ttttggagga tcgagctcga cgataatgga ccgtttctgc ttagccagat agtcaagagc 300
aggctatgtc ctttcgtttt ggacggcaag cgccgctttc ttggggattt tcactagttt 360
ttcggtgact ggaggaagtt ctttgacggc cctcggcatc gttctaccct gagtgtcttt 420
tatgcccgtc tttaggcggc cccgtcaacg aataatgcat aaaaaaggaa gattcatat 479
gaa aat cgt aaa cgt tct gct cgc tat ttt att gac cgc aat cat gtt 527
Glu Asn Arg Lys Arg Ser Ala Arg Tyr Phe Ile Asp Arg Asn His Val
1 5 10 15
aag cgg ttg ttt gta ccc tta aga aag aaa ggc gaa aaa cag cgc acc 575
Lys Arg Leu Phe Val Pro Leu Arg Lys Lys Gly Glu Lys Gln Arg Thr
20 25 30
gca tca gca cca gct caa aga agt gca ggc ggc cgt tta tta att cag 623
Ala Ser Ala Pro Ala Gln Arg Ser Ala Gly Gly Arg Leu Leu Ile Gln
35 40 45

10294.204.ST25.txt

gga ggc gac ggg agg gct tct gcc gat tca gac aag gga tat ggg cgt Gly Gly Asp Gly Arg Ala Ser 55 Ala Asp Ser Asp Lys 60 Gly Tyr Gly Arg	671
gcc aat cta tca aaa ata ccc tat cga ttt tca cag gct gtc ccc ccg Ala Asn Leu Ser Lys 70 Ile Pro Tyr Arg Phe 75 Ser Gln Ala Val Pro 80	719
gta tat ggc tta gcc gcc ggg cac atc cta tta aaa cgg cgg aga gta Val Tyr Gly Leu Ala 85 Ala Gly His Ile 90 Leu Leu Lys Arg Arg 95 Val	767
ctt gta cgt tct tgt cga tgt gga aaa aaa gcc gac ggt caa gct cat Leu Val Arg Ser 100 Cys Arg Cys Gly 105 Lys Lys Ala Asp Gly 110 Gln Ala His	815
tta tgt aaa aat gtc gga aat gat cag gga gtt aaa gct tcg ggt cga Leu Cys Lys 115 Asn Val Gly Asn 120 Asp Gln Gly Val Lys 125 Ala Ser Gly Arg	863
aat gta tca aga tca gca caa gta tcc gcc gta tca aaa agt cgt atc Asn Val 130 Ser Arg Ser Ala 135 Gln Val Ser Ala Val 140 Ser Lys Ser Arg Ile	911
caa gaa ctt att cat gct tta cca tta aaa gct cgg act gaa aga ggc Gln Glu Leu Ile His 150 Ala Leu Pro Leu Lys 155 Ala Arg Thr Glu Arg Gly 160	959
gcc ttc tgt cac gag tcc gct ttc ggg cac ctc gct gcc gct tct cgt Ala Phe Cys His 165 Glu Ser Ala Phe Gly 170 His Leu Ala Ala Ala Ser Arg 175	1007
cga tta aaa agg cga cat tca agt gga tta ccg gat gga ttt ggc caa Arg Leu Lys 180 Arg His Ser Ser Gly 185 Leu Pro Asp Gly 190 Phe Gly Gln	1055
gct gat gaa gaa gtc gaa aaa aac ggt aaa gcc ggg cga gga agt cca Ala Asp Glu 195 Glu Val Glu Lys 200 Asn Gly Lys Ala Gly 205 Arg Gly Ser Pro	1103
aga ttt gat gtg gga aga gac gcc ttt cgt tcc ggc gtt ttc ggt aaa Arg Phe 210 Asp Val Gly Arg Asp 215 Ala Phe Arg Ser 220 Gly Val Phe Gly Lys	1151
gta cac agt gaa tta caa aca gga acc tgt ttt tct cga ata gaa tat Val His Ser Glu Leu 220 Gln Thr Gly Thr Cys 235 Phe Ser Arg Ile Glu Tyr 240	1199
cgg tca aaa tgcaagtatc agtcatgaac ctttctcctc ggcatacaat Arg Ser Lys	1248
gaggagaaaag gttttttcat gtatgccgaa aaaatttccc taagctgtca tattgaaata	1308
ggacaacgtc atacactata gtgtcctgtt tttgattgat gaagaagtaa aaaattgaaa	1368
aggattggaa gtccgggagg ggatcacttg gaaaaggctcg atattttcaa ggatatcgct	1428
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acgtttatca aaaaatttat ggagctagtg gtgctccga atatcaacaa tgaagcagac	1548
cgggcgcgcg cacaagatga gctcccccaa agtgccgctg gcaaaaccat tatgacaacc	1608
tgaaccgaag tttgttccga atcaggcaat gtcagttcat gtcagtgacg gactcgatgt	1668
gaatataagg cttgtcgact gc	1690

10294.204.ST25.txt

<210> 44
 <211> 243
 <212> PRT
 <213> Bacillus licheniformis

<400> 44

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Lys Arg Leu Phe Val Pro Leu Arg Lys Lys Gly Glu Lys Gln Arg Thr
 20 25 30

Ala Ser Ala Pro Ala Gln Arg Ser Ala Gly Gly Arg Leu Leu Ile Gln
 35 40 45

Gly Gly Asp Gly Arg Ala Ser Ala Asp Ser Asp Lys Gly Tyr Gly Arg
 50 55 60

Ala Asn Leu Ser Lys Ile Pro Tyr Arg Phe Ser Gln Ala Val Pro Pro
 65 70 75 80

Val Tyr Gly Leu Ala Ala Gly His Ile Leu Leu Lys Arg Arg Arg Val
 85 90 95

Leu Val Arg Ser Cys Arg Cys Gly Lys Lys Ala Asp Gly Gln Ala His
 100 105 110

Leu Cys Lys Asn Val Gly Asn Asp Gln Gly Val Lys Ala Ser Gly Arg
 115 120 125

Asn Val Ser Arg Ser Ala Gln Val Ser Ala Val Ser Lys Ser Arg Ile
 130 135 140

Gln Glu Leu Ile His Ala Leu Pro Leu Lys Ala Arg Thr Glu Arg Gly
 145 150 155 160

Ala Phe Cys His Glu Ser Ala Phe Gly His Leu Ala Ala Ala Ser Arg
 165 170 175

Arg Leu Lys Arg Arg His Ser Ser Gly Leu Pro Asp Gly Phe Gly Gln
 180 185 190

Ala Asp Glu Glu Val Glu Lys Asn Gly Lys Ala Gly Arg Gly Ser Pro
 195 200 205

Arg Phe Asp Val Gly Arg Asp Ala Phe Arg Ser Gly Val Phe Gly Lys
 210 215 220

Val His Ser Glu Leu Gln Thr Gly Thr Cys Phe Ser Arg Ile Glu Tyr
 225 230 235 240

Arg Ser Lys

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<210> 45
<211> 1759
<212> DNA
<213> Bacillus licheniformis
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<220>
<221> CDS
<222> (476) .. (1267)

[illegible]

10294.204.ST25.txt

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Ala Ile Gly Lys Pro Glu Ser Val Pro Ala Gly Lys Tyr Ala Lys Glu				
	150	155	160	
acg ttg acg aac ctt gac gta tgg tct aaa gtg caa tct aaa gtc gtc				1006
Thr Leu Thr Asn Leu Asp Val Trp Ser Lys Val Gln Ser Lys Val Val				
	165	170	175	
tac agc aaa gat gta agg cag gtc ctt tct tat atc gaa aca ggc aac				1054
Tyr Ser Lys Asp Val Arg Gln Val Leu Ser Tyr Ile Glu Thr Gly Asn				
	180	185	190	
gcg gat gcc gga atc gtt tac cgg acg gac gcc ctt tca tca gat cag				1102
Ala Asp Ala Gly Ile Val Tyr Arg Thr Asp Ala Leu Ser Ser Asp Gln				
	195	200	205	
gtc gag acc gta gag acg gcg aaa agc gat ctg cat aca ccg att gtc				1150
Val Glu Thr Val Glu Thr Ala Lys Ser Asp Leu His Thr Pro Ile Val				
	210	215	220	225
tat ccg ctc gga att gtg aaa aat aca aag cac agg gaa cag tct gag				1198
Tyr Pro Leu Gly Ile Val Lys Asn Thr Lys His Arg Glu Gln Ser Glu				
	230	235	240	
gaa ttt tat caa ttc ctg caa agc gac caa gcc gtc aag gcg atg gaa				1246
Glu Phe Tyr Gln Phe Leu Gln Ser Asp Gln Ala Val Lys Ala Met Glu				
	245	250	255	
aag tac gga ttt aag aag ggc tgaccgccgt tatgcttgag gagttcttat				1297
Lys Tyr Gly Phe Lys Lys Gly				
	260			
cccccaattga aatttccatc caagtatcag ccgcagcggg catcatcgcc gttttgcttg				1357
gaactgctgc agcgaggctc ctggcgaaca gaaactttaa aggcaagtcc attatcgaga				1417
cggtgatgat gctgccgctc gttctgcccgc cgaccgttgt cggaattttt ttaattgtga				1477
tcttcggaag gcagagcgtg atcggacgct tgattgaaaa cgtgtttcaa gcgccggtta				1537
tttttacctg gtgggcagct gtgatcgccg cggcggttgt cgcgttcccg ttaatgtatc				1597
agtctgcaaa atccggattt ctggctgtcg accgcgacat cgaggatgca gcgaggggttg				1657
acggagcaaaa cgaatggagg gtgttcctct ttgtcaccgt tccccttgca tccaatggaa				1717
tcatgacggg gattgtgctc agctttgcga gggcgcttg cg				1759

<210> 46
 <211> 264
 <212> PRT
 <213> Bacillus licheniformis

<400> 46

Leu Lys Lys Ala Ile Leu Thr Val Ile Ala Val Leu Thr Ser Val Val
 1 5 10 15

Leu Phe Ala Gly Cys Gln Ala Glu Lys Gly Gly Ser Ala Lys Gly Gln
 20 25 30

Ser Glu Lys Val Gln Ile Thr Val Ser Ala Ala Ala Ser Leu Lys Asp
 35 40 45

10294.204.ST25.txt

Val Leu Thr Glu Leu Ser Ser Val Tyr Glu Lys Asp His Pro Asn Val
 50 55 60
 Ser Ile Lys Phe Asn Phe Gly Ser Ser Gly Ala Leu Gln Gln Gln Ile
 65 70 75 80
 Glu Gln Gly Ala Pro Ala Asp Leu Phe Phe Ser Ala Ala Glu Asp Lys
 85 90 95
 Phe Asn Arg Val Val Asp Gln Gly Leu Ile Asp Lys Lys Asp Ser Val
 100 105 110
 Lys Leu Val Glu Asn Ser Leu Val Leu Ile Val Pro Lys Gly Lys Ser
 115 120 125
 Gln His Val Asn Ser Phe Lys Asp Leu Ala Asp Asp Lys Val Glu Lys
 130 135 140
 Ile Ala Ile Gly Lys Pro Glu Ser Val Pro Ala Gly Lys Tyr Ala Lys
 145 150 155 160
 Glu Thr Leu Thr Asn Leu Asp Val Trp Ser Lys Val Gln Ser Lys Val
 165 170 175
 Val Tyr Ser Lys Asp Val Arg Gln Val Leu Ser Tyr Ile Glu Thr Gly
 180 185 190
 Asn Ala Asp Ala Gly Ile Val Tyr Arg Thr Asp Ala Leu Ser Ser Asp
 195 200 205
 Gln Val Glu Thr Val Glu Thr Ala Lys Ser Asp Leu His Thr Pro Ile
 210 215 220
 Val Tyr Pro Leu Gly Ile Val Lys Asn Thr Lys His Arg Glu Gln Ser
 225 230 235 240
 Glu Glu Phe Tyr Gln Phe Leu Gln Ser Asp Gln Ala Val Lys Ala Met
 245 250 255
 Glu Lys Tyr Gly Phe Lys Lys Gly
 260

<210> 47
 <211> 2449
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1946)

[illegible]

10294.204.ST25.txt

gtc aat ttc tct cag ccg gat tcg gac acg ctc aaa att gac ggt gta Val Asn Phe Ser Gln Pro Asp Ser Asp Thr Leu Lys Ile Asp Gly Val 205 210 215	1157
gaa gat cat aaa tcg gtc ttt gac ggc gcc gac ggc acg gta tac caa Glu Asp His Lys Ser Val Phe Asp Gly Ala Asp Gly Thr Val Tyr Gln 220 225 230 235	1205
aac gtt cag caa ttc att gac gaa gga aac tac agc tcc ggc gac aac Asn Val Gln Gln Phe Ile Asp Glu Gly Asn Tyr Ser Ser Gly Asp Asn 240 245 250	1253
cat acg atg aga gac ccg cat tat gtg gaa gac cgc ggc cat aaa tat His Thr Met Arg Asp Pro His Tyr Val Glu Asp Arg Gly His Lys Tyr 255 260 265	1301
ctc gta ttt gaa gcc aat acg gga aca aaa acc ggc tac caa gga gaa Leu Val Phe Glu Ala Asn Thr Gly Thr Lys Thr Gly Tyr Gln Gly Glu 270 275 280	1349
gac tcc cta ttc aac aga gcc tac tac ggg ggc agc aag aag ttc ttt Asp Ser Leu Phe Asn Arg Ala Tyr Tyr Gly Gly Ser Lys Lys Phe Phe 285 290 295	1397
aaa gaa gaa agc agc aag ctg ctg caa ggt gcg aac aaa aag aac gct Lys Glu Glu Ser Ser Lys Leu Leu Gln Gly Ala Asn Lys Lys Asn Ala 300 305 310 315	1445
tcg ctg gct aac ggc gct ctc gga atc atc gaa tta aat aac gat tat Ser Leu Ala Asn Gly Ala Leu Gly Ile Ile Glu Leu Asn Asn Asp Tyr 320 325 330	1493
aca ctg aaa aaa gtc atg aag cct ttg atc gcc tcc aat acg gtg aca Thr Leu Lys Lys Val Met Lys Pro Leu Ile Ala Ser Asn Thr Val Thr 335 340 345	1541
gat gaa atc gaa cgg gcc aac ctc ttc aaa atg aat gga aaa tgg tat Asp Glu Ile Glu Arg Ala Asn Leu Phe Lys Met Asn Gly Lys Trp Tyr 350 355 360	1589
ctg ttc aca gat tca aga gga tca aaa atg aca att gac ggc atc ggt Leu Phe Thr Asp Ser Arg Gly Ser Lys Met Thr Ile Asp Gly Ile Gly 365 370 375	1637
tca aaa gac att tat atg ctc ggc tat gta tca ggt tca tta acc gga Ser Lys Asp Ile Tyr Met Leu Gly Tyr Val Ser Gly Ser Leu Thr Gly 380 385 390 395	1685
cca ttc aag cct tta aac aaa tcc gga ctt gtt ttg cat atg gac cag Pro Phe Lys Pro Leu Asn Lys Ser Gly Leu Val Leu His Met Asp Gln 400 405 410	1733
gat tac aat gac atc acg ttt act tat tca cac ttt gcc gta ccg cag Asp Tyr Asn Asp Ile Thr Phe Thr Tyr Ser His Phe Ala Val Pro Gln 415 420 425	1781
aaa aaa ggc gac gaa gtc gtc att aca agc tac atc aca aac aga ggg Lys Lys Gly Asp Glu Val Val Ile Thr Ser Tyr Ile Thr Asn Arg Gly 430 435 440	1829
att tcg aac gag cat cac gcc acg ttt gca cca agc ttt ttg ctg aag Ile Ser Asn Glu His His Ala Thr Phe Ala Pro Ser Phe Leu Leu Lys 445 450 455	1877
atc aaa gga tca aaa aca tcc gtt gtc aaa aac agc atc ctt gaa cag Ile Lys Gly Ser Lys Thr Ser Val Val Lys Asn Ser Ile Leu Glu Gln 460 465 470 475	1925

10294.204.ST25.txt

gga caa cta acg gta aac aaa taaaacgaac gaaggaaaat gccggtgaac 1976
 Gly Gln Leu Thr Val Asn Lys
 480

atcggcattt tctttcgtat gtcattcttag aataaagcgg ggaattttct tgaagaaggc 2036
 agtatataag cggatcagca ttttaactgt ttgtcttgga atcttcatca tgatatttct 2096
 ttcagtccgg gaaacagaaa aaaagggaga atctccggat acaccggaat atcgtgcagc 2156
 tttccatttg acaaccctg acaaatggaa aaacgaccct caaaaaccg tctatttcaa 2216
 tggagaatat cattactact acctctataa ccgagactat ccggacggca atggaacaga 2276
 gtggcgccac gcagtatcag atgatctcgt cactggcag gataaagggg ttgccattcc 2336
 gaaatatacg aataaaaatg gcgatccctg gtccggttct gtcgttgtcg actcaaaaaa 2396
 cacagccggc ttcggcaaag ggacgatcgt ggcggttatg acgcagccgt cgg 2449

<210> 48
 <211> 482
 <212> PRT
 <213> Bacillus licheniformis
 <400> 48

Met Asn Ile Lys Asn Ile Ala Lys Lys Ala Ser Ala Leu Thr Val Ala
 1 5 10 15

Ala Ala Leu Leu Ala Gly Gly Ala Pro Gln Thr Phe Ala Lys Glu Thr
 20 25 30

Gln Asp Tyr Lys Lys Ser Tyr Gly Phe Ser His Ile Thr Arg His Asp
 35 40 45

Met Leu Lys Ile Pro Glu Gln Gln Lys Ser Glu Gln Phe Lys Val Pro
 50 55 60

Gln Phe Asp Pro Lys Thr Ile Lys Asn Ile Pro Ser Ala Lys Gly Tyr
 65 70 75 80

Asn Lys Asn Gly Glu Leu Ile Asp Leu Asp Val Trp Asp Ser Trp Pro
 85 90 95

Leu Gln Asn Ala Asp Gly Thr Val Ala Thr Tyr His Gly Tyr Asn Leu
 100 105 110

Val Phe Ala Leu Ala Gly Asp Pro Lys Asp Val Asp Asp Thr Ser Ile
 115 120 125

Tyr Leu Phe Tyr Gln Lys Lys Gly Glu Thr Ser Ile Asp Ser Trp Lys
 130 135 140

Asn Ala Gly Arg Val Phe Lys Asp Ser Asp Lys Phe Val Pro Asp Asp
 145 150 155 160

10294.204.ST25.txt

Pro Tyr Leu Lys His Gln Thr Gln Glu Trp Ser Gly Ser Ala Thr Leu
 165 170 175

Thr Lys Asp Gly Lys Val Arg Leu Phe Tyr Thr Ala Phe Ser Gly Thr
 180 185 190

Gln Tyr Gly Lys Gln Thr Leu Thr Thr Ala Gln Val Asn Phe Ser Gln
 195 200 205

Pro Asp Ser Asp Thr Leu Lys Ile Asp Gly Val Glu Asp His Lys Ser
 210 215 220

Val Phe Asp Gly Ala Asp Gly Thr Val Tyr Gln Asn Val Gln Gln Phe
 225 230 235 240

Ile Asp Glu Gly Asn Tyr Ser Ser Gly Asp Asn His Thr Met Arg Asp
 245 250 255

Pro His Tyr Val Glu Asp Arg Gly His Lys Tyr Leu Val Phe Glu Ala
 260 265 270

Asn Thr Gly Thr Lys Thr Gly Tyr Gln Gly Glu Asp Ser Leu Phe Asn
 275 280 285

Arg Ala Tyr Tyr Gly Gly Ser Lys Lys Phe Phe Lys Glu Glu Ser Ser
 290 295 300

Lys Leu Leu Gln Gly Ala Asn Lys Lys Asn Ala Ser Leu Ala Asn Gly
 305 310 315 320

Ala Leu Gly Ile Ile Glu Leu Asn Asn Asp Tyr Thr Leu Lys Lys Val
 325 330 335

Met Lys Pro Leu Ile Ala Ser Asn Thr Val Thr Asp Glu Ile Glu Arg
 340 345 350

Ala Asn Leu Phe Lys Met Asn Gly Lys Trp Tyr Leu Phe Thr Asp Ser
 355 360 365

Arg Gly Ser Lys Met Thr Ile Asp Gly Ile Gly Ser Lys Asp Ile Tyr
 370 375 380

Met Leu Gly Tyr Val Ser Gly Ser Leu Thr Gly Pro Phe Lys Pro Leu
 385 390 395 400

Asn Lys Ser Gly Leu Val Leu His Met Asp Gln Asp Tyr Asn Asp Ile
 405 410 415

Thr Phe Thr Tyr Ser His Phe Ala Val Pro Gln Lys Lys Gly Asp Glu
 420 425 430

10294.204.ST25.txt

Val Val Ile Thr Ser Tyr Ile Thr Asn Arg Gly Ile Ser Asn Glu His
 435 440 445

His Ala Thr Phe Ala Pro Ser Phe Leu Leu Lys Ile Lys Gly Ser Lys
 450 455 460

Thr Ser Val Val Lys Asn Ser Ile Leu Glu Gln Gly Gln Leu Thr Val
 465 470 475 480

Asn Lys

<210> 49
 <211> 1669
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (488)..(1168)

<400> 49
 gcaagaggcg gagagaaaaa acaagtcaag atcgagacc agatcgaata taaaaacggc 60
 acattgatga cggcttttaa agatcacgag ctcccaggag agaaaatcga ccagtataca 120
 gcgcaaaagc tgcaaaaact gctcagaaaa gttgtcacat ctgaaaaggg gacgggccgg 180
 cgcttcagcg atcttccgta cgatgtagcg ggaaaatcgg gcacagcgca gacaggcagg 240
 acgacagatg acaaaaaaac gctctatcat aaatggtttg ccggttattt tccggcggac 300
 aagccgaaat atgcgctcgt cgtcgtccat atggatacgc cggatagcaa ggctgcgaca 360
 aatgccgtat tttatgatat tgtaaaaaa gtatatgaaa ttgaaaagaa ccagacatag 420
 aagaatgcct caggtgatga taaaatagga agcgaggcaa gagggaaaaa ggagtgaat 480
 gaacttg agc gaa aca agg gaa tct cgt ttt gaa aat cgt gat aag cgc 529
 Ser Glu Thr Arg Glu Ser Arg Phe Glu Asn Arg Asp Lys Arg
 1 5 10
 agg aaa gcg aat ctt gtg ctt aac att tta ata ggc atc gta ttg gta 577
 Arg Lys Ala Asn Leu Val Leu Asn Ile Leu Ile Gly Ile Val Leu Val
 15 20 25 30
 tta atc gtt gtc gtt gcc agc agt ctg atg atg aac agt ccg aag gag 625
 Leu Ile Val Val Val Ala Ser Ser Leu Met Met Asn Ser Pro Lys Glu
 35 40 45
 cag gcg cag caa gat gtc tcg aaa aac gat tct gaa cag acg aca gaa 673
 Gln Ala Gln Gln Asp Val Ser Lys Asn Asp Ser Glu Gln Thr Thr Glu
 50 55 60
 gcg cct gct tcc gac aat aag aaa caa aca tct gat gaa gat gta aaa 721
 Ala Pro Ala Ser Asp Asn Lys Lys Gln Thr Ser Asp Glu Asp Val Lys
 65 70 75
 gat gag gac aaa gga aaa agc gat tct gcc gat aaa gaa gac agc gat 769
 Asp Glu Asp Lys Gly Lys Ser Asp Ser Ala Asp Lys Glu Asp Ser Asp
 80 85 90

10294.204.ST25.txt

tcc gac tca gac aag gat aaa gaa tct gct tca gac gag gac aag tca 817
 Ser Asp Ser Asp Lys Asp Lys Glu Ser Ala Ser Asp Glu Asp Lys Ser 110
 95 100 105
 aca tca gat gat ccg ttt gaa gga gcc gaa gtg aca gaa ggc ggt tca 865
 Thr Ser Asp Asp Pro Phe Glu Gly Ala Glu Val Thr Glu Gly Gly Ser 125
 115 120
 agc gcc aat gtt gaa aaa acg atc atc aat cct gac tgg gag cct gtc 913
 Ser Ala Asn Val Glu Lys Thr Ile Ile Asn Pro Asp Trp Glu Pro Val 140
 130 135
 ggc aca caa cag agc gga cag cat acc gca aca tat gat tcc tct tca 961
 Gly Thr Gln Gln Ser Gly Gln His Thr Ala Thr Tyr Asp Ser Ser Ser 155
 145 150
 caa gac tgg aag gaa atg ctt gaa gcc att tca tat gcg aca ggg gtt 1009
 Gln Asp Trp Lys Glu Met Leu Glu Ala Ile Ser Tyr Ala Thr Gly Val 170
 160 165
 tct aag gat aac atg acg gtg atc tgg ctc gga aac aac ggc agc ccg 1057
 Ser Lys Asp Asn Met Thr Val Ile Trp Leu Gly Asn Asn Gly Ser Pro 190
 175 180 185
 caa gat gcg aaa gga acc att cgg gcg aag gac act ggc gtc aaa tac 1105
 Gln Asp Ala Lys Gly Thr Ile Arg Ala Lys Asp Thr Gly Val Lys Tyr 205
 195 200
 cag gta gcc att act tgg gtt gac gga aaa ggc tgg aag ccg aca aaa 1153
 Gln Val Ala Ile Thr Trp Val Asp Gly Lys Gly Trp Lys Pro Thr Lys 220
 210 215
 gtt gaa caa ttg aaa taaagaaaa agcggccggt tgctaaaacc gggcgctttt 1208
 Val Glu Gln Leu Lys 225
 tttatgattc ggcttttaaaa tgaacgactg cgctgtagtg gatccgtccg tcaataaccg 1268
 ccgtatggtg ggaaaccgaa tggaccctca gcaaaatcgc ctggttggtt tcaatctgct 1328
 gactgatctt tttttcaagc tcctctaagc tcagtgcctc aaaaaactca attttatctt 1388
 tgatcagatc gagggccgaag ttcataaacc aatcctccat tcgtttcaag tcatttttta 1448
 ttaaagcaga gaagcggccg ggtgacaagg gaaatataac caagcctttt ttgtacccaa 1508
 aacgaatgac ttgtggtagg ataagaacta atcaatcgaa taaatcatac tatacttata 1568
 ggaattgtaa aaatagatgg agagtgcga caaatggga agagagttca ttcctttatt 1628
 tgagaactgg gcaaatctt atgatgatac agtagttggc c 1669

<210> 50
 <211> 227
 <212> PRT
 <213> Bacillus licheniformis

<400> 50

Ser Glu Thr Arg Glu Ser Arg Phe Glu Asn Arg Asp Lys Arg Arg Lys
 1 5 10 15

Ala Asn Leu Val Leu Asn Ile Leu Ile Gly Ile Val Leu Val Leu Ile
 20 25 30

10294.204.ST25.txt

Val Val Val Ala Ser Ser Leu Met Met Asn Ser Pro Lys Glu Gln Ala
 35 40 45

Gln Gln Asp Val Ser Lys Asn Asp Ser Glu Gln Thr Thr Glu Ala Pro
 50 55 60

Ala Ser Asp Asn Lys Lys Gln Thr Ser Asp Glu Asp Val Lys Asp Glu
 65 70 75 80

Asp Lys Gly Lys Ser Asp Ser Ala Asp Lys Glu Asp Ser Asp Ser Asp
 85 90 95

Ser Asp Lys Asp Lys Glu Ser Ala Ser Asp Glu Asp Lys Ser Thr Ser
 100 105 110

Asp Asp Pro Phe Glu Gly Ala Glu Val Thr Glu Gly Gly Ser Ser Ala
 115 120 125

Asn Val Glu Lys Thr Ile Ile Asn Pro Asp Trp Glu Pro Val Gly Thr
 130 135 140

Gln Gln Ser Gly Gln His Thr Ala Thr Tyr Asp Ser Ser Ser Gln Asp
 145 150 155 160

Trp Lys Glu Met Leu Glu Ala Ile Ser Tyr Ala Thr Gly Val Ser Lys
 165 170 175

Asp Asn Met Thr Val Ile Trp Leu Gly Asn Asn Gly Ser Pro Gln Asp
 180 185 190

Ala Lys Gly Thr Ile Arg Ala Lys Asp Thr Gly Val Lys Tyr Gln Val
 195 200 205

Ala Ile Thr Trp Val Asp Gly Lys Gly Trp Lys Pro Thr Lys Val Glu
 210 215 220

Gln Leu Lys
 225

<210> 51
 <211> 1700
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (437)..(1213)

<400> 51
 tccccgggttt actgagatgt gctcgccgtt ttctgcaccg gtgcgtacgg ctacagcatg 60
 gccacaact acaaccgcat tccgcgccc gccgtcgtct ttgtcgagga cggggaagcg 120
 cagctcgtca ttcagagaga gacgtatgag gatatcgtca agctggatct gccgctgaaa 180

10294.204.ST25.txt

tcgaaagtca aacaataaaaa aaatggagat tccctaagag ggggggtctcc aattttaatt	240
caagcacgaa aaacacttcc cggtgatcgg gaggtgtttt ttgttaaaaa gatcatgaca	300
tgcatagaac agcgaccggg ctaattgtat ataatatcgt gaatttaaca aaaaatttac	360
aaaggagatg ataaaggcga tgaccagggg gaaaaggatg agaattgctg atttggttga	420
tttagaggcg gagtag atg aaa ccg gcc aaa gta tcc cta ctc cac cga ttg	472
Met Lys Pro Ala Lys Val Ser Leu Leu His Arg Leu	
1 5 10	
ctc cag tgc ctg aag caa tgt gtc gat tgt tac aca gta gat cgt gtg	520
Leu Gln Cys Leu Lys Gln Cys Val Asp Cys Tyr Thr Val Asp Arg Val	
15 20 25	
aca gca ata aac att ttt gtg aat att tta ttg att tcg gct gtg atc	568
Thr Ala Ile Asn Ile Phe Val Asn Ile Leu Leu Ile Ser Ala Val Ile	
30 35 40	
tca ttc cca tat tct gct gcg gcc cat ggc gca aca cag tcc ggc gat	616
Ser Phe Pro Tyr Ser Ala Ala Ala His Gly Ala Thr Gln Ser Gly Asp	
45 50 55 60	
caa tat tca gct ttt gaa gaa ttg gag cgg aat gaa gat cca gct tct	664
Gln Tyr Ser Ala Phe Glu Glu Leu Glu Arg Asn Glu Asp Pro Ala Ser	
65 70 75	
tac cga att acg gag aag aac gca aga gtg ccg atg ctc atc atg gcc	712
Tyr Arg Ile Thr Glu Lys Asn Ala Arg Val Pro Met Leu Ile Met Ala	
80 85 90	
atc cat gga ggc ggc atc gaa ccc gga acg agc gaa atc gcc aat gaa	760
Ile His Gly Gly Gly Ile Glu Pro Gly Thr Ser Glu Ile Ala Asn Glu	
95 100 105	
gtg tcc aaa aac tat tcc ctg tac ttg ttt gaa ggg ctg aaa tca tca	808
Val Ser Lys Asn Tyr Ser Leu Tyr Leu Phe Glu Gly Leu Lys Ser Ser	
110 115 120	
ggc aat acg gac ctt cac att aca agc acg cgt ttt gac gag cca gcg	856
Gly Asn Thr Asp Leu His Ile Thr Ser Thr Arg Phe Asp Glu Pro Ala	
125 130 135 140	
gcg ctc gca att act gca agc cac cag tat gtc atg tcg ctc cac ggc	904
Ala Leu Ala Ile Thr Ala Ser His Gln Tyr Val Met Ser Leu His Gly	
145 150 155	
tat tac agt gaa gac cgc gat att aaa gta ggc ggc aca gac cgc gct	952
Tyr Tyr Ser Glu Asp Arg Asp Ile Lys Val Gly Gly Thr Asp Arg Ala	
160 165 170	
aaa atc aga ata ttg gtt gat gag ctg aac cgc tcg ggg ttt gcc gct	1000
Lys Ile Arg Ile Leu Val Asp Glu Leu Asn Arg Ser Gly Phe Ala Ala	
175 180 185	
gaa atg ctg ggg aca gat gac aag tat gcc gga acc cat ccg aat aac	1048
Glu Met Leu Gly Thr Asp Asp Lys Tyr Ala Gly Thr His Pro Asn Asn	
190 195 200	
atc gcc aac aag tcg ctt tcc ggg ctg agc att cag ctt gaa atg agc	1096
Ile Ala Asn Lys Ser Leu Ser Gly Leu Ser Ile Gln Leu Glu Met Ser	
205 210 215 220	
acg ggt ttc cgc aaa tct tta ttc gac cgg ttt aca cta aaa gac agg	1144
Thr Gly Phe Arg Lys Ser Leu Phe Asp Arg Phe Thr Leu Lys Asp Arg	
225 230 235	

10294.204.ST25.txt

gcg gcg acg caa aac gaa acg ttt tac cga ttt aca aag ctg ctg aca 1192
 Ala Ala Thr Gln Asn Glu Thr Phe Tyr Arg Phe Thr Lys Leu Leu Thr
 240 245 250

gat ttt att cat gaa aac tat gaagaagacg gaggggattt cccctctgca 1243
 Asp Phe Ile His Glu Asn Tyr
 255

aaaataaaac acccccttca agtgtgaact gacccgttaa aatgagactt agaaaaaaca 1303

cctatgctgc ctgtcccctg tattccagtg gggacaggta gtttaatttt gcctgaattc 1363

gtacatgatt atatcgatac atgtattgat ttacaatttg tactacttta gaattggata 1423

tagatgctct actttgagcg ttaaatacctt ccgacttttag cgaggagtga aaggattcaa 1483

tgacggcatt atcatggcag tttccttttc gagacatgct tgttggaatg cctttttctt 1543

tggccaaatt ctgatatgca tgtgaagtat agacagatcc ctggtcgcta tgaagaagaa 1603

ccctactggg ttacgtaatt ctaacagctt ccctcaatgt gtctaatact aggttaaata 1663

tctggctcgt acctattttg taagcactat ttgtgtt 1700

<210> 52
 <211> 259
 <212> PRT
 <213> Bacillus licheniformis

<400> 52

Met Lys Pro Ala Lys Val Ser Leu Leu His Arg Leu Leu Gln Cys Leu
 1 5 10 15

Lys Gln Cys Val Asp Cys Tyr Thr Val Asp Arg Val Thr Ala Ile Asn
 20 25 30

Ile Phe Val Asn Ile Leu Leu Ile Ser Ala Val Ile Ser Phe Pro Tyr
 35 40 45

Ser Ala Ala Ala His Gly Ala Thr Gln Ser Gly Asp Gln Tyr Ser Ala
 50 55 60

Phe Glu Glu Leu Glu Arg Asn Glu Asp Pro Ala Ser Tyr Arg Ile Thr
 65 70 75 80

Glu Lys Asn Ala Arg Val Pro Met Leu Ile Met Ala Ile His Gly Gly
 85 90 95

Gly Ile Glu Pro Gly Thr Ser Glu Ile Ala Asn Glu Val Ser Lys Asn
 100 105 110

Tyr Ser Leu Tyr Leu Phe Glu Gly Leu Lys Ser Ser Gly Asn Thr Asp
 115 120 125

Leu His Ile Thr Ser Thr Arg Phe Asp Glu Pro Ala Ala Leu Ala Ile
 130 135 140

10294.204.ST25.txt

Thr Ala Ser His Gln Tyr Val Met Ser Leu His Gly Tyr Tyr Ser Glu
 145 150 155 160

Asp Arg Asp Ile Lys Val Gly Gly Thr Asp Arg Ala Lys Ile Arg Ile
 165 170 175

Leu Val Asp Glu Leu Asn Arg Ser Gly Phe Ala Ala Glu Met Leu Gly
 180 185 190

Thr Asp Asp Lys Tyr Ala Gly Thr His Pro Asn Asn Ile Ala Asn Lys
 195 200 205

Ser Leu Ser Gly Leu Ser Ile Gln Leu Glu Met Ser Thr Gly Phe Arg
 210 215 220

Lys Ser Leu Phe Asp Arg Phe Thr Leu Lys Asp Arg Ala Ala Thr Gln
 225 230 235 240

Asn Glu Thr Phe Tyr Arg Phe Thr Lys Leu Leu Thr Asp Phe Ile His
 245 250 255

Glu Asn Tyr

<210> 53
 <211> 1519
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (472)..(1026)

<400> 53
 cggaatgatg gagcctccat ctttttcaaa aaacagaaag cgcaagtaaa ccaagtcaaa 60
 cgcgacaaat ataatcaaaa acagctgaat cgaattccac aaagaatgag atctgaaaat 120
 ttccagtgc aagcgggtgaa tcgttaagaa aatcacaaat cccatttgag caatcacgct 180
 aaagatcatg ccaaccccgaa taaaccagaa aagaacagac agaattctca atacctcgaa 240
 ggaaagaaac agctccttat atcttcccca ctctatggca aaaccgacaa tacttgtagt 300
 caaagctccg acaccaata cggaaaagaa aaatcggacg agattacggc ttttcattgt 360
 agacttccca acccctaaat aaaccgctgt aacagcgata ttttgttatg tataaatttt 420
 taaaagacat tcatattaaa ggtaagacga gttttcgaaa ggagcttaag c atg ttc 477
 Met Phe
 1

aag acc gca atg cta tcg ata agc tgt ttt ctg ttt cta tct gta aca 525
 Lys Thr Ala Met Leu Ser Ile Ser Cys Phe Leu Phe Leu Ser Val Thr
 5 10 15

gct tgt gct ccc acg gac caa gca gct gag atg gac tat gat caa acc 573
 Ala Cys Ala Pro Thr Asp Gln Ala Ala Glu Met Asp Tyr Asp Gln Thr

10294.204.ST25.txt
30

20 25 30

aaa aaa atg gtt gtc gat ata tta aag aca gat gac gga aaa aaa gcg 621
Lys Lys Met Val Val Asp Ile Leu Lys Thr Asp Asp Gly Lys Lys Ala
35 40 45 50

att caa gaa ata tta aat gat gac aaa tta aat gaa aca ctt gta atg 669
Ile Gln Glu Ile Leu Asn Asp Asp Lys Leu Asn Glu Thr Leu Val Met
55 60 65

gat gaa aaa act gtc aaa gaa acc gtt gaa aaa aca atg acc tcc aaa 717
Asp Glu Lys Thr Val Lys Glu Thr Val Glu Lys Thr Met Thr Ser Lys
70 75 80

aaa gga gct gaa ttt tgg aaa aaa gtc ttt gaa gat cca aaa ttc gct 765
Lys Gly Ala Glu Phe Trp Lys Lys Val Phe Glu Asp Pro Lys Phe Ala
85 90 95

gaa ggc ttt gcc aaa aca ctt caa aat gaa cat gaa aaa gtg ctg aaa 813
Glu Gly Phe Ala Lys Thr Leu Gln Asn Glu His Glu Lys Val Leu Lys
100 105 110

aaa ctg atg aaa gat cct gag tac caa aaa atg ctg atg cag gtc atg 861
Lys Leu Met Lys Asp Pro Glu Tyr Gln Lys Met Leu Met Gln Val Met
115 120 125 130

cag gat cct gaa atg gcc aaa aaa tac ggt gaa ctt gtc aga agc cag 909
Gln Asp Pro Glu Met Ala Lys Lys Tyr Gly Glu Leu Val Arg Ser Gln
135 140 145

gaa ttc cga agc cac ctg cag gaa gtc ata tct gac act ctg aca agc 957
Glu Phe Arg Ser His Leu Gln Glu Val Ile Ser Asp Thr Leu Thr Ser
150 155 160

cct ctt tac aga aag cag ttt gaa gag gaa ctg aaa aaa gct gct gct 1005
Pro Leu Tyr Arg Lys Gln Phe Glu Glu Glu Leu Lys Lys Ala Ala Ala
165 170 175

gaa agc atg aaa gaa gaa atg aaaggcggcg aagaaaaaca aagctgagcc 1056
Glu Ser Met Lys Glu Glu Met
180 185

gctttttcatt ccctaaaagc ttcttctgcg gaggaagctt tttttgctct ttaagctttt 1116

gcgccaatgc tttcgtcgat ttttttggcg atatccaaat aaatggcgcc ggtcgggtgg 1176

ctttcatcat aaacggacgg cgcaaattcg ctgtcatccc aatccggctg cttcagcgga 1236

attttgccca gaattggaac gcctagtgtcc tctgcgagct tttcgcttcc gcctttgccg 1296

aatacatatt ctttctcgcc tgttttgacg ctttcgtaat aagccatatt ttcaacgata 1356

cccacgattt catgatcggc cttcaaggcc atcgcgcccg ctcttgagc gacaaacggc 1416

gcagtagggg gcggcgctga cagatcacc tctttgcagc ttggaagcat tgagtgaaca 1476

tcaagcgcta catcgctgt tcccggcggc aggtctaaga taa 1519

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 <212> PRT
 <213> Bacillus licheniformis

<400> 54

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1 5 10 15

10294.204.ST25.txt

Val Thr Ala Cys Ala Pro Thr Asp Gln Ala Ala Glu Met Asp Tyr Asp
20 25 30

Gln Thr Lys Lys Met Val Val Asp Ile Leu Lys Thr Asp Asp Gly Lys
35 40 45

Lys Ala Ile Gln Glu Ile Leu Asn Asp Asp Lys Leu Asn Glu Thr Leu
50 55 60

Val Met Asp Glu Lys Thr Val Lys Glu Thr Val Glu Lys Thr Met Thr
65 70 75 80

Ser Lys Lys Gly Ala Glu Phe Trp Lys Lys Val Phe Glu Asp Pro Lys
85 90 95

Phe Ala Glu Gly Phe Ala Lys Thr Leu Gln Asn Glu His Glu Lys Val
100 105 110

Leu Lys Lys Leu Met Lys Asp Pro Glu Tyr Gln Lys Met Leu Met Gln
115 120 125

Val Met Gln Asp Pro Glu Met Ala Lys Lys Tyr Gly Glu Leu Val Arg
130 135 140

Ser Gln Glu Phe Arg Ser His Leu Gln Glu Val Ile Ser Asp Thr Leu
145 150 155 160

Thr Ser Pro Leu Tyr Arg Lys Gln Phe Glu Glu Glu Leu Lys Lys Ala
165 170 175

Ala Ala Glu Ser Met Lys Glu Glu Met
180 185

<210> 55
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<212> DNA
<213> Bacillus licheniformis

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<222> (501)..(1901)

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gtggaggctc tggggattga tgatgatcat cgtgcctttt tccgcggtat agacgctttg 300
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atgcgggcgcg	ttcatctcgcg	taaataccttt	tctctgcata	tattgaatcg	aaaaagaatg	420										
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taacaaacgg	gagggatcgt	atg	aaa	aag	tta	tgt	tgc	ctg	atc	ttg	gtc	ttg	533			
		Met	Lys	Lys	Leu	Cys	Cys	Leu	Ile	Leu	Val	Leu				
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gtt	ttt	tcc	gcg	ggc	tgt	act	cag	caa	aag	gca	tca	acg	gaa	gag	gac	581
Val	Phe	Ser	Ala	Gly	Cys	Thr	Gln	Gln	Lys	Ala	Ser	Thr	Glu	Glu	Asp	
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Gly	Ala	Leu	Glu	Ile	Asn	Trp	Leu	Val	Pro	Leu	His	Thr	Pro	Gln	Pro	
		30					35					40				
ccg	aaa	gag	aag	gcg	ctt	gac	atc	att	gaa	gac	aaa	acg	aat	aca	aag	677
Pro	Lys	Glu	Lys	Ala	Leu	Asp	Ile	Ile	Glu	Asp	Lys	Thr	Asn	Thr	Lys	
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ctg	aag	ctc	atc	tgg	gtt	ccg	gat	tca	aca	aaa	gaa	gag	cgg	atc	aat	725
Leu	Lys	Leu	Ile	Trp	Val	Pro	Asp	Ser	Thr	Lys	Glu	Glu	Arg	Ile	Asn	
60					65					70					75	
aca	acc	ctt	gca	agc	gga	aac	atg	cct	aaa	gta	atg	aca	ttg	cct	gat	773
Thr	Thr	Leu	Ala	Ser	Gly	Asn	Met	Pro	Lys	Val	Met	Thr	Leu	Pro	Asp	
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ctt	gaa	gat	tca	gcg	gtt	gtc	agc	gcg	ctg	cg	tcg	gga	atg	ttc	tgg	821
Leu	Glu	Asp	Ser	Ala	Val	Val	Ser	Ala	Leu	Arg	Ser	Gly	Met	Phe	Trp	
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gaa	atc	gga	ccg	tat	ttc	aaa	gac	tat	ccg	aat	tta	aga	aaa	ctt	gat	869
Glu	Ile	Gly	Pro	Tyr	Phe	Lys	Asp	Tyr	Pro	Asn	Leu	Arg	Lys	Leu	Asp	
		110					115					120				
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Lys	Thr	Ile	Leu	Lys	Asn	Ile	Ser	Val	Asp	Gly	Lys	Val	Tyr	Gly	Ile	
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tat	aga	gaa	agg	ccg	atg	gcc	agg	cag	gga	gtc	gtg	att	cg	aaa	gac	965
Tyr	Arg	Glu	Arg	Pro	Met	Ala	Arg	Gln	Gly	Val	Val	Ile	Arg	Lys	Asp	
140					145					150					155	
tgg	ctc	gac	aat	ctc	gga	ttg	gaa	atg	ccg	gaa	acc	gtt	gat	gac	ctt	1013
Trp	Leu	Asp	Asn	Leu	Gly	Leu	Glu	Met	Pro	Glu	Thr	Val	Asp	Asp	Leu	
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tat	aaa	ata	gcg	aaa	gca	ttt	aca	gaa	cag	gac	ccc	gat	caa	aac	gga	1061
Tyr	Lys	Ile	Ala	Lys	Ala	Phe	Thr	Glu	Gln	Asp	Pro	Asp	Gln	Asn	Gly	
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10294.204.ST25.txt

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att cag ggg aaa gcg gga atc tat atc ggc gcg atg agc gat gcc atg 1349
 Ile Gln Gly Lys Ala Gly Ile Tyr Ile Gly Ala Met Ser Asp Ala Met 280
 270

aac ttg cgt gat cag gga ctc gct ttg aac ccc ggc ttt cag ctt gat 1397
 Asn Leu Arg Asp Gln Gly Leu Ala Leu Asn Pro Gly Phe Gln Leu Asp 295
 285

atc gca aac cgg atc aag ggc ccc gac ggc aag gag cgc aca tgg gcg 1445
 Ile Ala Asn Arg Ile Lys Gly Pro Asp Gly Lys Glu Arg Thr Trp Ala 315
 300

ctc ggc ggg cat ggc ggg atg ttc gcc att tcg aaa tca agc gtc aag 1493
 Leu Gly Gly His Gly Gly Met Phe Ala Ile Ser Lys Ser Ser Val Lys 330
 320

act gaa aaa gag gtc aga aaa atc ctc gca ttt ttt gac aga atc gct 1541
 Thr Glu Lys Glu Val Arg Lys Ile Leu Ala Phe Phe Asp Arg Ile Ala 345
 335

gaa gaa gac ctc aac aat ttg atg ttg tat gga ata gaa ggc gta cac 1589
 Glu Glu Asp Leu Asn Asn Leu Met Leu Tyr Gly Ile Glu Gly Val His 360
 350

tat gaa aag aaa ggg ggg agc ggc tat ttt cga aag cag gaa aac tac 1637
 Tyr Glu Lys Lys Gly Gly Ser Gly Tyr Phe Arg Lys Gln Glu Asn Tyr 375
 365

cat ctg tgg gaa gcg gaa att cag ccg tta aac cag ctg att ggc gtc 1685
 His Leu Trp Glu Ala Glu Ile Gln Pro Leu Asn Gln Leu Ile Gly Val 395
 380

aat aaa caa gct tta aaa agc gct gaa gat ccg ctc cgc gcc aaa aat 1733
 Asn Lys Gln Ala Leu Lys Ser Ala Glu Asp Pro Leu Arg Ala Lys Asn 410
 400

gaa aag ctt gag gag gac aac cgg gca atc gca gtc cag aat ccg gcc 1781
 Glu Lys Leu Glu Glu Asp Asn Arg Ala Ile Ala Val Gln Asn Pro Ala 425
 415

gaa ccg ctg tat tct gcc gca cag atg gac agg gga aca gaa ttg aag 1829
 Glu Pro Leu Tyr Ser Ala Ala Gln Met Asp Arg Gly Thr Glu Leu Lys 440
 430

aaa atc att gat gac gcc aca ttt caa ttt att ctc ggg gaa atc aat 1877
 Lys Ile Ile Asp Asp Ala Thr Phe Gln Phe Ile Leu Gly Glu Ile Asn 455
 445

gaa aaa gct ttg acc agg cag tcc tgaaatggga gaagcatggc ggcggaaaga 1931
 Glu Lys Ala Leu Thr Arg Gln Ser 465

tcatgaaaga actgaatgaa gatctgaaaa aagcaaacta aacagaaaac cctttccatt 1991

tttttgaaaa ggaaagggtt tttcatcgta ttcgctccaa gttcattttc tttaaattct 2051

gcaaaataaa caatataatt ccatcatagg acgaaaagga ggaagcgata tgcagactgc 2111

cgttatatat gcacacccaa atccaaacag tttcaacgga gccattttta atcaagtcatt 2171

aaaggcgctt gaggacggtg agcattttta tgacgtcatt gatttgtata gagaccggtt 2231

tgatcccgtt ctattatttg atgaaaagaa aaggcgctca gatatgaatc gcgatccgga 2291

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 <212> PRT
 <213> Bacillus licheniformis

<400> 56

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 35 40 45

Leu Asp Ile Ile Glu Asp Lys Thr Asn Thr Lys Leu Lys Leu Ile Trp
 50 55 60

Val Pro Asp Ser Thr Lys Glu Glu Arg Ile Asn Thr Thr Leu Ala Ser
 65 70 75 80

Gly Asn Met Pro Lys Val Met Thr Leu Pro Asp Leu Glu Asp Ser Ala
 85 90 95

Val Val Ser Ala Leu Arg Ser Gly Met Phe Trp Glu Ile Gly Pro Tyr
 100 105 110

Phe Lys Asp Tyr Pro Asn Leu Arg Lys Leu Asp Lys Thr Ile Leu Lys
 115 120 125

Asn Ile Ser Val Asp Gly Lys Val Tyr Gly Ile Tyr Arg Glu Arg Pro
 130 135 140

Met Ala Arg Gln Gly Val Val Ile Arg Lys Asp Trp Leu Asp Asn Leu
 145 150 155 160

Gly Leu Glu Met Pro Glu Thr Val Asp Asp Leu Tyr Lys Ile Ala Lys
 165 170 175

Ala Phe Thr Glu Gln Asp Pro Asp Gln Asn Gly Lys Asp Asp Thr Phe
 180 185 190

Gly Leu Ala Asp Arg Asn Asp Leu Thr Phe Gly Ala Phe Lys Thr Leu
 195 200 205

Ala Ser Tyr Phe Gly Ala Pro Asn Glu Trp Gly Thr Asp Glu Asp Gly
 210 215 220

10294.204.ST25.txt

Asn Leu Phe Pro Tyr Phe Lys His Glu Ala Tyr Lys Asp Ala Met Ala
 225 230 235 240
 Tyr Met Lys Lys Leu Tyr Glu Glu Gly Leu Met Asn Arg Asp Phe Ala
 245 250 255
 Val Thr Ser Lys Thr Gln Gln Gln Asp Leu Val Ile Gln Gly Lys Ala
 260 265 270
 Gly Ile Tyr Ile Gly Ala Met Ser Asp Ala Met Asn Leu Arg Asp Gln
 275 280 285
 Gly Leu Ala Leu Asn Pro Gly Phe Gln Leu Asp Ile Ala Asn Arg Ile
 290 295 300
 Lys Gly Pro Asp Gly Lys Glu Arg Thr Trp Ala Leu Gly Gly His Gly
 305 310 315 320
 Gly Met Phe Ala Ile Ser Lys Ser Ser Val Lys Thr Glu Lys Glu Val
 325 330 335
 Arg Lys Ile Leu Ala Phe Phe Asp Arg Ile Ala Glu Glu Asp Leu Asn
 340 345 350
 Asn Leu Met Leu Tyr Gly Ile Glu Gly Val His Tyr Glu Lys Lys Gly
 355 360 365
 Gly Ser Gly Tyr Phe Arg Lys Gln Glu Asn Tyr His Leu Trp Glu Ala
 370 375 380
 Glu Ile Gln Pro Leu Asn Gln Leu Ile Gly Val Asn Lys Gln Ala Leu
 385 390 395 400
 Lys Ser Ala Glu Asp Pro Leu Arg Ala Lys Asn Glu Lys Leu Glu Glu
 405 410 415
 Asp Asn Arg Ala Ile Ala Val Gln Asn Pro Ala Glu Pro Leu Tyr Ser
 420 425 430
 Ala Ala Gln Met Asp Arg Gly Thr Glu Leu Lys Lys Ile Ile Asp Asp
 435 440 445
 Ala Thr Phe Gln Phe Ile Leu Gly Glu Ile Asn Glu Lys Ala Leu Thr
 450 455 460
 Arg Gln Ser
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<210> 57
 <211> 1589
 <212> DNA

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<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1388)

<400> 57

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cagcagggtgc ctgaagatct gattgaagct acagaagcat ttggttcaac gacaagccag      240
cggctcttta aagtgcagct gccgctcgcg acgaaaacca ttctggccgg tatcaatcaa      300
agcatcatgc ttgctttgtc aatggtcggt attgcatcaa tggtaggcgc gcccggactc      360
ggagaagaag tttaccgggc tgtgaccag ctgcaaacgg gtaccgggtgt agaaaccgga      420
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gcg gta ctc aca ttg ggt ctg gct gcc tgc gga agc agc aat aat aat      581
Ala Val Leu Thr Leu Gly Leu Ala Ala Cys Gly Ser Ser Asn Asn Asn
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gaa aat gcg tca gta ggc gat caa gtc aat tat aaa att acc ggc att      629
Glu Asn Ala Ser Val Gly Asp Gln Val Asn Tyr Lys Ile Thr Gly Ile
                        30          35          40

gat cct gga gcg ggc att atg aat gcg acg gac cag gcg ctc aag gac      677
Asp Pro Gly Ala Gly Ile Met Asn Ala Thr Asp Gln Ala Leu Lys Asp
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tac gat ctc agc aag tgg act gta acg tca gga tca agc tca gca atg      725
Tyr Asp Leu Ser Lys Trp Thr Val Thr Ser Gly Ser Ser Ser Ala Met
                        60          65          70          75

aca gcc gca ttg aaa aaa gct tat gac aaa aaa gat ccg atc atc att      773
Thr Ala Ala Leu Lys Lys Ala Tyr Asp Lys Lys Asp Pro Ile Ile Ile
                        80          85          90

acg ggc tgg acg ccg cat tgg atg ttt gca aaa tac gat ctg aaa tat      821
Thr Gly Trp Thr Pro His Trp Met Phe Ala Lys Tyr Asp Leu Lys Tyr
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tta aaa gat cct aaa ggt tcc tac ggc gat gcc gaa gaa atc cat act      869
Leu Lys Asp Pro Lys Gly Ser Tyr Gly Asp Ala Glu Glu Ile His Thr
                        110          115          120

gtt acg cgc aaa gga ttc aag gac gac cat ccg ggc gca aac aag ctg      917
Val Thr Arg Lys Gly Phe Lys Asp Asp His Pro Gly Ala Asn Lys Leu
                        125          130          135

ctc agc caa ttc agc tgg aca gag gat gat atg gga gaa gtc atg ctt      965
Leu Ser Gln Phe Ser Trp Thr Glu Asp Asp Met Gly Glu Val Met Leu
                        140          145          150          155

gcc gtt cag gaa ggc aaa aaa ccg gaa gaa gct gca gca gac ttc gtg      1013
Ala Val Gln Glu Gly Lys Lys Pro Glu Glu Ala Ala Ala Asp Phe Val
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aaa aaa cat caa gat cta gtt aag aaa tgg aca aag ggc gtc gat aag 1061
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 175 180

cgg acg gtg aaa aaa tta agc tcg gct atg tgg cat ggg aca gcg aaa 1109
 Arg Thr Val Lys Lys Leu Ser Ser Ala Met Trp His Gly Thr Ala Lys
 190 195 200

atg cga gca cga atg tca tcg caa agt tct tta aga cta ggg ata cag 1157
 Met Arg Ala Arg Met Ser Ser Gln Ser Ser Leu Arg Leu Gly Ile Gln
 205 210 215

cgt acg ctc agc cca agt aga agc agg ccc gat gtg agc tgg cat gca 1205
 Arg Thr Leu Ser Pro Ser Arg Ser Arg Pro Asp Val Ser Trp His Ala
 220 225 230 235

aaa tgg aag cgt cga tgc ttc act tgc tgc atg gct gcc gca acg caa 1253
 Lys Trp Lys Arg Arg Cys Phe Thr Cys Cys Met Ala Ala Ala Thr Gln
 240 245 250

tca aac ata tgc tta aaa ata caa agg caa ata cga aga tat cgg tac 1301
 Ser Asn Ile Cys Leu Lys Ile Gln Arg Gln Ile Arg Arg Tyr Arg Tyr
 255 260 265

tcg cat gac agg cgt aaa aat tgg cct tgt cgt tcc gac ata tat gaa 1349
 Ser His Asp Arg Arg Lys Asn Trp Pro Cys Arg Ser Asp Ile Tyr Glu
 270 275 280

aga tgt caa ttc aat cga aga ctt gaa aaa ata acg aac aaagccggcg 1398
 Arg Cys Gln Phe Asn Arg Arg Leu Glu Lys Ile Thr Asn
 285 290 295

aacccatctc gccggcttat ttttgccgga aagggataac cgctcatcac ccgaatcctc 1458
 ccggatgcaa aaaaaacatc ctaaaacggt aaaccgcttt aggatgctgg actcaactga 1518
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<210> 58
 <211> 296
 <212> PRT
 <213> Bacillus licheniformis

<400> 58

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35 40 45

Ile Met Asn Ala Thr Asp Gln Ala Leu Lys Asp Tyr Asp Leu Ser Lys
50 55 60

Trp Thr Val Thr Ser Gly Ser Ser Ser Ala Met Thr Ala Ala Leu Lys
65 70 75 80

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Lys Ala Tyr Asp Lys Lys Asp Pro Ile Ile Ile Thr Gly Trp Thr Pro
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 His Trp Met Phe Ala Lys Tyr Asp Leu Lys Tyr Leu Lys Asp Pro Lys
 100 105 110
 Gly Ser Tyr Gly Asp Ala Glu Glu Ile His Thr Val Thr Arg Lys Gly
 115 120 125
 Phe Lys Asp Asp His Pro Gly Ala Asn Lys Leu Leu Ser Gln Phe Ser
 130 135 140
 Trp Thr Glu Asp Asp Met Gly Glu Val Met Leu Ala Val Gln Glu Gly
 145 150 155 160
 Lys Lys Pro Glu Glu Ala Ala Ala Asp Phe Val Lys Lys His Gln Asp
 165 170 175
 Leu Val Lys Lys Trp Thr Lys Gly Val Asp Lys Arg Thr Val Lys Lys
 180 185 190
 Leu Ser Ser Ala Met Trp His Gly Thr Ala Lys Met Arg Ala Arg Met
 195 200 205
 Ser Ser Gln Ser Ser Leu Arg Leu Gly Ile Gln Arg Thr Leu Ser Pro
 210 215 220
 Ser Arg Ser Arg Pro Asp Val Ser Trp His Ala Lys Trp Lys Arg Arg
 225 230 235 240
 Cys Phe Thr Cys Cys Met Ala Ala Ala Thr Gln Ser Asn Ile Cys Leu
 245 250 255
 Lys Ile Gln Arg Gln Ile Arg Arg Tyr Arg Tyr Ser His Asp Arg Arg
 260 265 270
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 275 280 285
 Arg Arg Leu Glu Lys Ile Thr Asn
 290 295

<210> 59
 <211> 1682
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1181)

<400> 59
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60

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gccatcagca ttgccaagcg gacgaggacg attgtctggc agaataattat ttttgcactc	240
ggcgttaaag gagtttttct catcctgggt gcttttggca tcgcgacgat gtgggaagcc	300
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cacgaatgcg gcttgtcttg ttaaaatgaa agaggttatc aaactggcat actaaaaaat	480
aagaataatg aggtgtctaa gtg aag aag aaa cag cag tca ccg atg aaa ttt	533
Val Lys Lys Lys Gln Gln Ser Pro Met Lys Phe	
1 5 10	
gca gtg att atg aca gtc gtg gtc gtt ttt ctg atc ggc gca ctt gtc	581
Ala Val Ile Met Thr Val Val Val Val Phe Leu Ile Gly Ala Leu Val	
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Val Ile Asn Asn Gln Thr Gln Asn Ala Ser Gln Thr Phe Asp Asp Lys	
30 35 40	
cct tca act gaa gga cag ccg ctt cta ggc aac aaa gat gcg gct gta	677
Pro Ser Thr Glu Gly Gln Pro Leu Leu Gly Asn Lys Asp Ala Ala Val	
45 50 55	
acg atc acg gaa ttc gga gat tac aaa tgt ccc agc tgc aaa cag tgg	725
Thr Ile Thr Glu Phe Gly Asp Tyr Lys Cys Pro Ser Cys Lys Gln Trp	
60 65 70 75	
act gag acc gtc ttt ccg gat ttg aaa aag gat tac atc gat aaa gat	773
Thr Glu Thr Val Phe Pro Asp Leu Lys Lys Asp Tyr Ile Asp Lys Asp	
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caa gtt aat ttt tca tat att aac ttc gtc aat gaa cag cac ggc aga	821
Gln Val Asn Phe Ser Tyr Ile Asn Phe Val Asn Glu Gln His Gly Arg	
95 100 105	
ggc tct gaa ttg agc gcc ctc gct tcc gag cag gta tgg aag gaa gat	869
Gly Ser Glu Leu Ser Ala Leu Ala Ser Glu Gln Val Trp Lys Glu Asp	
110 115 120	
ccg gat tca ttc tgg aag ttc cat gag gcg ttg tac aag gcg cag cct	917
Pro Asp Ser Phe Trp Lys Phe His Glu Ala Leu Tyr Lys Ala Gln Pro	
125 130 135	
gac aat gac acg atg gaa aac gag tgg gcg acg ccg gca aaa ttg gcg	965
Asp Asn Asp Thr Met Glu Asn Glu Trp Ala Thr Pro Ala Lys Leu Ala	
140 145 150 155	
gac atc acg gaa gcc aat acg aaa atc aaa cgc gat aag ctt gtc agc	1013
Asp Ile Thr Glu Ala Asn Thr Lys Ile Lys Arg Asp Lys Leu Val Ser	
160 165 170	
agc tta aat gac aaa acg ttc gct gag caa tta aaa acg gac aat tcg	1061
Ser Leu Asn Asp Lys Thr Phe Ala Glu Gln Leu Lys Thr Asp Asn Ser	
175 180 185	
ctc atc aac aaa tac ggt gta gac tcg acg ccg acg atc ttt gtc aac	1109
Leu Ile Asn Lys Tyr Gly Val Asp Ser Thr Pro Thr Ile Phe Val Asn	
190 195 200	
ggc gta aaa atc gac aaa ccg ttt gat tat gac aaa atc aaa gaa acg	1157

10294.204.ST25.txt

Gly Val Lys Ile Asp Lys Pro Phe Asp Tyr Asp Lys Ile Lys Glu Thr
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 Ile Glu Lys Glu Leu Lys Gly Gln
 220 225
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<400> 60

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 35 40 45
 Gln Pro Leu Leu Gly Asn Lys Asp Ala Ala Val Thr Ile Thr Glu Phe
 50 55 60
 Gly Asp Tyr Lys Cys Pro Ser Cys Lys Gln Trp Thr Glu Thr Val Phe
 65 70 75 80
 Pro Asp Leu Lys Lys Asp Tyr Ile Asp Lys Asp Gln Val Asn Phe Ser
 85 90 95
 Tyr Ile Asn Phe Val Asn Glu Gln His Gly Arg Gly Ser Glu Leu Ser
 100 105 110
 Ala Leu Ala Ser Glu Gln Val Trp Lys Glu Asp Pro Asp Ser Phe Trp
 115 120 125
 Lys Phe His Glu Ala Leu Tyr Lys Ala Gln Pro Asp Asn Asp Thr Met
 130 135 140
 Glu Asn Glu Trp Ala Thr Pro Ala Lys Leu Ala Asp Ile Thr Glu Ala
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145

150

155

160

Asn Thr Lys Ile Lys Arg Asp Lys Leu Val Ser Ser Leu Asn Asp Lys
 165 170 175

Thr Phe Ala Glu Gln Leu Lys Thr Asp Asn Ser Leu Ile Asn Lys Tyr
 180 185 190

Gly Val Asp Ser Thr Pro Thr Ile Phe Val Asn Gly Val Lys Ile Asp
 195 200 205

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 agcagcaciaa tatgttggtt tctgtatttt tatagcatat attagttttt gtgaaaaaat 480
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 Met Lys Arg Phe Phe Ser Val Ile Ile Leu Gly
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 Gly Arg Asp Val Leu Gly Ser Lys Asp Gly Trp Gly Ala Tyr Gly Lys
 30 35 40
 gga acg acc gga ggc gct gac gct tct tct gat cag gta tat acg gtc 677
 Gly Thr Thr Gly Gly Ala Asp Ala Ser Ser Asp Gln Val Tyr Thr Val
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 aaa aac cgc aag cag ctt gtt gag gca tta ggg gga gac aat aaa aag 725
 Lys Asn Arg Lys Gln Leu Val Glu Ala Leu Gly Gly Asp Asn Lys Lys

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aag aaa tgg ggg aaa aag gag ccg aca gga aag ctt gaa gag gca agg Lys Lys Trp Gly Lys Lys Glu Pro Thr Gly Lys Leu Glu Glu Ala Arg 125 130 135				917
ctc cgc tcg aaa gat aat caa aag gaa cgg gtc ttg atc aga gtc ggt Leu Arg Ser Lys Asp Asn Gln Lys Glu Arg Val Leu Ile Arg Val Gly 140 145 150 155				965
tcg aac aca acg att atc ggg ctc gga gat gat gcg aaa atc gtc ggc Ser Asn Thr Thr Ile Ile Gly Leu Gly Asp Asp Ala Lys Ile Val Gly 160 165 170				1013
gga ggc ctt tat gtc aaa aac gcg gaa aac gtc att atc cgc aat atc Gly Gly Leu Tyr Val Lys Asn Ala Glu Asn Val Ile Ile Arg Asn Ile 175 180 185				1061
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cag cct gat gag ctg act gaa acg cat ttc ggg cgc gaa ttc cag cat Gln Pro Asp Glu Leu Thr Glu Thr His Phe Gly Arg Glu Phe Gln His 240 245 250				1253
cac gac gga ctg ctt gat atc aaa aag cag tcg gat ttc att acg gtg His Asp Gly Leu Leu Asp Ile Lys Lys Gln Ser Asp Phe Ile Thr Val 255 260 265				1301
tca tac agc ata ttt tca gga cat tct aaa aac acg att atc gga tca Ser Tyr Ser Ile Phe Ser Gly His Ser Lys Asn Thr Ile Ile Gly Ser 270 275 280				1349
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cac aat ctc tac gaa aat ata aaa gag cgg gca ccg cgc gtc cgc tac His Asn Leu Tyr Glu Asn Ile Lys Glu Arg Ala Pro Arg Val Arg Tyr 300 305 310 315				1445
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 Lys Val Phe Lys Gly Asp Ala Leu Tyr Glu Lys Asp Thr Ile Val Asn
 365 370 375
 aac caa aaa agc gtc gca aaa att gat gtt gtc agc aca tac aac aaa 1685
 Asn Gln Lys Ser Val Ala Lys Ile Asp Val Val Ser Thr Tyr Asn Lys
 380 385 390
 gca aac aat gcg tct att aaa aaa tcg gcc ggc tgg aag ccg acg ctg 1733
 Ala Asn Asn Ala Ser Ile Lys Lys Ser Ala Gly Trp Lys Pro Thr Leu
 400 405 410
 ttt gaa aaa atc gac gac gca gaa gat gtg ccg gca atc gtt gaa gcg 1781
 Phe Glu Lys Ile Asp Asp Ala Glu Asp Val Pro Ala Ile Val Glu Ala
 415 420 425
 cac gca ggc gca gga aaa ctg aag taatcaagca aagcggacat gcagatgatg 1835
 His Ala Gly Ala Gly Lys Leu Lys
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 35 40 45
 Ala Asp Ala Ser Ser Asp Gln Val Tyr Thr Val Lys Asn Arg Lys Gln
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 Leu Val Glu Ala Leu Gly Gly Asp Asn Lys Lys Asn Ser Glu Asn Asp
 65 70 75 80

10294.204.ST25.txt

Thr Pro Lys Ile Ile Tyr Val Lys Gly Thr Ile Asn Leu Ser Val Asp
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 100 105 110
 Ser Ile Glu Ala Tyr Leu Lys Ala Tyr Asp Pro Lys Lys Trp Gly Lys
 115 120 125
 Lys Glu Pro Thr Gly Lys Leu Glu Glu Ala Arg Leu Arg Ser Lys Asp
 130 135 140
 Asn Gln Lys Glu Arg Val Leu Ile Arg Val Gly Ser Asn Thr Thr Ile
 145 150 155 160
 Ile Gly Leu Gly Asp Asp Ala Lys Ile Val Gly Gly Gly Leu Tyr Val
 165 170 175
 Lys Asn Ala Glu Asn Val Ile Ile Arg Asn Ile Glu Phe Glu Asn Ala
 180 185 190
 Tyr Asp Phe Phe Pro Gly Trp Asp Pro Thr Asp Gly Ser Ser Gly Asn
 195 200 205
 Trp Asn Ser Glu Tyr Asp Asn Leu Leu Ile Glu Met Ser Lys Asn Ile
 210 215 220
 Trp Ile Asp His Cys Ser Phe Asn Asp Gly Asp Gln Pro Asp Glu Leu
 225 230 235 240
 Thr Glu Thr His Phe Gly Arg Glu Phe Gln His His Asp Gly Leu Leu
 245 250 255
 Asp Ile Lys Lys Gln Ser Asp Phe Ile Thr Val Ser Tyr Ser Ile Phe
 260 265 270
 Ser Gly His Ser Lys Asn Thr Ile Ile Gly Ser Ser Asp Ser Tyr Lys
 275 280 285
 Ala Asp Asn Gly His Leu Arg Val Thr Phe His His Asn Leu Tyr Glu
 290 295 300
 Asn Ile Lys Glu Arg Ala Pro Arg Val Arg Tyr Gly Lys Val His Ile
 305 310 315 320
 Tyr Asn Asn Tyr Phe Lys Ser Thr Lys Asp Ser Tyr Asn Tyr Ser Trp
 325 330 335
 Gly Val Gly Tyr Ser Ser Lys Ile Tyr Ala Glu Asp Asn Tyr Phe Asp
 340 345 350

10294.204.ST25.txt

Leu Pro Glu Gly Thr Lys Pro Gln Lys Leu Met Lys Val Phe Lys Gly
 355 360 365

Asp Ala Leu Tyr Glu Lys Asp Thr Ile Val Asn Asn Gln Lys Ser Val
 370 375 380

Ala Lys Ile Asp Val Val Ser Thr Tyr Asn Lys Ala Asn Asn Ala Ser
 385 390 395 400

Ile Lys Lys Ser Ala Gly Trp Lys Pro Thr Leu Phe Glu Lys Ile Asp
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Lys Leu Lys
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 <212> DNA
 <213> Bacillus licheniformis

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 tggcaaata tagtatgata tttgaaagac ggggtcccgt cgaatcggt gaaaaacaaa 240
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 gccaagggat ctttttttgt ttatcaggaa atttatgaaa attaaagact gctgaaacat 420
 aatcttaaca gtgcgaacct atactttggc aagagaagag caaa agg gga gtg gat 476
 Arg Gly Val Asp
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gat gtg tca gct tta ttc aaa aaa ttg atg tta tct tca ttg atc ggg 524
 Asp Val Ser Ala Leu Phe Lys Lys Leu Met Leu Ser Ser Leu Ile Gly
 5 10 15 20

gtt tcc atc ggg tca gcg ctg ttt gca ccg aat gcg ggt gca caa gag 572
 Val Ser Ile Gly Ser Ala Leu Phe Ala Pro Asn Ala Gly Ala Gln Glu
 25 30 35

ccg gcg gtg aag cct aaa aaa gtg gat gtc att gca cac aga ggc gct 620
 Pro Ala Val Lys Pro Lys Lys Val Asp Val Ile Ala His Arg Gly Ala
 40 45 50

tcg gga tat gcg ccg gaa aac acg atg gct gct ttt gat aaa gcg ctt 668
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Gln	Met	Lys	Ala	Asp	Tyr	Ile	Glu	Leu	Asp	Val	Gln	Met	Ser	Lys	Asp		
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Gly	Glu	Leu	Val	Ile	Ile	His	Asp	Thr	Thr	Val	Asn	Arg	Thr	Thr	Asp		
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Ile	Asp	Ser	Val	Leu	Pro	Val	Ala	Val	Lys	Asp	Leu	Thr	Leu	Ala	Glu		
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ctg	cgc	aag	ctt	gat	gcc	ggc	agc	ttc	ttc	ggt	ccg	cag	ttc	gca	gga	860	
Leu	Arg	Lys	Leu	Asp	Ala	Gly	Ser	Phe	Phe	Gly	Pro	Gln	Phe	Ala	Gly		
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Glu	Arg	Ile	Pro	Thr	Phe	Glu	Glu	Val	Leu	Asp	Arg	Tyr	Lys	Gly	Lys		
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Val	Gly	Met	Leu	Ile	Glu	Leu	Lys	Glu	Pro	Ala	Arg	Tyr	Pro	Gly	Ile		
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gaa	gga	aaa	gtg	tca	gca	gca	ttg	aaa	gag	cgg	aga	atg	gat	aag	cct	1004	
Glu	Gly	Lys	Val	Ser	Ala	Ala	Leu	Lys	Glu	Arg	Arg	Met	Asp	Lys	Pro		
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Lys	Asn	Gly	Lys	Ile	Ile	Val	Gln	Ser	Phe	Asp	Phe	Asn	Ser	Val	Tyr		
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aaa	att	cat	cag	ctg	ctt	cca	tcg	atg	ccg	aca	ggt	gtc	ttg	acg	tca	1100	
Lys	Ile	His	Gln	Leu	Leu	Pro	Ser	Met	Pro	Thr	Gly	Val	Leu	Thr	Ser		
			200					205					210				
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Lys	Ala	Ala	Asp	Leu	Thr	Asp	Ala	Lys	Leu	Lys	Glu	Phe	Ser	Gly	Tyr		
			215				220					225					
gcc	aaa	tac	gtg	aac	gcc	aac	ttg	aaa	aat	gtg	gcc	gct	gat	cct	acg	1196	
Ala	Lys	Tyr	Val	Asn	Ala	Asn	Leu	Lys	Asn	Val	Ala	Ala	Asp	Pro	Thr		
	230					235					240						
ctt	gtg	ccg	aga	att	cat	gcg	ctc	ggc	atg	aag	ata	cgc	cct	tgg	acc	1244	
Leu	Val	Pro	Arg	Ile	His	Ala	Leu	Gly	Met	Lys	Ile	Arg	Pro	Trp	Thr		
	245				250					255					260		
gtc	cgc	tcc	cgc	gat	gaa	gtg	cct	ccg	cta	tca	agg	ccc	gcg	tgg	aac	1292	
Val	Arg	Ser	Arg	Asp	Glu	Val	Pro	Pro	Leu	Ser	Arg	Pro	Ala	Trp	Asn		
				265					270					275			
ggg	att	gtg	aca	aaa	ctt	tcc	cga	cta	ttg	ttc	caa	aaa	agt	acg	gga	1340	
Gly	Ile	Val	Thr	Lys	Leu	Ser	Arg	Leu	Leu	Phe	Gln	Lys	Ser	Thr	Gly		
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gcc	cca	ata	aaa	aac	cct	gaag	ttt	gct	ttga	agg	gct	tttta	attta			1388	
Ala	Pro	Ile	Lys	Asn	Pro												
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 35 40 45

His Arg Gly Ala Ser Gly Tyr Ala Pro Glu Asn Thr Met Ala Ala Phe
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Asp Lys Ala Leu Gln Met Lys Ala Asp Tyr Ile Glu Leu Asp Val Gln
 65 70 75 80

Met Ser Lys Asp Gly Glu Leu Val Ile Ile His Asp Thr Thr Val Asn
 85 90 95

Arg Thr Thr Asp Ile Asp Ser Val Leu Pro Val Ala Val Lys Asp Leu
 100 105 110

Thr Leu Ala Glu Leu Arg Lys Leu Asp Ala Gly Ser Phe Phe Gly Pro
 115 120 125

Gln Phe Ala Gly Glu Arg Ile Pro Thr Phe Glu Glu Val Leu Asp Arg
 130 135 140

Tyr Lys Gly Lys Val Gly Met Leu Ile Glu Leu Lys Glu Pro Ala Arg
 145 150 155 160

Tyr Pro Gly Ile Glu Gly Lys Val Ser Ala Ala Leu Lys Glu Arg Arg
 165 170 175

Met Asp Lys Pro Lys Asn Gly Lys Ile Ile Val Gln Ser Phe Asp Phe
 180 185 190

Asn Ser Val Tyr Lys Ile His Gln Leu Leu Pro Ser Met Pro Thr Gly
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200 205

195

Val Leu Thr Ser Lys Ala Ala Asp Leu Thr Asp Ala Lys Leu Lys Glu
210 215 220

Phe Ser Gly Tyr Ala Lys Tyr Val Asn Ala Asn Leu Lys Asn Val Ala
225 230 235 240

Ala Asp Pro Thr Leu Val Pro Arg Ile His Ala Leu Gly Met Lys Ile
245 250 255

Arg Pro Trp Thr Val Arg Ser Arg Asp Glu Val Pro Pro Leu Ser Arg
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Met Arg Ser Leu Leu Arg Ser Ala Met Ile Leu
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Cys Met Ile Phe Leu Val Phe Ile Pro Ile Ala Ser Gly Ala Ala Ala
15 20 25
tct gaa cag aag cgg ttt gtt tat gat gaa gcc ggg ctt ctg acc aaa 629
Ser Glu Gln Lys Arg Phe Val Tyr Asp Glu Ala Gly Leu Leu Thr Lys
30 35 40
cag gaa atc gag aag ctg gaa acg ctg gca gcc aaa ttg ggc gcc gaa 677
Gln Glu Ile Glu Lys Leu Glu Thr Leu Ala Ala Lys Leu Gly Ala Glu
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Arg Glu Thr Asp Phe Ile Val Thr Thr Asn Asp Thr Asn Gly Arg			
60	65	70	
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Asp Val Lys Lys Tyr Ala Glu Asp Phe Tyr Asp Glu Lys Ala Pro Gly			
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Tyr Gln Lys Lys His Gly Asn Ala Ala Val Leu Thr Val Asp Met Glu			
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His Arg Glu Val Tyr Leu Ala Gly Phe Lys Lys Ala Glu Glu Tyr Leu			
	110	115	
aat gac gcc agg ctg gac aaa att aga gaa aaa atc acg ccg gat ata			917
Asn Asp Ala Arg Leu Asp Lys Ile Arg Glu Lys Ile Thr Pro Asp Ile			
	125	130	
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Ser Asp Lys His Tyr Glu Ala Ala Phe Glu Met Phe Met Lys Ala Ala			
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His Asp Asp Met Glu Lys Lys Pro Trp Ala Asp Ser Ile Phe Phe Lys			
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	175	180	
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Ala Ile Met Lys Tyr Asn Ser Gly Gly Lys Val Thr Val Ser Ala Ser			
	190	195	
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Thr Tyr Met Asn Gly Asp Thr Ser Gly Val Ile Arg Asn Asn Asp Glu			
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cgg gga agc ttt tagaaaggga aaggaagagc ttaaattggtg ttttttagaa			1305
Arg Gly Ser Phe			
	255		
atcaatttgc aaatgtagta gagtgggatg aatttcgcga tgatatgatt ttctataaat			1365
ggaacaaccg cgaaatcaaa aaggggagcc ggctgatcat tcgccccggt caggatgccg			1425
tcttttttaaa caacggaaaa attgaaggca ttttccagga tgagggcgac tatgatattg			1485
aatccgaaat tattcctttt ttatccactt taaaagggtt taaatttggtc tttaacagcg			1545
ggatgcgcgc cgaagtcctg tttgtcaaca cgaaggaatt taccgtcaag tgggggacga			1605
agaatgccat caatatcccg gctgcaggac ttccgggcgg catgccgatc agggcgaacg			1665
gaagatttaa ctttaagggtg aatgattatg tcgcattaat cgataaaatt gccggtgtga			1725

10294.204.ST25.txt

aagatcagta tgttgtggaa gatatcaaaa tacggatcac atc

1768

<210> 66
 <211> 255
 <212> PRT
 <213> Bacillus licheniformis

<400> 66

Met Arg Ser Leu Leu Arg Ser Ala Met Ile Leu Cys Met Ile Phe Leu
 1 5 10 15
 Val Phe Ile Pro Ile Ala Ser Gly Ala Ala Ala Ser Glu Gln Lys Arg
 20 25 30
 Phe Val Tyr Asp Glu Ala Gly Leu Leu Thr Lys Gln Glu Ile Glu Lys
 35 40 45
 Leu Glu Thr Leu Ala Ala Lys Leu Gly Ala Glu Arg Glu Thr Asp Phe
 50 55 60
 Ile Ile Val Thr Thr Asn Asp Thr Asn Gly Arg Asp Val Lys Lys Tyr
 65 70 75 80
 Ala Glu Asp Phe Tyr Asp Glu Lys Ala Pro Gly Tyr Gln Lys Lys His
 85 90 95
 Gly Asn Ala Ala Val Leu Thr Val Asp Met Glu His Arg Glu Val Tyr
 100 105 110
 Leu Ala Gly Phe Lys Lys Ala Glu Glu Tyr Leu Asn Asp Ala Arg Leu
 115 120 125
 Asp Lys Ile Arg Glu Lys Ile Thr Pro Asp Ile Ser Asp Lys His Tyr
 130 135 140
 Glu Ala Ala Phe Glu Met Phe Met Lys Ala Ala His Asp Asp Met Glu
 145 150 155 160
 Lys Lys Pro Trp Ala Asp Ser Ile Phe Phe Lys Thr Trp Phe Gln Leu
 165 170 175
 Leu Val Ser Ala Val Ile Ala Gly Ile Ala Val Ala Ile Met Lys Tyr
 180 185 190
 Asn Ser Gly Gly Lys Val Thr Val Ser Ala Ser Thr Tyr Met Asn Gly
 195 200 205
 Asp Thr Ser Gly Val Ile Arg Asn Asn Asp Glu Tyr Ile Arg Thr Thr
 210 215 220
 Val Thr Lys Gln Arg Lys Pro Ser Asn Asn Lys Ser Ser Gly Gly Gly
 225 230 235 240

10294.204.ST25.txt

Thr Thr Ser Gly Gly His Ser His Ser Gly Ser Arg Gly Ser Phe
 245 250 255

<210> 67
 <211> 2206
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1703)

<400> 67
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 cggtataaat catgccgtcg aatttttcggt ccctgattga agaaaaagtt gtataaaact 120
 gttccaaatg ctgccttggt gtatgttttg gcgtgtgtgt agacgggtatt aaaaaagtgga 180
 aatatacctg taaaggagaa ttcccgagca tcctgagcag ctgtgtctcg gtcttgattt 240
 tctgcggcat cagattaaga atcacaatat ttaaagggtct gatgtcctga tgaaaagccc 300
 gtttttcac catgacaaaa atattttcac tttcaagaat ctgctttgct ggcaaattga 360
 taggtatggt gataggcaac acgccacctc cggttttctc cgctgatttt tcttcatatc 420
 ggagcgacag tcgtgcgtta agctggcagc tgacatcgta tgaattaaaa ggaatcttga 480
 acaactgccg gccgaagggtg atg ttt tat gac ttg gaa ttt gcc gat ata cta 533
 Met Phe Tyr Asp Leu Glu Phe Ala Asp Ile Leu
 1 5 10
 acg ccg ctc cgc gaa cag ctt cag ttc tgc ctg atg att gaa gcg ggt 581
 Thr Pro Leu Arg Glu Gln Leu Gln Phe Cys Leu Met Ile Glu Ala Gly
 15 20 25
 gcg gga atg aac acg act gaa cag ttt gag agc tta ttt aaa aac agg 629
 Ala Gly Met Asn Thr Thr Glu Gln Phe Glu Ser Leu Phe Lys Asn Arg
 30 35 40
 ccg ctg aag gtg gaa gct gag cag gtg aca gag cat gat ttg gct tta 677
 Pro Leu Lys Val Glu Ala Glu Gln Val Thr Glu His Asp Leu Ala Leu
 45 50 55
 atg ctg ttc acc tcg ggc acg acg gga aac ccg aaa ggc tgc atg gtc 725
 Met Leu Phe Thr Ser Gly Thr Thr Gly Asn Pro Lys Gly Cys Met Val
 60 65 70 75
 aac cac ggc agt ctg gcc gca tac ttg aca gag gtg aac gtg aaa tcg 773
 Asn His Gly Ser Leu Ala Ala Tyr Leu Thr Glu Val Asn Val Lys Ser
 80 85 90
 aag cag ctg aaa ggc acg cgc ttt tta gcg agc cac ccg ctc tat cat 821
 Lys Gln Leu Lys Gly Thr Arg Phe Leu Ala Ser His Pro Leu Tyr His
 95 100 105
 atg agc tcg ctc aac cat gtt ttt cag gcg gct ttt gaa gga att gcc 869
 Met Ser Ser Leu Asn His Val Phe Gln Ala Ala Phe Glu Gly Ile Ala
 110 115 120
 ctt tat ttc tta tgg gat ccc gaa ccg ttt gaa atc ctg cag gag atc 917
 Leu Tyr Phe Leu Trp Asp Pro Glu Pro Phe Glu Ile Leu Gln Glu Ile
 125 130 135

10294.204.ST25.txt

gag aag aaa cgc att cat atg atg atg gcg ttt cct tcc gtc tac acc Glu Lys Lys Arg Ile His Met Met Met Ala Phe Pro Ser Val Tyr Thr 140 145 150 155	965
tac atg ctg gag gaa atg aaa aga cat cca ttc gac ctg tca tct gtg Tyr Met Leu Glu Glu Met Lys Arg His Pro Phe Asp Leu Ser Ser Val 160 165 170	1013
aaa atg ctt gtt tcc ggc ggc acc aag gtg ccg gcg cgg ctg att aag Lys Met Leu Val Ser Gly Gly Thr Lys Val Pro Ala Arg Leu Ile Lys 175 180 185	1061
gag tac aat gac cat gga atc atg atg gtg cag ggg tac ggc agc aca Glu Tyr Asn Asp His Gly Ile Met Met Val Gln Gly Tyr Gly Ser Thr 190 195 200	1109
gaa gca tgg acg gtc agc gta tgg cgg cct gac atg ggc tgg gat aaa Glu Ala Trp Thr Val Ser Val Trp Arg Pro Asp Met Gly Trp Asp Lys 205 210 215	1157
gtc act tca gcc ggc aag ccg att ccg caa gtc agc ata aaa atc gaa Val Thr Ser Ala Gly Lys Pro Ile Pro Gln Val Ser Ile Lys Ile Glu 220 225 230 235	1205
gac cct gat aca cat gaa gag ctg ccg acg gga gaa gtc gga gaa gtc Asp Pro Asp Thr His Glu Glu Leu Pro Thr Gly Glu Val Gly Glu Val 240 245 250	1253
gtc gtc aaa agc ccg tat gtt ttt gaa ggg tat tac caa aat cct tcc Val Val Lys Ser Pro Tyr Val Phe Glu Gly Tyr Tyr Gln Asn Pro Ser 255 260 265	1301
gcc acg caa aag gtg ctg aaa gac ggc tgg ttc tat atg ggg gac tcc Ala Thr Gln Lys Val Leu Lys Asp Gly Trp Phe Tyr Met Gly Asp Ser 270 275 280	1349
ggc aaa ctc gat gaa gac gga ttt tta tat att acc ggc cgg tat aaa Gly Lys Leu Asp Glu Asp Gly Phe Leu Tyr Ile Thr Gly Arg Tyr Lys 285 290 295	1397
gac gtc att gtc tac gga ggc gac aac att tat ccg gac caa gtg gaa Asp Val Ile Val Tyr Gly Gly Asp Asn Ile Tyr Pro Asp Gln Val Glu 300 305 310 315	1445
gaa atc atc gat caa gtg ccc gga gta gtt gaa tct gcc gtc atc ggc Glu Ile Ile Asp Gln Val Pro Gly Val Val Glu Ser Ala Val Ile Gly 320 325 330	1493
gtc ccg gat gaa atg tac ggc gag gtt ccg agg gcg tat gtg gtg aaa Val Pro Asp Glu Met Tyr Gly Glu Val Pro Arg Ala Tyr Val Val Lys 335 340 345	1541
aat gaa agc gcc ggc ctc aag aag gag gac att atc gcg tat tgc aaa Asn Glu Ser Ala Gly Leu Lys Lys Glu Asp Ile Ile Ala Tyr Cys Lys 350 355 360	1589
gag cgc ctg tcc gac tat aaa att cct gaa atc gtc ttt atc gac agc Glu Arg Leu Ser Asp Tyr Lys Ile Pro Glu Ile Val Phe Ile Asp Ser 365 370 375	1637
ctt ccg aaa aac agg ctc ggc aaa atc gtc aaa aaa gat ctg cgt gaa Leu Pro Lys Asn Arg Leu Gly Lys Ile Val Lys Lys Asp Leu Arg Glu 380 385 390 395	1685
ctg gca gtc aaa ggg cag tgagcgcaat gattgaccga aagcttatcc Leu Ala Val Lys Gly Gln 400	1733

10294.204.ST25.txt

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agcattggat aagctttttg tgctgattcc ttgcatcagc tgccgttttt tgtaacgttt 1793
tccagtgcta aaccactac aacattagga ggtgttgaca attgaaatcg aaatggagtg 1853
caatggtggt tattgccggt cttttattgc tggccggatg cggtgcaactg aaggaggctg 1913
atcccccgcg cggcagatca gcgcaaaaaa cggaagcctc gttttctgaa gctgaacagc 1973
gatttgcgct cgccttgttt caagacatga taaaagaaga agggagccgg aaaaacatct 2033
tcctctcgcc ttacagtatt cagcaggcac ttttgatgac ggcaaacggt gccgcgggag 2093
acagcagaaa ggacctgatc agcactttac atctcagcca ggcggatatg gcatcgatca 2153
acgggatatc aaaatctggt aatcgttctc ttgaaacgct gcctcacggt gaa 2206

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<210> 68
 <211> 401
 <212> PRT
 <213> Bacillus licheniformis

<400> 68

Met Phe Tyr Asp Leu Glu Phe Ala Asp Ile Leu Thr Pro Leu Arg Glu
1 5 10 15

Gln Leu Gln Phe Cys Leu Met Ile Glu Ala Gly Ala Gly Met Asn Thr
20 25 30

Thr Glu Gln Phe Glu Ser Leu Phe Lys Asn Arg Pro Leu Lys Val Glu
35 40 45

Ala Glu Gln Val Thr Glu His Asp Leu Ala Leu Met Leu Phe Thr Ser
50 55 60

Gly Thr Thr Gly Asn Pro Lys Gly Cys Met Val Asn His Gly Ser Leu
65 70 75 80

Ala Ala Tyr Leu Thr Glu Val Asn Val Lys Ser Lys Gln Leu Lys Gly
85 90 95

Thr Arg Phe Leu Ala Ser His Pro Leu Tyr His Met Ser Ser Leu Asn
100 105 110

His Val Phe Gln Ala Ala Phe Glu Gly Ile Ala Leu Tyr Phe Leu Trp
115 120 125

Asp Pro Glu Pro Phe Glu Ile Leu Gln Glu Ile Glu Lys Lys Arg Ile
130 135 140

His Met Met Met Ala Phe Pro Ser Val Tyr Thr Tyr Met Leu Glu Glu
145 150 155 160

Met Lys Arg His Pro Phe Asp Leu Ser Ser Val Lys Met Leu Val Ser
165 170 175

10294.204.ST25.txt

Gly Gly Thr Lys Val Pro Ala Arg Leu Ile Lys Glu Tyr Asn Asp His
 180 185 190
 Gly Ile Met Met Val Gln Gly Tyr Gly Ser Thr Glu Ala Trp Thr Val
 195 200 205
 Ser Val Trp Arg Pro Asp Met Gly Trp Asp Lys Val Thr Ser Ala Gly
 210 215 220
 Lys Pro Ile Pro Gln Val Ser Ile Lys Ile Glu Asp Pro Asp Thr His
 225 230 235 240
 Glu Glu Leu Pro Thr Gly Glu Val Gly Glu Val Val Val Lys Ser Pro
 245 250 255
 Tyr Val Phe Glu Gly Tyr Tyr Gln Asn Pro Ser Ala Thr Gln Lys Val
 260 265 270
 Leu Lys Asp Gly Trp Phe Tyr Met Gly Asp Ser Gly Lys Leu Asp Glu
 275 280 285
 Asp Gly Phe Leu Tyr Ile Thr Gly Arg Tyr Lys Asp Val Ile Val Tyr
 290 295 300
 Gly Gly Asp Asn Ile Tyr Pro Asp Gln Val Glu Glu Ile Ile Asp Gln
 305 310 315 320
 Val Pro Gly Val Val Glu Ser Ala Val Ile Gly Val Pro Asp Glu Met
 325 330 335
 Tyr Gly Glu Val Pro Arg Ala Tyr Val Val Lys Asn Glu Ser Ala Gly
 340 345 350
 Leu Lys Lys Glu Asp Ile Ile Ala Tyr Cys Lys Glu Arg Leu Ser Asp
 355 360 365
 Tyr Lys Ile Pro Glu Ile Val Phe Ile Asp Ser Leu Pro Lys Asn Arg
 370 375 380
 Leu Gly Lys Ile Val Lys Lys Asp Leu Arg Glu Leu Ala Val Lys Gly
 385 390 395 400

Gln

<210> 69
 <211> 1547
 <212> DNA
 <213> Bacillus licheniformis

<220>

10294.204.ST25.txt

<221> CDS

<222> (501)..(1046)

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tggctccgcc tgatcgtttc atcccctgta tatccataga tttcagcggc ttcaaccatc      180
at ttgcccgt tcttgctgat ggaaacgagc aatgcttctt tttcaatata cttttgcacc      240
cgctcccggg aggtcccaaa aaaatTTTTT tgcaaaaaaa aatTTTTTccc cataaggctc      300
tagtgttatg agaaaaaaat ccgggaacgg aatcaaggac cataaaaaatt ttttctggcc      360
aacccaaaac cccggtgcgt ttaagtcgtc ataaataaga aaccagcgga ggaaaaattt      420
ttctcgcaac cctcttgtaa tctatctgac gttattgtaa catttgtaat ataagagata      480
tatttaagga gagaggacca ttg aaa aag tta atc gtt tgt tta tta gct gtt      533
                      Leu Lys Lys Leu Ile Val Cys Leu Leu Ala Val
                      1                      5                      10

tta ctg atc ttg cct gcc gga gcg tcc ctc gca gcg aaa aat caa aca      581
Leu Leu Ile Leu Pro Ala Gly Ala Ser Leu Ala Ala Lys Asn Gln Thr
                      15                      20                      25

tca ggg aat tta aca aat aag caa gtc atg caa tta acc ttg cag gca      629
Ser Gly Asn Leu Thr Asn Lys Gln Val Met Gln Leu Thr Leu Gln Ala
                      30                      35                      40

cgg gag cac ttt tgg aat acg atg agc ggc cac aat cca aaa gcg aaa      677
Arg Glu His Phe Trp Asn Thr Met Ser Gly His Asn Pro Lys Ala Lys
                      45                      50                      55

aac tca act tgc cca tcc aaa aca ttt gaa tac cgc ggt ctt cca tat      725
Asn Ser Thr Cys Pro Ser Lys Thr Phe Glu Tyr Arg Gly Leu Pro Tyr
60                      65                      70                      75

acg tat atg tgc agt gaa ttc agc aca aaa gca aaa tta aca gac tac      773
Thr Tyr Met Cys Ser Glu Phe Ser Thr Lys Ala Lys Leu Thr Asp Tyr
80                      85                      90

ttg acg ccg gtt ttc aca aaa gac gcc att aaa aaa ggc ttg gaa aaa      821
Leu Thr Pro Val Phe Thr Lys Asp Ala Ile Lys Lys Gly Leu Glu Lys
95                      100

tac aac atc att tct tat aaa gga aaa atg gcc gtg cct gtc ggc gat      869
Tyr Asn Ile Ile Ser Tyr Lys Gly Lys Met Ala Val Pro Val Gly Asp
110                      115                      120

ggg gac aac ctc tta gga tgg gac aag gca aaa atc aaa ctg atc tct      917
Gly Asp Asn Leu Leu Gly Trp Asp Lys Ala Lys Ile Lys Leu Ile Ser
125                      130                      135

caa aaa aac aat acc cgc act tat gaa ttt tcc gta ccg gca ttg gat      965
Gln Lys Asn Asn Thr Arg Thr Tyr Glu Phe Ser Val Pro Ala Leu Asp
140                      145                      150                      155

gga tcg gtg act gcg aaa aga aag atc acg ttt gtg aaa gaa aac aac      1013
Gly Ser Val Thr Ala Lys Arg Lys Ile Thr Phe Val Lys Glu Asn Asn
160                      165                      170

aaa tgg aaa atc aat cag ctc gat gct gcc atc taaacgaaaa agctaattgc      1066
Lys Trp Lys Ile Asn Gln Leu Asp Ala Ile
                      175                      180

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10294.204.ST25.txt

taaaaacgga cattagcttt tttccgtcaa acggtcagtt caacgatggt gccgtcagga 1126
 tccagaatga ctctttcata atacccgtct cccgtgacgc gcggctttcc ggcaacctgg 1186
 tatecttcct tttcaaagcg gctcgtcatc tcgtcaacct cttgccgcga ccctaaggaa 1246
 aacgccatat gtgcatagcc ggaagcggtc tcctctcctt ttgcaaggtc ggggcgtctc 1306
 atcagctcaa gccgtgttcc cgattcaaac tggatgaaat atgattcgaa atgctttttc 1366
 ggattgacat atttttcatt cgtctttccg tgaaaaaaac gggatatagaa atctttcatt 1426
 tcctctaaat tgttcgcca tatggcgatg tgttcgattt tcataaatct ccctccatt 1486
 tcatattacc atatagatcc tctgcctttt tttacacttt tttaaattga taagtattca 1546
 t 1547

<210> 70
 <211> 182
 <212> PRT
 <213> Bacillus licheniformis

<400> 70

Leu Lys Lys Leu Ile Val Cys Leu Leu Ala Val Leu Leu Ile Leu Pro
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Ala Gly Ala Ser Leu Ala Ala Lys Asn Gln Thr Ser Gly Asn Leu Thr
 20 25 30

Asn Lys Gln Val Met Gln Leu Thr Leu Gln Ala Arg Glu His Phe Trp
 35 40 45

Asn Thr Met Ser Gly His Asn Pro Lys Ala Lys Asn Ser Thr Cys Pro
 50 55 60

Ser Lys Thr Phe Glu Tyr Arg Gly Leu Pro Tyr Thr Tyr Met Cys Ser
 65 70 75 80

Glu Phe Ser Thr Lys Ala Lys Leu Thr Asp Tyr Leu Thr Pro Val Phe
 85 90 95

Thr Lys Asp Ala Ile Lys Lys Gly Leu Glu Lys Tyr Asn Ile Ile Ser
 100 105 110

Tyr Lys Gly Lys Met Ala Val Pro Val Gly Asp Gly Asp Asn Leu Leu
 115 120 125

Gly Trp Asp Lys Ala Lys Ile Lys Leu Ile Ser Gln Lys Asn Asn Thr
 130 135 140

Arg Thr Tyr Glu Phe Ser Val Pro Ala Leu Asp Gly Ser Val Thr Ala
 145 150 155 160

Lys Arg Lys Ile Thr Phe Val Lys Glu Asn Asn Lys Trp Lys Ile Asn
 165 170 175

Gln Leu Asp Ala Ala Ile
180

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<210> 71
<211> 1621
<212> DNA
<213> Bacillus licheniformis
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<220>
<221> CDS
<222> (271) .. (1122)

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gtgctgtatt	cagccgctcg	tttgccatat	tcacagtttt	tgtattggct	ggcggattgc											180		
tatatattt	tatt	gacttgcaaa	cgcaaaaaat	cttaggatat	tcgagtgggt	gggcgggaaa											240	
gcccagccgt	tttttatgct	gactcgattt	tctgaaacat	aatgaaaaga	aaatcgtatt											294		
tgatgtaaag	cttcttgaga	ggatgaaaat	gat	gaa	aag	aag	cat	cgg	cac	ctt						342		
			Asp	Glu	Lys	Lys	His	Arg	His	Leu						390		
			1				5									438		
tta	aat	tta	cgg	act	gac	aat	tta	ata	ttc	gcg	agt	agg	tta	agg	gaa	342		
Leu	Asn	Leu	Arg	Thr	Asp	Asn	Leu	Ile	Phe	Ala	Ser	Arg	Leu	Arg	Glu			
	10					15					20							
gcc	gat	tct	tgt	gat	gca	cgg	agg	tca	ttc	gaa	ttg	ccg	cga	gga	att	390		
Ala	Asp	Ser	Cys	Asp	Ala	Arg	Arg	Ser	Phe	Glu	Leu	Pro	Arg	Gly	Ile			
25					30					35				40				
tgg	gta	tcg	aga	tct	tta	tta	gag	ccg	att	ctc	tat	cat	cac	gcc	ttc	438		
Trp	Val	Ser	Arg	Ser	Leu	Leu	Glu	Pro	Ile	Leu	Tyr	His	His	Ala	Phe			
				45					50					55				
ccg	tgc	agg	gta	tgg	ccg	gac	atc	gaa	aga	aat	cgg	gga	cag	ttt	gga	486		
Pro	Cys	Arg	Val	Trp	Pro	Asp	Ile	Glu	Arg	Asn	Arg	Gly	Gln	Phe	Gly			
			60					65					70					
act	tgc	ctg	cta	tta	cat	atg	aaa	ctg	ctt	gat	cat	tta	aat	atc	aag	534		
Thr	Cys	Leu	Leu	Leu	His	Met	Lys	Leu	Leu	Asp	His	Leu	Asn	Ile	Lys			
		75					80					85						
aaa	gtt	cat	gtg	gtt	gcg	gtg	tca	gcc	ggc	ggg	cca	agc	gga	ata	tgt	582		
Lys	Val	His	Val	Val	Ala	Val	Ser	Ala	Gly	Gly	Pro	Ser	Gly	Ile	Cys			
	90					95					100							
ttt	gca	tcc	aaa	tac	tcg	gaa	aga	gta	gaa	tcc	tta	att	ttg	caa	agc	630		
Phe	Ala	Ser	Lys	Tyr	Ser	Glu	Arg	Val	Glu	Ser	Leu	Ile	Leu	Gln	Ser			
105					110					115					120			
gct	gtc	aca	aag	cag	tgg	ctg	aca	gcg	aag	gat	att	gaa	tat	aaa	gtt	678		
Ala	Val	Thr	Lys	Gln	Trp	Leu	Thr	Ala	Lys	Asp	Ile	Glu	Tyr	Lys	Val			
				125					130					135				
ggt	cag	atc	atc	ttt	cgg	ccg	cct	gtt	gaa	aag	gcc	gta	tgg	aag	ctg	726		
Gly	Gln	Ile	Ile	Phe	Arg	Pro	Pro	Val	Glu	Lys	Ala	Val	Trp	Lys	Leu			
			140					145					150					
ata	tcg	gcg	ctt	aac	aat	cga	ttt	ccg	gaa	tgg	atc	ttt	aag	aaa	atg	774		
Ile	Ser	Ala	Leu	Asn	Asn	Arg	Phe	Pro	Glu	Trp	Ile	Phe	Lys	Lys	Met			
		155					160					165						

10294.204.ST25.txt

cta tcc tcc ttt act aca ctt cct gct gat cag gcg atg ctg aaa gtc 822
 Leu Ser Ser Phe Thr Thr Leu Pro Ala Asp Gln Ala Met Leu Lys Val
 170 175 180
 acg gag gga gat att gaa gaa atg aga aaa atg aac aac aga cag cgt 870
 Thr Glu Gly Asp Ile Glu Glu Met Arg Lys Met Asn Asn Arg Gln Arg
 185 190 195 200
 tca agt cga ggg ttc ttg ctt gat tta aaa aat ata gac gat tta tct 918
 Ser Ser Arg Gly Phe Leu Leu Asp Leu Lys Asn Ile Asp Asp Leu Ser
 205 210 215
 ttc cat cat ttg aag gag att tct tgt ccg gta tta att atg cat tgc 966
 Phe His His Leu Lys Glu Ile Ser Cys Pro Val Leu Ile Met His Cys
 220 225 230
 cga tat gat cgt gtt gtt cca gcc gag cat gct ttt cat gca aaa aaa 1014
 Arg Tyr Asp Arg Val Val Pro Ala Glu His Ala Phe His Ala Lys Lys
 235 240 245
 ctg att cct ttt tca gaa gtc tat cag gca gac agc tgg ggt cat ctc 1062
 Leu Ile Pro Phe Ser Glu Val Tyr Gln Ala Asp Ser Trp Gly His Leu
 250 255 260
 att tgg ctg gga aca gag ggt aaa tct gtc tca cag aag gtc atc agc 1110
 Ile Trp Leu Gly Thr Glu Gly Lys Ser Val Ser Gln Lys Val Ile Ser
 265 270 275 280
 ttt tta aaa acc acatcatctt gatcataaga tgaataaaat tttaggatcg 1162
 Phe Leu Lys Thr
 cagcctaccc gcaaatgaag tagtgcaatt ttttaatacaa gagcagaatg atctttccga 1222
 acagaactga tgaacgtcgt acaagacttg caaataagat gaatgagaaa tcctccctgg 1282
 ccgggttttcg gagcacaagg gaaacttatg tataagaatc tattccgata gagggacagg 1342
 tacgggatga atcattgatt accgttgcct gcgatttccc aggggggaga gagttggtaa 1402
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 ctttggtgtt ggatatttca atttgggcct gctgaatgga tatggcgag tttggcttgc 1522
 ggcaagcggc agcttcttcc taaactcgcg attgaaacga tgcggctatg caatatggtg 1582
 aaacgttgca tgaaaaactt aacatttttaa aaatccagc 1621

<210> 72
 <211> 284
 <212> PRT
 <213> Bacillus licheniformis

<400> 72

Asp Glu Lys Lys His Arg His Leu Leu Asn Leu Arg Thr Asp Asn Leu
 1 5 10 15

Ile Phe Ala Ser Arg Leu Arg Glu Ala Asp Ser Cys Asp Ala Arg Arg
 20 25 30

Ser Phe Glu Leu Pro Arg Gly Ile Trp Val Ser Arg Ser Leu Leu Glu
 35 40 45

10294.204.ST25.txt

Pro Ile Leu Tyr His His Ala Phe Pro Cys Arg Val Trp Pro Asp Ile
 50 55 60
 Glu Arg Asn Arg Gly Gln Phe Gly Thr Cys Leu Leu Leu His Met Lys
 65 70 75 80
 Leu Leu Asp His Leu Asn Ile Lys Lys Val His Val Val Ala Val Ser
 85 90 95
 Ala Gly Gly Pro Ser Gly Ile Cys Phe Ala Ser Lys Tyr Ser Glu Arg
 100 105 110
 Val Glu Ser Leu Ile Leu Gln Ser Ala Val Thr Lys Gln Trp Leu Thr
 115 120 125
 Ala Lys Asp Ile Glu Tyr Lys Val Gly Gln Ile Ile Phe Arg Pro Pro
 130 135 140
 Val Glu Lys Ala Val Trp Lys Leu Ile Ser Ala Leu Asn Asn Arg Phe
 145 150 155 160
 Pro Glu Trp Ile Phe Lys Lys Met Leu Ser Ser Phe Thr Thr Leu Pro
 165 170 175
 Ala Asp Gln Ala Met Leu Lys Val Thr Glu Gly Asp Ile Glu Glu Met
 180 185 190
 Arg Lys Met Asn Asn Arg Gln Arg Ser Ser Arg Gly Phe Leu Leu Asp
 195 200 205
 Leu Lys Asn Ile Asp Asp Leu Ser Phe His His Leu Lys Glu Ile Ser
 210 215 220
 Cys Pro Val Leu Ile Met His Cys Arg Tyr Asp Arg Val Val Pro Ala
 225 230 235 240
 Glu His Ala Phe His Ala Lys Lys Leu Ile Pro Phe Ser Glu Val Tyr
 245 250 255
 Gln Ala Asp Ser Trp Gly His Leu Ile Trp Leu Gly Thr Glu Gly Lys
 260 265 270
 Ser Val Ser Gln Lys Val Ile Ser Phe Leu Lys Thr
 275 280

<210> 73
 <211> 1630
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<220>

10294.204.ST25.txt

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<222> (256)..(1131)

<400> 73

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tttttgGCCA ttatatgaat tcggccagcg ttgaatatTTT cctcttttca gggaaatttc	180
cgaagcggcg attcaaaaat ccgcaaactt atcttacaat agaaaaagtt ctgaatgatc	240
gagtagggag agatc gtt agt atg aaa gta tcg gtt ctg ttt gtc ttg ctt	291
Val Ser Met Lys Val Ser Val Leu Phe Val Leu Leu	
1 5 10	
gCG gca att tta tgg gga acg acg gga aca acc cag gca ttt gCG ccg	339
Ala Ala Ile Leu Trp Gly Thr Thr Gly Thr Thr Gln Ala Phe Ala Pro	
15 20 25	
aaa gag gCG gca cct ctt gtg ttc ggc gct gtc aga atg gct gtc ggc	387
Lys Glu Ala Ala Pro Leu Val Phe Gly Ala Val Arg Met Ala Val Gly	
30 35 40	
ggc atc acc ctg ctc ttg ttc gCG gct ttc cgc ggt caa ttg aaa cga	435
Gly Ile Thr Leu Leu Phe Ala Ala Phe Arg Gly Gln Leu Lys Arg	
45 50 55 60	
agc ggc tgg ccc gtt aaa acg ctg atc atc gca gca ttg agc atg gca	483
Ser Gly Trp Pro Val Lys Thr Leu Ile Ile Ala Ala Leu Ser Met Ala	
65 70 75	
ttt tac cag cct ttc ttt ttt tca gcc gtc agc ctg tca gga atc gcc	531
Phe Tyr Gln Pro Phe Phe Phe Ser Ala Val Ser Leu Ser Gly Ile Ala	
80 85 90	
gtc gga acg gtc gtc gcc atc ggc agc gct ccg att att gcc ggc tgc	579
Val Gly Thr Val Val Ala Ile Gly Ser Ala Pro Ile Ile Ala Gly Cys	
95 100 105	
ctc gaa tgg ctg gtg ttc aaa aag gtt ccg cag acg aaa tgg tgg atc	627
Leu Glu Trp Leu Val Phe Lys Lys Val Pro Gln Thr Lys Trp Trp Ile	
110 115 120	
gca act gct gca gCG ata gca ggc gta gcc tta tta ttc att ccc tcc	675
Ala Thr Ala Ala Ala Ile Ala Gly Val Ala Leu Leu Phe Ile Pro Ser	
125 130 135 140	
gcc tca tcg ggg ggg agc ttt ctc ggc ata ctg ctc gca ctt ggc gcc	723
Ala Ser Ser Gly Gly Ser Phe Leu Gly Ile Leu Leu Ala Leu Gly Ala	
145 150 155	
ggt ctt tcc ttt gcc gtc tac acg ctg aca agc aag aaa ctc ctg caa	771
Gly Leu Ser Phe Ala Val Tyr Thr Leu Thr Ser Lys Lys Leu Leu Gln	
160 165 170	
aag caa aag ccg gag gct gtc aca ggc acc gta ttc ttt tta agc gct	819
Lys Gln Lys Pro Glu Ala Val Thr Gly Thr Val Phe Phe Leu Ser Ala	
175 180 185	
gta ttg ctt gcc ccg ttg ttg ttt ctg tac gat ctc ggc tgg atc tca	867
Val Leu Leu Ala Pro Leu Leu Phe Leu Tyr Asp Leu Gly Trp Ile Ser	
190 195 200	
tcg gtt cag gga atg gct gtc agc ctc tat atc ggg gtc att gca acc	915
Ser Val Gln Gly Met Ala Val Ser Leu Tyr Ile Gly Val Ile Ala Thr	
205 210 215 220	

10294.204.ST25.txt

gga gcc gcg tac ctg tta ttt acg aca gga ttg gca aaa gtg ccc gcc 963
 Gly Ala Ala Tyr Leu Leu Phe Thr Thr Gly Leu Ala Lys Val Pro Ala
 225 230 235
 tca acg gcg gtg acg ctg tcg ctt gct gaa ccg ctt aca gcg tcg ctg 1011
 Ser Thr Ala Val Thr Leu Ser Leu Ala Glu Pro Leu Thr Ala Ser Leu
 240 245 250
 ttg gga acc gtg ctt gtc agg gaa tcg ctg cct ctt gtt tcc tgg gcc 1059
 Leu Gly Thr Val Leu Val Arg Glu Ser Leu Pro Leu Val Ser Trp Ala
 255 260 265
 ggg atc gcc ctg ctt ctt tta ggc att ttt tat att tcc tat cag ccc 1107
 Gly Ile Ala Leu Leu Leu Leu Gly Ile Phe Tyr Ile Ser Tyr Gln Pro
 270 275 280
 aaa aag gat aaa ata aac gct gaa cagatgaaag cgtaaaaaaa acccgcccgg 1161
 Lys Lys Asp Lys Ile Asn Ala Glu
 285 290
 ggatatacgg gcggggttttc atgttgcttt gttattcatc caaaccgatg gacaaatatt 1221
 ttgtttccaa atacggctcg atgccttcca gtccgctttc gcgtccgata ccgctttcct 1281
 tcatgccgcc gaaaggcgcc tgaacgggtg acgggtccgcc gtcattccag ccgagaatgc 1341
 cgtaatcaag gttttcggat aaatagatgc cgcgggcggtg gttttccgta aagaagtatg 1401
 ccgctaaacc gtaaggcgta tcattggcga gcttgaccgc ttcgtccagc gttttaaaag 1461
 acgtaatcgg cgcaacgggg ccgaatgttt cctcatgcat gatcgtcatt gaaggatcaa 1521
 catccgtcag cactgtcggg tggacaaaagt agcatgattt ctcatcatcg ctttcatatt 1581
 cggcgccgat gagaactttc gcccctttat tcaccgcgtc attgatttg 1630

<210> 74
 <211> 292
 <212> PRT
 <213> Bacillus licheniformis

<400> 74

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20 25 30

Pro Leu Val Phe Gly Ala Val Arg Met Ala Val Gly Gly Ile Thr Leu
35 40 45

Leu Leu Phe Ala Ala Phe Arg Gly Gln Leu Lys Arg Ser Gly Trp Pro
50 55 60

Val Lys Thr Leu Ile Ile Ala Ala Leu Ser Met Ala Phe Tyr Gln Pro
65 70 75 80

Phe Phe Phe Ser Ala Val Ser Leu Ser Gly Ile Ala Val Gly Thr Val
85 90 95

10294.204.ST25.txt

Val Ala Ile Gly Ser Ala Pro Ile Ile Ala Gly Cys Leu Glu Trp Leu
 100 105 110

Val Phe Lys Lys Val Pro Gln Thr Lys Trp Trp Ile Ala Thr Ala Ala
 115 120 125

Ala Ile Ala Gly Val Ala Leu Leu Phe Ile Pro Ser Ala Ser Ser Gly
 130 135 140

Gly Ser Phe Leu Gly Ile Leu Leu Ala Leu Gly Ala Gly Leu Ser Phe
 145 150 155 160

Ala Val Tyr Thr Leu Thr Ser Lys Lys Leu Leu Gln Lys Gln Lys Pro
 165 170 175

Glu Ala Val Thr Gly Thr Val Phe Phe Leu Ser Ala Val Leu Leu Ala
 180 185 190

Pro Leu Leu Phe Leu Tyr Asp Leu Gly Trp Ile Ser Ser Val Gln Gly
 195 200 205

Met Ala Val Ser Leu Tyr Ile Gly Val Ile Ala Thr Gly Ala Ala Tyr
 210 215 220

Leu Leu Phe Thr Thr Gly Leu Ala Lys Val Pro Ala Ser Thr Ala Val
 225 230 235 240

Thr Leu Ser Leu Ala Glu Pro Leu Thr Ala Ser Leu Leu Gly Thr Val
 245 250 255

Leu Val Arg Glu Ser Leu Pro Leu Val Ser Trp Ala Gly Ile Ala Leu
 260 265 270

Leu Leu Leu Gly Ile Phe Tyr Ile Ser Tyr Gln Pro Lys Lys Asp Lys
 275 280 285

Ile Asn Ala Glu
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<210> 75
 <211> 2140
 <212> DNA
 <213> Bacillus licheniformis

<220>
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 <222> (501)..(1637)

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 gaatacaagt gattatttag attttaatga agaaaacaaa aacaatgata atggaaaaga 120
 ttacagtaat gcctacactg atatggactg tgaggcgatg actgaagata ttaatcattt 180

10294.204.ST25.txt

gaaatctgcc aatcctgagg tgtatcaaaa gctgcagaag atggacatta ccgctgcggc	240
gggatacaga acagaggata ctgtaagttt ttccccttac tataccgcaa gcggaaaaca	300
taaaataaac agtgatgata tcgttttcggt cgaaagtcaa cacggtgaca tattaggcga	360
tctcattgat aaaaagccag aaattgaagt aagaggttcc ggtgtaacca atcctggaca	420
tatttatgaa attgaagact ctgaatttgt tgacttgatt cgagaggtca acaaaaaaga	480
agcagaatag gagaaggctcg atg aaa aag aaa ggg ttt ata agt ata ttt ttt	533
Met Lys Lys Lys Gly Phe Ile Ser Ile Phe Phe	
1 5 10	
tta ata gtg ttt cta ctg ctc gcc acc acc ggc tgc ggc aaa gat gat	581
Leu Ile Val Phe Leu Leu Leu Ala Thr Thr Gly Cys Gly Lys Asp Asp	
15 20 25	
gtt cag gaa gcc atc tat aaa aaa ggc ttg ccc aaa gaa gac agt cca	629
Val Gln Glu Ala Ile Tyr Lys Lys Gly Leu Pro Lys Glu Asp Ser Pro	
30 35 40	
gca ttt aga gaa ttt atg aga cat gaa ctt gat tta gcg aca gac gca	677
Ala Phe Arg Glu Phe Met Arg His Glu Leu Asp Leu Ala Thr Asp Ala	
45 50 55	
act ctt agt tat caa aat agt aca tat acg att atg cgc agt gat aaa	725
Thr Leu Ser Tyr Gln Asn Ser Thr Tyr Thr Ile Met Arg Ser Asp Lys	
60 65 70 75	
aag ggg cta cgg tac tat caa tat aca gat caa gaa gta gac gat ttt	773
Lys Gly Leu Arg Tyr Tyr Gln Tyr Thr Asp Gln Glu Val Asp Asp Phe	
80 85 90	
tac agt ccc ttt ctt tcg gct aat aaa tat cct gcg aca aaa tta tat	821
Tyr Ser Pro Phe Leu Ser Ala Asn Lys Tyr Pro Ala Thr Lys Leu Tyr	
95 100 105	
gat ttg aaa aca act gaa ttt tta act aaa gaa aaa ctt atc cac aat	869
Asp Leu Lys Thr Thr Glu Phe Leu Thr Lys Glu Lys Leu Ile His Asn	
110 115 120	
aaa ctt gaa tat aat ctg ccg gaa atg aca tta gat aaa aag aat gtt	917
Lys Leu Glu Tyr Asn Leu Pro Glu Met Thr Leu Asp Lys Lys Asn Val	
125 130 135	
cta aaa gtg aaa aca aaa agc gga gaa aaa ata gag ttt cca tca	965
Leu Lys Val Lys Thr Lys Ser Gly Glu Lys Lys Ile Glu Phe Pro Ser	
140 145 150 155	
gcc aag gat aaa aaa gta cat ctg gcg tta gca gct gtt agc aaa gac	1013
Ala Lys Asp Lys Lys Val His Leu Ala Leu Ala Ala Val Ser Lys Asp	
160 165 170	
agc atg ctt ata caa gtg gac gta tat gaa aaa ttt aaa aat ggt gac	1061
Ser Met Leu Ile Gln Val Asp Val Tyr Glu Lys Phe Lys Asn Gly Asp	
175 180 185	
ctt gga gac aga caa ata tat tat ctt ttt tta aaa agt gat ctt tca	1109
Leu Gly Asp Arg Gln Ile Tyr Tyr Leu Phe Leu Lys Ser Asp Leu Ser	
190 195 200	
aaa tac cgg att gtt aaa gaa gag gaa tta aat tca aca att gag tct	1157
Lys Tyr Arg Ile Val Lys Glu Glu Glu Leu Asn Ser Thr Ile Glu Ser	
205 210 215	
ggg aaa ctg aag gaa tac tta tcc gta ttt cca aat gta gcg aag gat	1205

10294.204.ST25.txt

Gly 220	Lys	Leu	Lys	Glu	Tyr 225	Leu	Ser	Val	Phe	Pro 230	Asn	Val	Ala	Lys	Asp 235	
gga	gca	tat	cgt	aag	tta	ttt	gat	aaa	tac	att	ttt	gat	gaa	aag	aaa	1253
Gly	Ala	Tyr	Arg	Lys 240	Leu	Phe	Asp	Lys	Tyr 245	Ile	Phe	Asp	Glu	Lys 250	Lys	
aac	aaa	ggt	agg	aaa	atc	aaa	aac	act	gat	att	ctg	agc	aaa	gac	ggt	1301
Asn	Lys	Val	Arg 255	Lys	Ile	Lys	Asn	Thr 260	Asp	Ile	Leu	Ser	Lys 265	Asp	Gly	
aag	tat	ggt	tat	att	aac	gga	gca	aaa	gaa	aaa	gaa	aca	aat	gta	atg	1349
Lys	Tyr	Val 270	Tyr	Ile	Asn	Gly	Ala 275	Lys	Glu	Lys	Glu	Thr 280	Asn	Val	Met	
cct	gat	ggt	atc	caa	cag	ata	caa	aca	atg	gat	aat	tat	cta	aaa	gga	1397
Pro	Asp 285	Gly	Ile	Gln	Gln	Ile 290	Gln	Thr	Met	Asp	Asn 295	Tyr	Leu	Lys	Gly	
aat	gaa	aaa	tat	gaa	gct	caa	ttt	aag	att	gat	ttc	aaa	caa	att	gca	1445
Asn	Glu	Lys	Tyr	Glu	Ala 305	Gln	Phe	Lys	Ile	Asp 310	Phe	Lys	Gln	Ile	Ala 315	
aaa	gag	atg	gat	tta	aac	gcg	ggt	gat	gcg	agg	ata	gct	aat	att	cat	1493
Lys	Glu	Met	Asp	Leu 320	Asn	Ala	Gly	Asp	Ala 325	Arg	Ile	Ala	Asn	Ile 330	His	
tat	ttt	aat	aaa	gat	tat	gta	gtt	ttg	tat	att	tct	tat	cat	ggg	aag	1541
Tyr	Phe	Asn	Lys 335	Asp	Tyr	Val	Val	Leu 340	Tyr	Ile	Ser	Tyr	His 345	Gly	Lys	
aca	att	ggt	aca	gca	ggt	tct	gtt	aat	gta	ctt	att	gat	tta	caa	aaa	1589
Thr	Ile	Gly 350	Thr	Ala	Gly	Ser	Val 355	Asn	Val	Leu	Ile	Asp 360	Leu	Gln	Lys	
aac	aaa	caa	cag	cca	acg	gct	tat	tta	gtt	gat	tta	gga	att	gaa	tca	1637
Asn	Lys 365	Gln	Gln	Pro	Thr	Ala 370	Tyr	Leu	Val	Asp	Leu 375	Gly	Ile	Glu	Ser	
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attgggacaa	gccttctgct	tcctactttcc	ttatccaatt	taagagaagt	tcttgacagaa											1757
agcgtacaat	gacgaaagaa	tgacagcagcg	tttggaacac	tcgttaatgc	tcgtttcggg											1817
agcggacgga	aaaatcgtcg	gcttttgcaa	ctactccttt	gtcagagaag	gaggggtagc											1877
ctatctcgca	gccgtttatt	tagctccgga	ataccaggga	aaaggcatcg	gaaccgcatt											1937
attggaagag	gggatgaacc	atttaaagg	agtgaaaaag	atctttgtag	agggttga											1997
agaaaaccgc	accggaaaaa	actttttaca	ggcgaagggt	tttgaggatg	tcgccgaata											2057
tgatgaagat	ttcgaagggc	atatacctcaa	aacagtcaga	atggccttgc	acgtataatc											2117
ccgctttcac	ttcgttaactt	gga														2140

<210> 76
 <211> 379
 <212> PRT
 <213> Bacillus licheniformis

<400> 76

Met Lys Lys Lys Gly Phe Ile Ser Ile Phe Phe Leu Ile Val Phe Leu
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10294.204.ST25.txt

Leu Leu Ala Thr Thr Gly Cys Gly Lys Asp Asp Val Gln Glu Ala Ile
 20 25 30

Tyr Lys Lys Gly Leu Pro Lys Glu Asp Ser Pro Ala Phe Arg Glu Phe
 35 40 45

Met Arg His Glu Leu Asp Leu Ala Thr Asp Ala Thr Leu Ser Tyr Gln
 50 55 60

Asn Ser Thr Tyr Thr Ile Met Arg Ser Asp Lys Lys Gly Leu Arg Tyr
 65 70 75 80

Tyr Gln Tyr Thr Asp Gln Glu Val Asp Asp Phe Tyr Ser Pro Phe Leu
 85 90 95

Ser Ala Asn Lys Tyr Pro Ala Thr Lys Leu Tyr Asp Leu Lys Thr Thr
 100 105 110

Glu Phe Leu Thr Lys Glu Lys Leu Ile His Asn Lys Leu Glu Tyr Asn
 115 120 125

Leu Pro Glu Met Thr Leu Asp Lys Lys Asn Val Leu Lys Val Lys Thr
 130 135 140

Lys Ser Gly Glu Lys Lys Ile Glu Phe Pro Ser Ala Lys Asp Lys Lys
 145 150 155 160

Val His Leu Ala Leu Ala Ala Val Ser Lys Asp Ser Met Leu Ile Gln
 165 170 175

Val Asp Val Tyr Glu Lys Phe Lys Asn Gly Asp Leu Gly Asp Arg Gln
 180 185 190

Ile Tyr Tyr Leu Phe Leu Lys Ser Asp Leu Ser Lys Tyr Arg Ile Val
 195 200 205

Lys Glu Glu Glu Leu Asn Ser Thr Ile Glu Ser Gly Lys Leu Lys Glu
 210 215 220

Tyr Leu Ser Val Phe Pro Asn Val Ala Lys Asp Gly Ala Tyr Arg Lys
 225 230 235 240

Leu Phe Asp Lys Tyr Ile Phe Asp Glu Lys Lys Asn Lys Val Arg Lys
 245 250 255

Ile Lys Asn Thr Asp Ile Leu Ser Lys Asp Gly Lys Tyr Val Tyr Ile
 260 265 270

Asn Gly Ala Lys Glu Lys Glu Thr Asn Val Met Pro Asp Gly Ile Gln
 275 280 285

10294.204.ST25.txt

Gln Ile Gln Thr Met Asp Asn Tyr Leu Lys Gly Asn Glu Lys Tyr Glu
 290 295 300

Ala Gln Phe Lys Ile Asp Phe Lys Gln Ile Ala Lys Glu Met Asp Leu
 305 310 315 320

Asn Ala Gly Asp Ala Arg Ile Ala Asn Ile His Tyr Phe Asn Lys Asp
 325 330 335

Tyr Val Val Leu Tyr Ile Ser Tyr His Gly Lys Thr Ile Gly Thr Ala
 340 345 350

Gly Ser Val Asn Val Leu Ile Asp Leu Gln Lys Asn Lys Gln Gln Pro
 355 360 365

Thr Ala Tyr Leu Val Asp Leu Gly Ile Glu Ser
 370 375

<210> 77
 <211> 1387
 <212> DNA
 <213> Bacillus licheniformis

<220>
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 <222> (501)..(884)

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 atctggatgg aaaagctttt gcagatatga ttctgtacgg cgacacccat ctgtctcaaa 180
 acgcaaagt agttgatgag ttaaactgat ttccggttcc ggacggagat acgggaacga 240
 acactaatct gtcgatgaca tccggtgcga aagaagtggg gcaaatcgac accgccaata 300
 tcggcaaagt ggcacaaagc ctgtcaaggg ggcttctgat gggggcgagg ggaaactcgg 360
 gcgtcatttt atcccagctg ttcagaggct ttggcaaact gattgaacag aaatcggaaa 420
 ttaacgcgaa agaatttgcc gccgcgttcc aggccggagt ggacaccgcc tacaaggccg 480
 tcataaacia gcttctacag atg tct acc agc agc att gtc gtt ctc ttg att 533
 Met Ser Thr Ser Ser Ile Val Val Leu Leu Ile
 1 5 10
 tgc gcc gcg ctc atc atc tac gcg gtc gct tca tac atc tat cag cag 581
 Cys Ala Ala Leu Ile Ile Tyr Ala Val Ala Ser Tyr Ile Tyr Gln Gln
 15 20 25
 cgc att atg aaa acc ttg aca gaa gaa gaa ttc cgg gca ggc tat cgc 629
 Arg Ile Met Lys Thr Leu Thr Glu Glu Glu Phe Arg Ala Gly Tyr Arg
 30 35 40
 aaa gcg cag ctc atc gat gtg cgc gag ccg aat gag tat gaa ggc ggc 677
 Lys Ala Gln Leu Ile Asp Val Arg Glu Pro Asn Glu Tyr Glu Gly Gly
 45 50 55

10294.204.ST25.txt

cac att ttg ggt gcg aga aac att ccg ctt tca cag ctt aag caa aga 725
 His Ile Leu Gly Ala Arg Asn Ile Pro Leu Ser Gln Leu Lys Gln Arg 75
 60 65 70

aaa agc gaa atc cgg cct gac aaa ccg gtt tac ctg tac tgc caa aac 773
 Lys Ser Glu Ile Arg Pro Asp Lys Pro Val Tyr Leu Tyr Cys Gln Asn 90
 80 85

aac gtc aga agc gga agg gcc gcc caa acg ctc cgc aaa cac ggc tgt 821
 Asn Val Arg Ser Gly Arg Ala Ala Gln Thr Leu Arg Lys His Gly Cys 105
 95 100

aag gag att tac aac ctg aaa ggc ggg ttc aaa aaa tgg ggc gga aaa 869
 Lys Glu Ile Tyr Asn Leu Lys Gly Gly Phe Lys Lys Trp Gly Gly Lys 120
 110 115

att aaa acg aaa aat taataaccga agctgtctct gctatggaag gcttcagttg 924
 Ile Lys Thr Lys Asn 125

agtccagcat cctaaagcgg ttttaacgttt taggatgttt tttttgcatc cgggaggatt 984

cgggtgatga gcggttatcc ctttccggca aaaataagcc ggcgagatgg gttcgccggc 1044

tttgttcggt attttttcaa gtcttcgatt gaattgacat ctttcatata tgtcggaaacg 1104

acaaggccaa tttttacgcc tgtcatgcta gtaccgatat cttcgtatatt gcctttgtat 1164

ttttcagcat atgttttatt gcgttgccggc agccatgcag caagtgaagc atcgacgctt 1224

ccattttgca tgccagggtca catcgggcct gcttctactt gggctgagcg tacgggtgtat 1284

ccctagtctt caagaacttt gcgatgacat tcgtgctcgc attttcgctg tcccatgccca 1344

catagccgag cttaattttt tcaccgtccg cttatcgacg ccc 1387

<210> 78
 <211> 128
 <212> PRT
 <213> Bacillus licheniformis

<400> 78

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Ile Tyr Ala Val Ala Ser Tyr Ile Tyr Gln Gln Arg Ile Met Lys Thr
20 25 30

Leu Thr Glu Glu Glu Phe Arg Ala Gly Tyr Arg Lys Ala Gln Leu Ile
35 40 45

Asp Val Arg Glu Pro Asn Glu Tyr Glu Gly Gly His Ile Leu Gly Ala
50 55 60

Arg Asn Ile Pro Leu Ser Gln Leu Lys Gln Arg Lys Ser Glu Ile Arg
65 70 75 80

Pro Asp Lys Pro Val Tyr Leu Tyr Cys Gln Asn Asn Val Arg Ser Gly
85 90 95

Arg Ala Ala Gln Thr Leu Arg Lys His Gly Cys Lys Glu Ile Tyr Asn
100 105 110

Leu Lys Gly Gly Phe Lys Lys Trp Gly Gly Lys Ile Lys Thr Lys Asn
115 120 125

<210> 79
<211> 1486
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501) .. (983)

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Phe Gly Ile 15 Phe Leu Thr Ala Leu 20 Leu Ala Gly Ala Asn 25 Val Tyr

cgt acg gca atg gat cag aaa gaa aac ggc cac gag cag gct gcc gaa 629
Arg Thr Ala Met Asp Gln Lys Glu Asn Gly His Glu Gln Ala Ala Glu
30 35 40

aca gcc agg cag gaa gcc ggc tta aaa caa gtt gac agc gtg gag acg 677
Thr Ala Arg Gln Glu Ala Gly Leu Lys Gln Val Asp Ser Val Glu Thr
45 50 55

ttt gtc ggt aaa gaa aag cag tac att gtt aca ggg gca gac aaa aaa 725
Phe Val Gly Lys Glu Lys Gln Tyr Ile Val Thr Gly Ala Asp Lys Lys
60 65 70 75

ggc gac aaa atg tat gtt tgg gtg cct gct gac aaa aag cag aaa acg 773
Gly Asp Lys Met Tyr Val Trp Val Pro Ala Asp Lys Lys Gln Lys Thr
80 85 90

ctt tac aaa aaa gca tca gcc ggc att acc ggc cgc cag gct gca aaa 821
Leu Tyr Lys Lys Ala Ser Ala Gly Ile Thr Gly Arg Gln Ala Ala Lys
95 100 105

gct gtt cag gat gag ggc ctg atg tct gag ctt aaa gag gtg cac ctt 869
Ala Val Gln Asp Glu Gly Leu Met Ser Glu Leu Lys Glu Val His Leu
110 115 120

gca agg gaa ggc aat gtt cta ttg tgg gaa gtt aca tac tta aat aaa 917
Page 156

10294.204.ST25.txt

Ala Arg Glu Gly Asn Val Leu Leu Trp Glu Val Thr Tyr Leu Asn Lys
 125 130 135

gat ggg cag tac agt tta agc tat gtg gac ttt ata aac gga aaa att 965
 Asp Gly Gln Tyr Ser Leu Ser Tyr Val Asp Phe Ile Asn Gly Lys Ile
 140 145 150 155

cac aaa aat att acg cct tagacgaaac aggggggaaat cgagttgaat 1013
 His Lys Asn Ile Thr Pro
 160

ctagctaaaa gagtatcagc gttaacacca tctgcaacat tggcaatcac tgcaaaagca 1073
 aaagaattaa aagcggcagg gcacgacgtc atcgggtcttg gggcaggtga gccggatttt 1133
 aatacgcttg agcacatcat tgaagcggct gtccgttcga tgaacgaagg acataccaaa 1193
 tacacgcctt ccggcgggtct tgcggcgctg aaagacagca tccgcgataa attcaagcgc 1253
 gatcagggaa ttgaatacag ccaatcggaa gttattgtgt gcacaggtgc aaagcatgct 1313
 ctttacaccc tatttcaagt gctcctcgac gaaggggacg aagtgattat tccgactccg 1373
 tactgggtca gctatcctga acaagtcaag cttgcaggcg gcaaacctgt gtttgtggaa 1433
 ggccttgagg aaaacagctt caagatttct ccggagcagc tcgaaaaagc cgt 1486

<210> 80
 <211> 161
 <212> PRT
 <213> Bacillus licheniformis

<400> 80

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 20 25 30

Gln Lys Glu Asn Gly His Glu Gln Ala Ala Glu Thr Ala Arg Gln Glu
 35 40 45

Ala Gly Leu Lys Gln Val Asp Ser Val Glu Thr Phe Val Gly Lys Glu
 50 55 60

Lys Gln Tyr Ile Val Thr Gly Ala Asp Lys Lys Gly Asp Lys Met Tyr
 65 70 75 80

Val Trp Val Pro Ala Asp Lys Lys Gln Lys Thr Leu Tyr Lys Lys Ala
 85 90 95

Ser Ala Gly Ile Thr Gly Arg Gln Ala Ala Lys Ala Val Gln Asp Glu
 100 105 110

Gly Leu Met Ser Glu Leu Lys Glu Val His Leu Ala Arg Glu Gly Asn
 115 120 125

Val Leu Leu Trp Glu Val Thr Tyr Leu Asn Lys Asp Gly Gln Tyr Ser

140

Pro

gcc aga tgt gcg gcc atc gat tta gcg ggc cgt gac gtg ctt gaa gcc 869
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Page 158

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110	115	120	
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ggt gta gca atg gat ggt Gly Val Ala Met Asp Gly 140 145	atc gaa gtg aaa gca Ile Glu Val Lys Ala 150	aaa gcg aga atc acg Lys Ala Arg Ile Thr 155	965
ggt cgc gct aac atc gac Val Arg Ala Asn Ile Asp 160	cgc ctt gtc ggg gga Arg Leu Val Gly Gly 165	gcg ggc gaa gaa acg Ala Gly Glu Glu Thr 170	1013
atc att gcc cgt gtc ggc Ile Ile Ala Arg Val Gly 175	gaa ggg atc gtt tcg Glu Gly Ile Val Ser 180	aca atc ggt tct tcc Thr Ile Gly Ser Ser 185	1061
gat aat cat aaa aaa gtg Asp Asn His Lys Lys Val 190	ctt gaa aac cca gat Leu Glu Asn Pro Asp 195	atg att tca caa acc Met Ile Ser Gln Thr 200	1109
gta ttg agc aaa ggg ttg Val Leu Ser Lys Gly Leu 205 210	gat tca ggt aca gcg Asp Ser Gly Thr Ala 215	ttt gaa att cta tcg Phe Glu Ile Leu Ser 215	1157
atc gat atc gct gac gtt Ile Asp Ile Ala Asp Val 220 225	gac atc ggc aaa aac Asp Ile Gly Lys Asn 230	atc gga gcg att ctg Ile Gly Ala Ile Leu 235	1205
caa acc gac cag gct gaa Gln Thr Asp Gln Ala Glu 240	gcc gat aaa aac atc Ala Asp Lys Asn Ile 245	gcc cag gcg aaa gcg Ala Gln Ala Lys Ala 250	1253
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cgc gtc gaa gaa atg Arg Val Glu Glu Met 270	cgc gcc aaa gtc gtc Arg Ala Lys Val Val 275	gaa gcc gaa gtc Glu Ala Glu Glu Val 280	1349
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gac tac ctc aat atg Asp Tyr Leu Asn Met Lys 300 305	aaa aac atc gac gcc Lys Asn Ile Asp Ala 310	act gac atg cgc gat Thr Asp Met Arg Asp 315	1445
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10294.204.ST25.txt

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Ser Ala Leu Ala Ala Gly Val Lys Ile Ser Ile Phe Thr Leu Ile Gly
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Met Arg Leu Arg Arg Val Ile Pro Asn Arg Val Val Asn Pro Leu Ile
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Lys Ala His Lys Ala Gly Leu Asp Val Ala Ile Asn Gln Leu Glu Ser
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His Tyr Leu Ala Gly Gly Asn Val Asp Arg Val Val Asn Ala Leu Ile
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Ile Asp Leu Ala Gly Arg Asp Val Leu Glu Ala Val Gln Met Ser Val
115 120 125
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130 135 140
Gly Ile Glu Val Lys Ala Lys Ala Arg Ile Thr Val Arg Ala Asn Ile
145 150 155 160
Asp Arg Leu Val Gly Gly Ala Gly Glu Glu Thr Ile Ile Ala Arg Val
165 170 175
Gly Glu Gly Ile Val Ser Thr Ile Gly Ser Ser Asp Asn His Lys Lys
180 185 190
Val Leu Glu Asn Pro Asp Met Ile Ser Gln Thr Val Leu Ser Lys Gly
195 200 205
Leu Asp Ser Gly Thr Ala Phe Glu Ile Leu Ser Ile Asp Ile Ala Asp
210 215 220

10294.204.ST25.txt

Val Asp Ile Gly Lys Asn Ile Gly Ala Ile Leu Gln Thr Asp Gln Ala
225 230 235 240

Glu Ala Asp Lys Asn Ile Ala Gln Ala Lys Ala Glu Glu Arg Arg Ala
245 250 255

Met Ala Val Ala Gln Glu Gln Glu Met Arg Ala Arg Val Glu Glu Met
260 265 270

Arg Ala Lys Val Val Glu Ala Glu Ala Glu Val Pro Leu Ala Met Ser
275 280 285

Glu Ala Leu Arg Ser Gly Lys Ile Gly Val Met Asp Tyr Leu Asn Met
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Lys Asn Ile Asp Ala Asp Thr Asp Met Arg Asp Ser Phe Gly Lys Met
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Thr Lys Asp Gln Asn Glu Glu Asp His Lys
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ttcacggcgg tttcgcagct ctttttttct cttctattga aacagatcag gccataccaa 300
aaaggag gaa tac aaa atg agt caa gtc gaa ttt gaa ggt gta agt aaa 349
Glu Tyr Lys Met Ser Gln Val Glu Phe Glu Gly Val Ser Lys
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cga ata aaa ggc aga cca att gtc caa aat atc aca ttt caa att gcc 397
Arg Ile Lys Gly Arg Pro Ile Val Gln Asn Ile Thr Phe Gln Ile Ala
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Pro Gly Thr Ile Phe Gly Leu Leu Gly Pro Asn Gly Ala Gly Lys Thr
35 40 45
aca ctt atc aaa atg att gtc ggg atg gca aag ccg aca tca gga gat 493
Thr Leu Ile Lys Met Ile Val Gly Met Ala Lys Pro Thr Ser Gly Asp
50 55 60
atc cgc atc gac ggc tat tca gtt aaa agc aat tac gag gaa gcg gca 541
Ile Arg Ile Asp Gly Tyr Ser Val Lys Ser Asn Tyr Glu Glu Ala Ala
65 70 75

10294.204.ST25.txt

gcc cga gtc ggt tct gtt gtt gaa aac cca tcc ttt tat gag cac tta 589
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aca gga tac caa aac ctt aaa tat ctc ggc gga ttc cac agc cac gtg 637
 Thr Gly Tyr Gln Asn Leu Lys Tyr Leu Gly Gly Phe His Ser His Val
 95 100 105 110

tca aag gag cgc ata gaa gag atc gtt cag ctt gtt gat ttg aca gga 685
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 115 120 125

agt att cat aaa cca gtt aaa acg tat tca tta ggc atg aaa cag cgt 733
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gat gaa ccg aca aac ggc ctt gat cct cag gga atc att gat ttg cgc 829
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 160 165 170

gaa cac ctt cag tac ttg gcg aaa acc ttc aac aaa acg att ttg att 877
 Glu His Leu Gln Tyr Leu Ala Lys Thr Phe Asn Lys Thr Ile Leu Ile
 175 180 185 190

tcg agt cat ctt ctg tct gag gtt gag atg att tgt gat gaa tac ggc 925
 Ser Ser His Leu Leu Ser Glu Val Glu Met Ile Cys Asp Glu Tyr Gly
 195 200 205

gtc atg aaa aac gga gaa ctc ctg caa att aag agc aat cac cgc gat 973
 Val Met Lys Asn Gly Glu Leu Leu Gln Ile Lys Ser Asn His Arg Asp
 210 215 220

acc gat acg gtt cgt tat cgg ctt aca tta aac ggc cac gcc gat gaa 1021
 Thr Asp Thr Val Arg Tyr Arg Leu Thr Leu Asn Gly His Ala Asp Glu
 225 230 235

gcg gct gac ctg ttg aat gag tac cag tat gca ggc ggt ctc acg gaa 1069
 Ala Ala Asp Leu Leu Asn Glu Tyr Gln Tyr Ala Gly Gly Leu Thr Glu
 240 245 250

gat aaa aat gag att tat gtc ctt tgc atg gaa gaa gac att atg aaa 1117
 Asp Lys Asn Glu Ile Tyr Val Leu Cys Met Glu Glu Asp Ile Met Lys
 255 260 265 270

gtc gtt aat ctg tta atg gag aac aaa ata aga gtt ctg cat atg aag 1165
 Val Val Asn Leu Leu Met Glu Asn Lys Ile Arg Val Leu His Met Lys
 275 280 285

cag gaa aaa cag tcg ata gaa caa agc ttt ctg gaa ttg atc aat aag 1213
 Gln Glu Lys Gln Ser Ile Glu Gln Ser Phe Leu Glu Leu Ile Asn Lys
 290 295 300

ggg tta ccg gca tta ggg tct tga aaaatgaact ttacaggctg atggtgacga 1267
 Gly Leu Pro Ala Leu Gly Ser

305

aaagtacctg gattgtgtta agcttgctgc ttgtcatgac aatcgctgtt gcatggatgg 1327

tcagcaatgg cgaaaaggag aaggagacag gtaactggaa agagcaatta accgttcaaa 1387

acgctcagta tgaaagagaa atgagagagc tgagcccagc gggtcccaaa taccaatttt 1447

taaaagaaga gatcgcggtc aatcaatacc ggcttgagca taatttgccg ctttctgcga 1507

10294.204.ST25.txt

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 <400> 84

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Thr Ile Phe Gly Leu Leu Gly Pro Asn Gly Ala Gly Lys Thr Thr Leu
 35 40 45

Ile Lys Met Ile Val Gly Met Ala Lys Pro Thr Ser Gly Asp Ile Arg
 50 55 60

Ile Asp Gly Tyr Ser Val Lys Ser Asn Tyr Glu Glu Ala Ala Ala Arg
 65 70 75 80

Val Gly Ser Val Val Glu Asn Pro Ser Phe Tyr Glu His Leu Thr Gly
 85 90 95

Tyr Gln Asn Leu Lys Tyr Leu Gly Gly Phe His Ser His Val Ser Lys
 100 105 110

Glu Arg Ile Glu Glu Ile Val Gln Leu Val Asp Leu Thr Gly Ser Ile
 115 120 125

His Lys Pro Val Lys Thr Tyr Ser Leu Gly Met Lys Gln Arg Leu Gly
 130 135 140

Leu Ala Val Ala Leu Leu His Asp Pro Glu Phe Leu Ile Leu Asp Glu
 145 150 155 160

Pro Thr Asn Gly Leu Asp Pro Gln Gly Ile Ile Asp Leu Arg Glu His
 165 170 175

Leu Gln Tyr Leu Ala Lys Thr Phe Asn Lys Thr Ile Leu Ile Ser Ser
 180 185 190

His Leu Leu Ser Glu Val Glu Met Ile Cys Asp Glu Tyr Gly Val Met
 195 200 205

Lys Asn Gly Glu Leu Leu Gln Ile Lys Ser Asn His Arg Asp Thr Asp
210 215 220

Thr Val Arg Tyr Arg Leu Thr Leu Asn Gly His Ala Asp Glu Ala Ala
225 230 235 240

Asp Leu Leu Asn Glu Tyr Gln Tyr Ala Gly Gly Leu Thr Glu Asp Lys
245 250 255

Asn Glu Ile Tyr Val Leu Cys Met Glu Glu Asp Ile Met Lys Val Val
260 265 270

Asn Leu Leu Met Glu Asn Lys Ile Arg Val Leu His Met Lys Gln Glu
275 280 285

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 60 65 70 75
 tca aaa gca aaa ccg cac aaa gtc att aca gtc tat aaa tat gat gtc 773
 Ser Lys Ala Lys Pro His Lys Val Ile Thr Val Tyr Lys Tyr Asp Val
 80 85 90
 ggc aga atg ccg ggc gct gtt ttg gat gta agc ccg aaa gct ttt aga 821
 Gly Arg Met Pro Gly Ala Val Leu Asp Val Ser Pro Lys Ala Phe Arg
 95 100 105
 gct ttg gga ttt ccg aca agc aaa gga aag gta gcc gga cat tat aca 869
 Ala Leu Gly Phe Pro Thr Ser Lys Gly Lys Val Ala Gly His Tyr Thr
 110 115 120
 tat aaa aaa taggagaaat gaagcaagaa aaatcgtttt cttgcttctt 918
 Tyr Lys Lys
 125
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 agccgcaggc gcatttgcg ccgtccgcta tttcgtccc gaaaaagcgg agccggcaaa 1038
 gagcggcggg tccagacctgc ttgtatcgat aaccgatcag aagctgatga ccgcttacta 1098
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<210> 86
 <211> 126
 <212> PRT
 <213> Bacillus licheniformis

<400> 86

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20 25 30

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35 40 45

Gly Lys Arg Leu Gly His Trp Asp Cys Ala Thr Lys Met Gly Phe Asp
50 55 60

Val Pro Arg Lys Gly Thr Lys Ile Arg Ala Tyr Ser Lys Ala Lys Pro
65 70 75 80

10294.204.ST25.txt

His Lys Val Ile Thr Val Tyr Lys Tyr Asp Val Gly Arg Met Pro Gly
 85 90 95

Ala Val Leu Asp Val Ser Pro Lys Ala Phe Arg Ala Leu Gly Phe Pro
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Thr Ser Lys Gly Lys Val Ala Gly His Tyr Thr Tyr Lys Lys
 115 120 125

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 <211> 1957
 <212> DNA
 <213> Bacillus licheniformis

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 <222> (501)..(1454)

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 cgttctgaga ggacgatcgg tctcgccgtc ctgaaagacc attatttgtc gccggcggca 360
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 taactcaa at aaggacttct caagatgaca aatattcctgt atattgataa tgataattat 480
 tatcaattgg aggattaaat atg acg aaa aag caa tat tct tat ata ttc acc 533
 Met Thr Lys Lys Gln Tyr Ser Tyr Ile Phe Thr
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 ctt tta ctc gct ttc gct gta ttt ctt tca ggc tgt caa agc ggc cag 581
 Leu Leu Leu Ala Phe Ala Val Phe Leu Ser Gly Cys Gln Ser Gly Gln
 15 20 25
 aaa cag gct gca tca gag aaa aat gaa gag aaa aca aga gtg gtg aaa 629
 Lys Gln Ala Ala Ser Glu Lys Asn Glu Glu Lys Thr Arg Val Val Lys
 30 35 40
 acc atc aac gga aat gtc act gta ccg gct aat ccg aag cgc gtc gtg 677
 Thr Ile Asn Gly Asn Val Thr Val Pro Ala Asn Pro Lys Arg Val Val
 45 50 55
 acg att ggc tat gcg gga acc atg ctt gca ttc ggg atc aag ccg ctt 725
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 gga gaa acg gga aag tac ctc gga agt cct tat att aaa gat caa gtt 773
 Gly Glu Thr Gly Lys Tyr Leu Gly Ser Pro Tyr Ile Lys Asp Gln Val
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 tca gga ata aag gat atc ggg gga aaa gac ggt ttt tca gta tct gtg 821
 Ser Gly Ile Lys Asp Ile Gly Gly Lys Asp Gly Phe Ser Val Ser Val
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 gaa aaa gtt ctt gaa ctt aaa ccc gat tta atc gta tcg atg acg aac 869
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10294.204.ST25.txt															
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Phe	Asn	Gln	Lys	Met	Lys	Ala	Ala	Arg	Ala	Lys	Ile	Lys	Asp	Ala	Ser
			175					180					185		1061
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Tyr	Val	Tyr	Gly	Ala	Tyr	Gly	Tyr	Arg	Gly	Gly	Glu	Ala	Ile	Tyr	Thr
		205				210					215				1157
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Gln	Leu	Gly	Leu	Thr	Pro	Pro	Glu	Ser	Val	Lys	Lys	Asp	Ala	Ile	Asp
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Thr	Ala	Asp	Gly	Tyr	Lys	Ala	Ile	Ser	Phe	Glu	Val	Leu	Pro	Lys	Tyr
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Ala	Gly	Asp	Tyr	Ile	Phe	Val	Asp	Glu	Ser	Tyr	Asn	Gly	Lys	Leu	Asp
			255					260					265		1301
cag	gac	aat	ccg	gtt	tgg	gca	tcg	ctt	gac	gcg	gtg	aaa	aaa	ggc	aag
Gln	Asp	Asn	Pro	Val	Trp	Ala	Ser	Leu	Asp	Ala	Val	Lys	Lys	Gly	Lys
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Val	Phe	Phe	Leu	Asp	Pro	Asp	Arg	Phe	Trp	Pro	Tyr	Asp	Pro	Asn	Ala
		285				290					295				1397
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Val	Gln	Ala	Gln	Ala	Glu	Glu	Ile	Ala	Asp	Met	Ile	Ser	Lys	Lys	Ala
		300			305					310					1445
aaa	aat	aaa	tag	aaa	agcg	ggg	agcc	gaa	aaga	atgatc	cgg	ctt	ccccg		1494
Lys	Asn	Lys													
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cccgcatctt	ggatggggat	gatataggcg	gcttcatctg	actcattatg	gtgggaatgc										1614
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ggaggcacga	tgccgaacat	tgcccacaat	acatgggtga	tcgtcagcgt	ttgatcgaat										1854
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10294.204.ST25.txt

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1957

<210> 88
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 <213> Bacillus licheniformis

<400> 88

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 35 40 45

Val Thr Val Pro Ala Asn Pro Lys Arg Val Val Thr Ile Gly Tyr Ala
 50 55 60

Gly Thr Met Leu Ala Phe Gly Ile Lys Pro Leu Gly Glu Thr Gly Lys
 65 70 75 80

Tyr Leu Gly Ser Pro Tyr Ile Lys Asp Gln Val Ser Gly Ile Lys Asp
 85 90 95

Ile Gly Gly Lys Asp Gly Phe Ser Val Ser Val Glu Lys Val Leu Glu
 100 105 110

Leu Lys Pro Asp Leu Ile Val Ser Met Thr Asn Asp Ser Lys Glu Tyr
 115 120 125

Glu Lys Leu Ser Lys Ile Ala Pro Thr Val Val Tyr Pro Phe Gly Thr
 130 135 140

Phe Lys Asp Ala Arg Asp Glu Met Lys Thr Phe Gly Lys Leu Leu Gly
 145 150 155 160

Lys Glu Lys Glu Ala Arg Glu Trp Thr Lys Thr Phe Asn Gln Lys Met
 165 170 175

Lys Ala Ala Arg Ala Lys Ile Lys Asp Ala Ser Val Lys Gly Glu Thr
 180 185 190

Phe Ser Leu Ile Gly Ala Tyr Ala Lys Ser Leu Tyr Val Tyr Gly Ala
 195 200 205

Tyr Gly Tyr Arg Gly Gly Glu Ala Ile Tyr Thr Gln Leu Gly Leu Thr
 210 215 220

Pro Pro Glu Ser Val Lys Lys Asp Ala Ile Asp Thr Ala Asp Gly Tyr
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10294.204.ST25.txt

225 230 235 240

Lys Ala Ile Ser Phe Glu Val Leu Pro Lys Tyr Ala Gly Asp Tyr Ile
 245 250 255

Phe Val Asp Glu Ser Tyr Asn Gly Lys Leu Asp Gln Asp Asn Pro Val
 260 265 270

Trp Ala Ser Leu Asp Ala Val Lys Lys Gly Lys Val Phe Phe Leu Asp
 275 280 285

Pro Asp Arg Phe Trp Pro Tyr Asp Pro Asn Ala Val Gln Ala Gln Ala
 290 295 300

Glu Glu Ile Ala Asp Met Ile Ser Lys Lys Ala Lys Asn Lys
 305 310 315

<210> 89
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 <213> Bacillus licheniformis

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 tcgaacgtcg acctttcaga agaattttcc gaaatgatta tcgcgagcg cggtttccag 180
 tccaatgcga aaatcattac aacctctgat gaaattcttc aggaactcgt caatctgaag 240
 cgataggagg gaaggaggcg ccctcgtgaa ggcgcctctt gataacacat gatcaaagtt 300
 acgcgattaa acggacagcc ctttattctg aatgcactat tcattgagca aattgaatgt 360
 tttccggata cgacaattac gctgtccaac ggaaaaaagt ttgttgtaa agaagatgaa 420
 gatacagttg tggatacaat cgtgtcattc tatcaaaaaa tccaaatact ttcttgtgac 480
 caaagaattg aggaatctga atg aat aaa aaa ctt cta gga att atg atg acg 533
 Met Asn Lys Lys 5 Leu Leu Gly Ile Met Met Thr 10
 1 5 10

att att ttg gca att gct gtg ttg gga acc gct gcg ttc ttt gtc atc 581
 ile ile leu ala ile ala val leu gly thr ala ala phe phe val ile 25
 15 20 25

aag gga agc gca agt gaa aaa gat caa aac gca gaa cct tcg atc gat 629
 lys gly ser ala ser glu lys asp gln asn ala glu pro ser ile asp 40
 30 35 40

gaa gtg gtc gaa tct tca gtt gaa gtc gcc gaa atc acg aca aac ttg 677
 glu val val glu ser ser val glu val ala glu ile thr thr asn leu 55
 45 50 55

aaa tca gac aat gta gtc cgt ttg tca atc aag ctt gaa acc gat tcg 725
 lys ser asp asn val val arg leu ser ile lys leu glu thr asp ser

10294.204.ST25.txt

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Ser Val Ile	Ser Leu Leu Ala Asn Thr	Asn Ala Asp Glu	Leu Ile Glu Gly	
	95	100	105	
caa aaa gga aaa gaa aaa ttt aaa gaa cag ctg aaa gaa aag ctg aac				869
Gln Lys Gly Lys Glu Lys Phe Lys Glu Gln Leu Lys Glu Lys Leu Asn				
	110	115	120	
acg aac tac atg aaa gag gga aaa gtg aaa act gtg tac att acc tcc				917
Thr Asn Tyr Met Lys Glu Gly Lys Val Lys Thr Val Tyr Ile Thr Ser				
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Phe Asn Leu Gln				
	140			
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tgaaatggac gccgacgagc tgaaaaaaga agagtccgtt aaaaaagtaa aagtctatga				1089
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	20	25	30	
Glu Lys Asp Gln Asn Ala Glu Pro Ser Ile Asp Glu Val Val Glu Ser				
	35	40	45	
Ser Val Glu Val Ala Glu Ile Thr Thr Asn Leu Lys Ser Asp Asn Val				
	50	55	60	
Val Arg Leu Ser Ile Lys Leu Glu Thr Asp Ser Lys Glu Ala Lys Glu				
	65	70	75	80
Glu Leu Glu Lys Arg Asp Phe Gln Ile Lys Asp Ser Val Ile Ser Leu				
	85	90	95	

10294.204.ST25.txt

Leu Ala Asn Thr Asn Ala Asp Glu Leu Glu Gly Gln Lys Gly Lys Glu
 100 105 110

Lys Phe Lys Glu Gln Leu Lys Glu Lys Leu Asn Thr Asn Tyr Met Lys
 115 120 125

Glu Gly Lys Val Lys Thr Val Tyr Ile Thr Ser Phe Asn Leu Gln
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 cagaatgaat gtcggatggt cgctctctgt tgtaaaagac ggactccgac gtctgaagac 180
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 aatcagccgg aatacagcga tcgcatgat aaagaaaacg gccagcgtaa taaaagaagg 360
 gatataattct cttttgtctt caggaaaata gagcataaac tgaatcagaa acggcgccat 420
 ttttcttcct ccctgaaatg atttttttac catttattta ttatgatacc attaggaggc 480
 agatgca gtg aac aac caa ttt caa gtc gga gat cgc gta aag ggc ttt 529
 Val Asn Asn Gln Phe Gln Val Gly Asp Arg Val Lys Gly Phe
 1 5 10
 tat aaa aca ggc gtc tac atc ggc gaa att acg gat gtt aaa ccg atg 577
 Tyr Lys Thr Gly Val Tyr Ile Gly Glu Ile Thr Asp Val Lys Pro Met
 15 20 25 30
 cac tac ctg gtc aaa atc ctc gcc gtg ctg acc cat ccg aag cag ggc 625
 His Tyr Leu Val Lys Ile Leu Ala Val Leu Thr His Pro Lys Gln Gly
 35 40 45
 gac ctt cat cat ccc aat cgg gca gac gtc cct ttt ttt cat gaa cga 673
 Asp Leu His His Pro Asn Arg Ala Asp Val Pro Phe Phe His Glu Arg
 50 55 60
 aaa gcg ctc gct tac ggt gaa cag acg aat atc ccg cac cgc atg gtg 721
 Lys Ala Leu Ala Tyr Gly Glu Gln Thr Asn Ile Pro His Arg Met Val
 65 70 75
 aag ccg ttc gat gaa gct gta ccg gat tat gcg gat tcg ctc cgc tca 769
 Lys Pro Phe Asp Glu Ala Val Pro Asp Tyr Ala Asp Ser Leu Arg Ser
 80 85 90
 gct ttg agc cgc tta aaa acg gat ctg caa aac gat tcg tcc gaa tac 817
 Ala Leu Ser Arg Leu Lys Thr Asp Leu Gln Asn Asp Ser Ser Glu Tyr
 95 100 105 110

10294.204.ST25.txt

gcg gca aaa tcg ctt gag ctt att cat ggg ctt gaa aaa gaa tat ttc 865
 Ala Ala Lys Ser Leu Glu Leu Ile His Gly Leu Glu Lys Glu Tyr Phe
 115 120 125

ctg cac aaa taaccaatc tgtttgcag attgggtttt ttatgtggcg 914
 Leu His Lys

tcggaaga cttttgagag gtcaaccggt tcgccgatcg tcgtcggctt cggattttcc 974
 aaatacttct tatcccggtc tacgagccga aacaacttat acgttgatcat cgcgtcgtca 1034
 agcgctttat gctgttttcc cggtcctgaa tcgccgtact cttccgctgc cttccacaaa 1094
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 cctttaaacg gaaacggaac atggttgaac atgcaatttt gcttcagcac tttcatatcc 1214
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<210> 92
 <211> 129
 <212> PRT
 <213> Bacillus licheniformis

<400> 92

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 20 25 30

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 35 40 45

His His Pro Asn Arg Ala Asp Val Pro Phe Phe His Glu Arg Lys Ala
 50 55 60

Leu Ala Tyr Gly Glu Gln Thr Asn Ile Pro His Arg Met Val Lys Pro
 65 70 75 80

Phe Asp Glu Ala Val Pro Asp Tyr Ala Asp Ser Leu Arg Ser Ala Leu
 85 90 95

Ser Arg Leu Lys Thr Asp Leu Gln Asn Asp Ser Ser Glu Tyr Ala Ala
 100 105 110

Lys Ser Leu Glu Leu Ile His Gly Leu Glu Lys Glu Tyr Phe Leu His
 115 120 125

Lys

10294.204.ST25.txt

<210> 93
<211> 1909
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<213> *Bacillus licheniformis*

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<221> CDS
<222> (501) .. (1406)
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[illegible]

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ttc act tcc acc gtc cag ctt tta agc gca aca gac aga aac aac aga 1061
 Phe Thr Ser Thr Val Gln Leu Leu Ser Ala Thr Asp Arg Asn Asn Arg
 175 180 185

atc tcc aca gtt atc gct gca gat aaa ggc aag aaa acg gtg aac gga 1109
 Ile Ser Thr Val Ile Ala Ala Asp Lys Gly Lys Lys Thr Val Asn Gly
 190 195 200

atc atc aac ggc tac gac tca gat aaa aag gcg ctt tcc atg gaa atc 1157
 Ile Ile Asn Gly Tyr Asp Ser Asp Lys Lys Ala Leu Ser Met Glu Ile
 205 210 215

atc gag cct gat gaa gac agg gaa gtg aaa aaa ggt gac ctc gtc gaa 1205
 Ile Glu Pro Asp Glu Asp Arg Glu Val Lys Lys Gly Asp Leu Val Glu
 220 225 230 235

act tcc ggt gcg ggc ggc gtt ttt cct aaa ggc ctg aca atc gga aaa 1253
 Thr Ser Gly Ala Gly Gly Val Phe Pro Lys Gly Leu Thr Ile Gly Lys
 240 245 250

gtg aca gag gtt gaa cca gat tcc tac ggt ttg acg aaa atc gct tat 1301
 Val Thr Glu Val Glu Pro Asp Ser Tyr Gly Leu Thr Lys Ile Ala Tyr
 255 260 265

gta gag ccg gca gcc gat) tat aac ctt gat aac gtc atc gtc gtc 1349
 Val Glu Pro Ala Ala Asp Met Tyr Asn Leu Asp Asn Val Ile Val Val
 270 275 280

gac aga acg ctt gat acg gtg gat gtc gac aag atg gac gat gag gag 1397
 Asp Arg Thr Leu Asp Thr Val Asp Val Asp Lys Met Asp Asp Glu Glu
 285 290 295

gaa ggg tcg tgaaacgctt ccttcttccc gtcgctcatga tgtttgtttt 1446
 Glu Gly Ser 300

agtatctgac agcgtctatg cggattttgt caacttgcct tttgtgacgg aagaacagca 1506
 gctcatcccg cgttttctgc tgcttgtctt agtttttatg acggcttatg tcaatcagcc 1566
 ttttgccatt acatatggat ttattttcgg actgtttatat gatattaatt acaccgacct 1626
 ttttaggtgta tatatgtttg gttttgccgg tatttgctat ttatcgtcaa aagcgttcaa 1686
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 tgaattttac caatatggcg tgcagatgct gatacgtccg gaaattatgc cgttccatca 1806
 atttgtgctc ggcaggctcc tgcccacgct tgcgctgaac gccgttggcg gccttctgct 1866
 catttaccgg ttcaaattggt tttttaccag tcttaagaaa gag 1909

<210> 94
 <211> 302
 <212> PRT
 <213> Bacillus licheniformis

<400> 94

Met Pro Gln Phe Phe Thr Asn Lys Arg Leu Met Leu Leu Leu Leu Cys
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10294.204.ST25.txt

Ile Ile Ile Leu Val Ala Met Ile Gly Phe Ser Leu Lys Asn Asp Arg
 20 25 30
 Asn Ala Thr Trp Pro Glu Lys Phe Ile Gly Asp Thr Thr Gly Val Phe
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 Gln Thr Ile Phe His Thr Pro Ala Gln Phe Phe Ala Gly Phe Phe Glu
 50 55 60
 Asn Ile Glu Asp Leu Lys Asn Thr Tyr Ser Glu Asn Glu Arg Leu Arg
 65 70 75 80
 Lys Lys Leu Asp Gly Gln Thr Gln Tyr Glu Ala Lys Leu Gln Glu Leu
 85 90 95
 Glu Asn Glu Asn Lys Ser Leu Arg Lys Glu Leu Gly His Leu Lys Ser
 100 105 110
 Ile Lys Asp Tyr Thr Pro Ile Leu Ala Thr Val Ile Ala Arg Asn Pro
 115 120 125
 Asp Lys Tyr Glu Trp Trp Asn Leu Ile Thr Ile Asn Lys Gly Ser Lys
 130 135 140
 His Gly Val Glu Lys Asp Met Ala Val Thr Asp Glu Asn Gly Asn Leu
 145 150 155 160
 Ile Gly Lys Ile Lys Ser Thr Lys Val Asn Asn Phe Thr Ser Thr Val
 165 170 175
 Gln Leu Leu Ser Ala Thr Asp Arg Asn Asn Arg Ile Ser Thr Val Ile
 180 185 190
 Ala Ala Asp Lys Gly Lys Lys Thr Val Asn Gly Ile Ile Asn Gly Tyr
 195 200 205
 Asp Ser Asp Lys Lys Ala Leu Ser Met Glu Ile Ile Glu Pro Asp Glu
 210 215 220
 Asp Arg Glu Val Lys Lys Gly Asp Leu Val Glu Thr Ser Gly Ala Gly
 225 230 235 240
 Gly Val Phe Pro Lys Gly Leu Thr Ile Gly Lys Val Thr Glu Val Glu
 245 250 255
 Pro Asp Ser Tyr Gly Leu Thr Lys Ile Ala Tyr Val Glu Pro Ala Ala
 260 265 270
 Asp Met Tyr Asn Leu Asp Asn Val Ile Val Val Asp Arg Thr Leu Asp
 275 280 285

10294.204.ST25.txt

Thr Val Asp Val Asp Lys Met Asp Asp Glu Glu Glu Gly Ser
 290 295 300

<210> 95
 <211> 1450
 <212> DNA
 <213> Bacillus licheniformis

<220>
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 <222> (121)..(951)

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 atg aca cat agc gca tta aag cat tta gat tat cac aat tgg gcg aat 168
 Met Thr His Ser Ala Leu Lys His Leu Asp Tyr His Asn Trp Ala Asn 15
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 caa agg gtg ctc acc cac ctg aaa agc ctg cct gaa gag ctg ttc acc 216
 Gln Arg Val Leu Thr His Leu Lys Ser Leu Pro Glu Glu Leu Phe Thr 30
 20
 cgg gaa atc aaa agc gtt ttt caa act gta tct gag gtt gtt acc cat 264
 Arg Glu Ile Lys Ser Val Phe Gln Thr Val Ser Glu Val Val Thr His 45
 35
 atg tgc ggc gct gac gac ctt agg ctg aaa gat acc acc ctc tta acc 312
 Met Cys Gly Ala Asp Asp Leu Arg Leu Lys Asp Thr Thr Leu Leu Thr 60
 50
 aga aag tgt ggg gga aag tat acc cgc aga acc gtt caa aaa atg aag 360
 Arg Lys Cys Gly Gly Lys Tyr Thr Arg Arg Thr Val Gln Lys Met Lys 80
 65
 cca aag ttt agg ttg cag tgt cag ttt aag aag aag cgc caa aag tac 408
 Pro Lys Phe Arg Leu Gln Cys Gln Phe Lys Lys Lys Arg Gln Lys Tyr 95
 85
 att tgt ggt gaa agg aat aat att ggg cgg aac act gtc aat ggt aat 456
 Ile Cys Gly Glu Arg Asn Asn Ile Gly Arg Asn Thr Val Asn Gly Asn 110
 100
 ttt aaa gca agc cga ttt aat gaa aaa tgg gta acc gac att acc tac 504
 Phe Lys Ala Ser Arg Phe Asn Glu Lys Trp Val Thr Asp Ile Thr Tyr 125
 115
 tta cat tat ggc tcc gat atg tta tat tta tca acg att atg gac tta 552
 Leu His Tyr Gly Ser Asp Met Leu Tyr Leu Ser Thr Ile Met Asp Leu 140
 130
 tat aac aac gaa ata gtg gct tac aaa ata ggt acg agc caa gat att 600
 Tyr Asn Asn Glu Ile Val Ala Tyr Lys Ile Gly Thr Ser Gln Asp Ile 160
 145
 aac cta gta tta gac aca ttg agg gaa gct gta gaa tta cgt aaa cca 648
 Asn Leu Val Leu Asp Thr Leu Arg Glu Ala Val Glu Leu Arg Lys Pro 175
 165
 gta ggg tta ctt ctt cat agc gac cag gga tct gtc tat act tca cat 696
 Val Gly Leu Leu Leu His Ser Asp Gln Gly Ser Val Tyr Thr Ser His 190
 180
 gca tat cag aat ttg gcc aaa gaa aaa ggc att acc aca agc atg tct 744
 Page 176

10294.204.ST25.txt

Ala Tyr Gln Asn Leu Ala Lys Glu Lys Gly Ile Thr Thr Ser Met Ser
 195 200 205

cga aaa gga aac tgc cat gat aat gcc gtc att gaa tcc ttt cac tcc 792
 Arg Lys Gly Asn Cys His Asp Asn Ala Val Ile Glu Ser Phe His Ser
 210 215 220

tcg cta aag tcg gaa gga ttt aac gct caa agt aga gca tct ata tcc 840
 Ser Leu Lys Ser Glu Gly Phe Asn Ala Gln Ser Arg Ala Ser Ile Ser
 225 230 235 240

aat tct aaa gta gta caa att gta aat caa tac atg tat cga tat aat 888
 Asn Ser Lys Val Val Gln Ile Val Asn Gln Tyr Met Tyr Arg Tyr Asn
 245 250 255

cat gta cga att cag gca aaa tta aac tac ctg tcc cca ctg gaa tac 936
 His Val Arg Ile Gln Ala Lys Leu Asn Tyr Leu Ser Pro Leu Glu Tyr
 260 265 270

agg gga cag gca gca taggtgtttt ttctaagtct cattttaacg ggtcagttca 991
 Arg Gly Gln Ala Ala

275

tctttacatg ccgggttttt gctttattca ggctgcttcg cgtccgcttc aagccgggcc 1051

actgctccag gcgacgcttt ttccaccgct ctggcggcta tgtcgtaagc ctcttcatac 1111

tgatatgcgt aaaaacagtt ttctgcttct ttcagctggt cggaaggat acggtcctgg 1171

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tcgtccgtct ttgttttcac ttccgtgaca agctgttccg cctcttgaag acgttcgttc 1291

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aggctgcgcg ccgtatcctt gattgtctgc ttcaattgc 1450

<210> 96
 <211> 277
 <212> PRT
 <213> Bacillus licheniformis

<400> 96

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 20 25 30

Arg Glu Ile Lys Ser Val Phe Gln Thr Val Ser Glu Val Val Thr His
 35 40 45

Met Cys Gly Ala Asp Asp Leu Arg Leu Lys Asp Thr Thr Leu Leu Thr
 50 55 60

Arg Lys Cys Gly Gly Lys Tyr Thr Arg Arg Thr Val Gln Lys Met Lys
 65 70 75 80

Pro Lys Phe Arg Leu Gln Cys Gln Phe Lys Lys Lys Arg Gln Lys Tyr
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10294.204.ST25.txt

85

90

95

Ile Cys Gly Glu Arg Asn Asn Ile Gly Arg Asn Thr Val Asn Gly Asn
 100 105 110

Phe Lys Ala Ser Arg Phe Asn Glu Lys Trp Val Thr Asp Ile Thr Tyr
 115 120 125

Leu His Tyr Gly Ser Asp Met Leu Tyr Leu Ser Thr Ile Met Asp Leu
 130 135 140

Tyr Asn Asn Glu Ile Val Ala Tyr Lys Ile Gly Thr Ser Gln Asp Ile
 145 150 155 160

Asn Leu Val Leu Asp Thr Leu Arg Glu Ala Val Glu Leu Arg Lys Pro
 165 170 175

Val Gly Leu Leu Leu His Ser Asp Gln Gly Ser Val Tyr Thr Ser His
 180 185 190

Ala Tyr Gln Asn Leu Ala Lys Glu Lys Gly Ile Thr Thr Ser Met Ser
 195 200 205

Arg Lys Gly Asn Cys His Asp Asn Ala Val Ile Glu Ser Phe His Ser
 210 215 220

Ser Leu Lys Ser Glu Gly Phe Asn Ala Gln Ser Arg Ala Ser Ile Ser
 225 230 235 240

Asn Ser Lys Val Val Gln Ile Val Asn Gln Tyr Met Tyr Arg Tyr Asn
 245 250 255

His Val Arg Ile Gln Ala Lys Leu Asn Tyr Leu Ser Pro Leu Glu Tyr
 260 265 270

Arg Gly Gln Ala Ala
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<210> 97
 <211> 2312
 <212> DNA
 <213> Bacillus licheniformis

<220>
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 <222> (501)..(1925)

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 cttaaacagg acaagagcga atcggttaaat aaggaaatca tgaggctcta ctttaacggg 180

10294.204.ST25.txt

ggaaaaaaga agaagcttag agctgttgat ttcgtcggaa cgattgctaa aattgacggc	240
gtctccgccg aggatatcgg gattatcacg atccaggagc aagggttcatt cgttgaaatt	300
ttaaaccggca aagggtccgct cgtcttagat gcgatgaaaa acacgacagt gaaagggaaa	360
ttgctgaaag tgcataaagc gaggaataa tcttaggctg ccgattttgt cgggagcttt	420
tttgctcgta ataaaccttg gataagcagc atatgatgga ttgtcaaaaa atgaaagcgt	480
tttaaaagag aggagaacaa atg aat atg aga aag tgt ttc atc caa gtc ctt	533
Met Asn Met Arg Lys Cys Phe Ile Gln Val Leu	1 5 10
gca ttg ctt ttc atc att gct gca tgt ttc gcg cca aac caa gcc tct	581
Ala Leu Leu Phe Ile Ile Ala Ala Cys Phe Ala Pro Asn Gln Ala Ser	15 20 25
gca caa act caa aaa cct gtt ttt tca gaa gtg acg gta cat gat cca	629
Ala Gln Thr Gln Lys Pro Val Phe Ser Glu Val Thr Val His Asp Pro	30 35 40
tcg att att aaa gcg aat ggc acg tac tat gtc ttc ggc tcc cat tta	677
Ser Ile Ile Lys Ala Asn Gly Thr Tyr Tyr Val Phe Gly Ser His Leu	45 50 55
gct tcg gcc aaa tcg acg gac ctg atg aat tgg acg caa att tcc tcg	725
Ala Ser Ala Lys Ser Thr Asp Leu Met Asn Trp Thr Gln Ile Ser Ser	60 65 70 75
agt gtc cac gac ggc aat cct ctg att ccg aac gtc tat gaa gaa tta	773
Ser Val His Asp Gly Asn Pro Leu Ile Pro Asn Val Tyr Glu Glu Leu	80 85 90
aaa gaa acc ttt gaa tgg gct gaa tct gat acg ttg tgg gca cct gat	821
Lys Glu Thr Phe Gln Glu Trp Ala Glu Ser Asp Thr Leu Trp Ala Pro Asp	95 100 105
gtc acc cag ctt gag gac ggc aag ttt tat atg tat tac aac gcc tgc	869
Val Thr Gln Leu Glu Asp Gly Lys Phe Tyr Met Tyr Tyr Asn Ala Cys	110 115 120
cgc ggg gat tct ccg aga tcc gcc ctc ggg ctt gct gtc gca gac gac	917
Arg Gly Asp Ser Pro Arg Ser Ala Leu Gly Leu Ala Val Ala Asp Asp	125 130 135
att gaa ggt cca tac aaa aat aaa ggc att ttt ctg aag tcg gga atg	965
Ile Glu Gly Pro Tyr Lys Asn Lys Gly Ile Phe Leu Lys Ser Gly Met	140 145 150 155
gat ggg atc agc aat gac ggg acg cct tat gac gcg aca aag cac cca	1013
Asp Gly Ile Ser Asn Asp Gly Thr Pro Tyr Asp Ala Thr Lys His Pro	160 165 170
aat gtc gtc gat ccc cac aca ttc ttt gat caa aac gga aag ctg tgg	1061
Asn Val Val Asp Pro His Thr Phe Phe Asp Gln Asn Gly Lys Leu Trp	175 180 185
atg gtg tac ggc tcc tat tcc ggc gga att ttt att tta gaa atg gac	1109
Met Val Tyr Gly Ser Tyr Ser Gly Gly Ile Phe Ile Leu Glu Met Asp	190 195 200
aag aaa acc gga ttt ccg ctt ccg gga cag gga tac ggc aaa aag ctg	1157
Lys Lys Thr Gly Phe Pro Leu Pro Gly Gln Gly Tyr Gly Lys Lys Leu	205 210 215
atc ggc ggc aac cac agc cgt att gaa ggc gca tat att ctc tac cat	1205
Ile Gly Gly Asn His Ser Arg Ile Glu Gly Ala Tyr Ile Leu Tyr His	

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220	225	230	235	
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Pro Glu Thr Gln Tyr Tyr Tyr Leu Tyr Met Ser Phe Gly Gly Leu Ala				
	240	245	250	
gct gac ggg ggt tac aac att cgc gtc gcc cgc tcc aaa aac cct gac				1301
Ala Asp Gly Gly Tyr Asn Ile Arg Val Ala Arg Ser Lys Asn Pro Asp				
	255	260	265	
ggg cct tat tat gat gca gaa ggc cac gcg atg att gac gtc cgc ggc				1349
Gly Pro Tyr Tyr Asp Ala Glu Gly His Ala Met Ile Asp Val Arg Gly				
	270	275	280	
aaa gaa gga acg ctt ttt gac gat cgt tca atc gaa ccg tac ggc gtc				1397
Lys Glu Gly Thr Leu Phe Asp Asp Arg Ser Ile Glu Pro Tyr Gly Val				
	285	290	295	
aaa ctg atg gga aat ttc tca ttt aac aat aaa aac ggc tat gtg tcg				1445
Lys Leu Met Gly Asn Phe Ser Phe Asn Asn Lys Asn Gly Tyr Val Ser				
	300	305	310	
ccg ggc cat aac tct gcc ttt tac gat gaa aaa agc ggt aaa tca tat				1493
Pro Gly His Asn Ser Ala Phe Tyr Asp Glu Lys Ser Gly Lys Ser Tyr				
	320	325	330	
tta atc ttc cac acc cgc ttc ccg gga cgg ggc gag gag cac gaa gtc				1541
Leu Ile Phe His Thr Arg Phe Pro Gly Arg Gly Glu Glu His Glu Val				
	335	340	345	
cgc gtc cac caa ttg ctg atg aac aaa caa ggc tgg ccg gtt gtc gcc				1589
Arg Val His Gln Leu Leu Met Asn Lys Gln Gly Trp Pro Val Val Ala				
	350	355	360	
cct cac cgc tat gcc gga gag aag ctt gaa aag gtg aaa aag tca gat				1637
Pro His Arg Tyr Ala Gly Glu Lys Leu Glu Lys Val Lys Lys Ser Asp				
	365	370	375	
gtg att ggc gat tac gaa ttg gtg agg cac ggc aaa gac atc tcc gca				1685
Val Ile Gly Asp Tyr Glu Leu Val Arg His Gly Lys Asp Ile Ser Ala				
	380	385	390	
gat att aaa gaa tcg aaa gaa atc cgc ttg aat caa aat ggc aaa ata				1733
Asp Ile Lys Glu Ser Lys Glu Ile Arg Leu Asn Gln Asn Gly Lys Ile				
	400	405	410	
aca ggc gca gta gcc gga acg tgg aag aac acg ggg cat aac aaa ata				1781
Thr Gly Ala Val Ala Gly Thr Trp Lys Asn Thr Gly His Asn Lys Ile				
	415	420	425	
gaa ctc aag atc gac gga aaa acc tac gat ggc gtg ttt ttg cgt cag				1829
Glu Leu Lys Ile Asp Gly Lys Thr Tyr Asp Gly Val Phe Leu Arg Gln				
	430	435	440	
tgg gat gcg gct tct gag cgt aag gtg atg acg ttt agt gcg ttg tct				1877
Trp Asp Ala Ala Ser Glu Arg Lys Val Met Thr Phe Ser Ala Leu Ser				
	445	450	455	
cgt gag gga gat gcg gtt tgg ggg agt agt tta aaa aga gcg gaa ttt				1925
Arg Glu Gly Asp Ala Val Trp Gly Ser Ser Leu Lys Arg Ala Glu Phe				
	460	465	470	
taaaaggaat ttcattctcta aaagcacatt cctgattaaa ggtatgtgct ttttaaata				1985
tttagatcaa atgggttgttt taatatggaa attcaggatg gattatacga taatacatat				2045
atgggtctttt ttactacata agttgttcgt gagattctat gaagaaaaat caacaagggg				2105

10294.204.ST25.txt

tgttgataaa atgggtttta aaaggagttt taaaataatg cctgggtgtca aacttaatat 2165
 aaataaaaaa agtggtggga tgacttttagg gggcaaaaat ggcaggataa cttataatac 2225
 ttctggcaaa gtaacaacaa gtgcaaaaat ccccgtaca ggtctatctt atagttccag 2285
 taaatctatt tcttcacac aaaaaca 2312

<210> 98
 <211> 475
 <212> PRT
 <213> Bacillus licheniformis

<400> 98

Met Asn Met Arg Lys Cys Phe Ile Gln Val Leu Ala Leu Leu Phe Ile
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Ile Ala Ala Cys Phe Ala Pro Asn Gln Ala Ser Ala Gln Thr Gln Lys
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Pro Val Phe Ser Glu Val Thr Val His Asp Pro Ser Ile Ile Lys Ala
35 40 45

Asn Gly Thr Tyr Tyr Val Phe Gly Ser His Leu Ala Ser Ala Lys Ser
50 55 60

Thr Asp Leu Met Asn Trp Thr Gln Ile Ser Ser Ser Val His Asp Gly
65 70 75 80

Asn Pro Leu Ile Pro Asn Val Tyr Glu Glu Leu Lys Glu Thr Phe Glu
85 90 95

Trp Ala Glu Ser Asp Thr Leu Trp Ala Pro Asp Val Thr Gln Leu Glu
100 105 110

Asp Gly Lys Phe Tyr Met Tyr Tyr Asn Ala Cys Arg Gly Asp Ser Pro
115 120 125

Arg Ser Ala Leu Gly Leu Ala Val Ala Asp Asp Ile Glu Gly Pro Tyr
130 135 140

Lys Asn Lys Gly Ile Phe Leu Lys Ser Gly Met Asp Gly Ile Ser Asn
145 150 155 160

Asp Gly Thr Pro Tyr Asp Ala Thr Lys His Pro Asn Val Val Asp Pro
165 170 175

His Thr Phe Phe Asp Gln Asn Gly Lys Leu Trp Met Val Tyr Gly Ser
180 185 190

Tyr Ser Gly Gly Ile Phe Ile Leu Glu Met Asp Lys Lys Thr Gly Phe
195 200 205

10294.204.ST25.txt

Pro Leu Pro Gly Gln Gly Tyr Gly Lys Lys Leu Ile Gly Gly Asn His
 210 215 220

Ser Arg Ile Glu Gly Ala Tyr Ile Leu Tyr His Pro Glu Thr Gln Tyr
 225 230 235 240

Tyr Tyr Leu Tyr Met Ser Phe Gly Gly Leu Ala Ala Asp Gly Gly Tyr
 245 250 255

Asn Ile Arg Val Ala Arg Ser Lys Asn Pro Asp Gly Pro Tyr Tyr Asp
 260 265 270

Ala Glu Gly His Ala Met Ile Asp Val Arg Gly Lys Glu Gly Thr Leu
 275 280 285

Phe Asp Asp Arg Ser Ile Glu Pro Tyr Gly Val Lys Leu Met Gly Asn
 290 295 300

Phe Ser Phe Asn Asn Lys Asn Gly Tyr Val Ser Pro Gly His Asn Ser
 305 310 315 320

Ala Phe Tyr Asp Glu Lys Ser Gly Lys Ser Tyr Leu Ile Phe His Thr
 325 330 335

Arg Phe Pro Gly Arg Gly Glu Glu His Glu Val Arg Val His Gln Leu
 340 345 350

Leu Met Asn Lys Gln Gly Trp Pro Val Val Ala Pro His Arg Tyr Ala
 355 360 365

Gly Glu Lys Leu Glu Lys Val Lys Lys Ser Asp Val Ile Gly Asp Tyr
 370 375 380

Glu Leu Val Arg His Gly Lys Asp Ile Ser Ala Asp Ile Lys Glu Ser
 385 390 395 400

Lys Glu Ile Arg Leu Asn Gln Asn Gly Lys Ile Thr Gly Ala Val Ala
 405 410 415

Gly Thr Trp Lys Asn Thr Gly His Asn Lys Ile Glu Leu Lys Ile Asp
 420 425 430

Gly Lys Thr Tyr Asp Gly Val Phe Leu Arg Gln Trp Asp Ala Ala Ser
 435 440 445

Glu Arg Lys Val Met Thr Phe Ser Ala Leu Ser Arg Glu Gly Asp Ala
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Val Trp Gly Ser Ser Leu Lys Arg Ala Glu Phe
 465 470 475

10294.204.ST25.txt

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<210> 99
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<212> DNA
<213> Bacillus licheniformis
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<220>
<221> CDS
<222> (501) .. (1325)
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[illegible]

10294.204.ST25.txt

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 160 165 170

tct ccg gtt gcc gcc gtc aat ctt gcc aat gcc tcg gcc att ccc gaa 1061
 Ser Pro Val Ala Ala Val Asn Leu Ala Asn Ala Ser Ala Ile Pro Glu
 175 180 185

gga gcg act gtg aaa agc gtt tct gcc gag gga acg ata tat cca agt 1109
 Gly Ala Thr Val Lys Ser Val Ser Ala Glu Gly Thr Ile Tyr Pro Ser
 190 195 200

ctc gga cac acc tac aga gaa gtc ctg aac aag gaa gaa ggc gtt tgg 1157
 Leu Gly His Thr Tyr Arg Glu Val Leu Asn Lys Glu Glu Gly Val Trp
 205 210 215

cac aca tcg gtt tca ggc ggc aca ctg ttt ccg gat cta aag cct gaa 1205
 His Thr Ser Val Ser Gly Gly Thr Leu Phe Pro Asp Leu Lys Pro Glu
 220 225 230 235

ctt gcg ctt ccc gtc aaa acg aca tgg aat gtg aga tac tat tcg ctc 1253
 Leu Ala Leu Pro Val Lys Thr Thr Trp Asn Val Arg Tyr Tyr Ser Leu
 240 245 250

gct tgg agc agt tca act tgg aga tcg ccg cag ctg aag atc aat tat 1301
 Ala Trp Ser Ser Ser Thr Trp Arg Ser Pro Gln Leu Lys Ile Asn Tyr
 255 260 265

caa tac gat tca aca tac ggc tgg taaacagatc caaatcccgg ccgatataaa 1355
 Gln Tyr Asp Ser Thr Tyr Gly Trp
 270 275

aagtaataga atgtaattgg catgaaagga gctcccatga atattagaga cagggtaaaa 1415

ctttcgcttt attccgagca gctgatgaag ccggccgccg cgaatgtgcc ggcaaagact 1475

aaaggctcca aaaggatgcc cgccagccaa acagacactc tctccatcag caaacaggct 1535

gaatcagccc aaaaaaatgc accgtcatta cggtcacaaa tgaacggcgt tcaatttgag 1595

atctataatc tttatgtgga caggcagcgt ttgaacagcc agatcgaagg ggcgctgcgg 1655

gagagcggaa tttccctttc cgaaagcgaa catctgacat tgcattgttg cggacataac 1715

cggattacag ttgaaggcat cgaagacgaa caaaaaagaa cccgtatcga agctgtttta 1775

aacgacagcg ataaacgggt cggtgcgcgt ctgttggggc acgcagaact gat 1828

<210> 100
 <211> 275
 <212> PRT
 <213> Bacillus licheniformis

<400> 100

Met Lys Lys Ser Leu Phe Leu Phe Val Phe Ser Leu Phe Leu Met Ala
 1 5 10 15

Ile Pro Ala Phe Ser Ala Ser Ala Asn Val Tyr Glu Asp Glu Tyr Glu
 20 25 30

Pro Asn Asn Ser Phe Ala Glu Ala Tyr Asp Val Gly Leu Trp Lys Tyr
 35 40 45

Lys Thr Ile Ser Ala Thr Ile His Ser Glu Ser Asp Lys Asp Tyr Tyr
 Page 184

10294.204.ST25.txt

50

55

60

Lys Phe Tyr Ala Thr Lys Gly Glu Gln Leu Ala Ile His Leu Lys Asn
 65 70 75 80
 Ile Pro Ala Asn Thr Asp Tyr Asp Leu Tyr Leu Phe Lys Asp Ala Tyr
 85 90 95
 Gly Tyr Pro Ala Val Gly Ser Ser Glu Arg Met Gly Asn Gln Asn Glu
 100 105 110
 Ile Ile Arg Leu Asp Val Pro Glu Thr Gly Arg Tyr Ile Ala Val Val
 115 120 125
 Met Ser Lys Asp Gly Ser Tyr Asp Gly Trp Gly Phe Tyr Arg Leu Glu
 130 135 140
 Phe Ile Asp Arg Met Lys Ser Gly Ala Tyr Thr Ala Asn Leu Ser Pro
 145 150 155 160
 Ser Ser Ile Ser Ser Pro Gly Gln Gly Val Val Ser Pro Val Ala Ala
 165 170 175
 Val Asn Leu Ala Asn Ala Ser Ala Ile Pro Glu Gly Ala Thr Val Lys
 180 185 190
 Ser Val Ser Ala Glu Gly Thr Ile Tyr Pro Ser Leu Gly His Thr Tyr
 195 200 205
 Arg Glu Val Leu Asn Lys Glu Glu Gly Val Trp His Thr Ser Val Ser
 210 215 220
 Gly Gly Thr Leu Phe Pro Asp Leu Lys Pro Glu Leu Ala Leu Pro Val
 225 230 235 240
 Lys Thr Thr Trp Asn Val Arg Tyr Tyr Ser Leu Ala Trp Ser Ser Ser
 245 250 255
 Thr Trp Arg Ser Pro Gln Leu Lys Ile Asn Tyr Gln Tyr Asp Ser Thr
 260 265 270
 Tyr Gly Trp
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<210> 101
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 <212> DNA
 <213> Bacillus licheniformis

<220>
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[illegible]

10294.204.ST25.txt

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Gly Arg Ile Ile Ala Thr Leu Gln Arg Asn Ala Ser Val Thr Ile Leu	205	210	215	
aac gaa cag cac gcc tgg tat gaa atc gaa ttt aat gga caa aaa ggc				1205
Asn Glu Gln His Gly Trp Tyr Glu Ile Glu Phe Asn Gly Gln Lys Gly	220	225	230	
tgg gcc gca agc cac tat att ctc gaa gga aac aaa cag aac agc gga				1253
Trp Ala Ala Ser His Tyr Ile Leu Glu Gly Asn Lys Gln Asn Ser Gly	235	240	245	
acc tcc gga aca agc agc agc tcc gaa gca aaa cgg cag ggc acc atc				1301
Thr Ser Gly Thr Ser Ser Ser Ser Glu Ala Lys Arg Gln Gly Thr Ile	250	255	260	
gtg tat gaa agc aca aat gtt aga agc ggg gcc tcg aca tcc tca gcg				1349
Val Tyr Glu Ser Thr Asn Val Arg Ser Gly Ala Ser Thr Ser Ser Ala	265	270	275	280
atc gtc aaa cgc acg gga aaa ggc gag tct tac ccg atc gtc tct aca				1397
Ile Val Lys Arg Thr Gly Lys Gly Glu Ser Tyr Pro Ile Val Ser Thr	285	290	295	
aaa gga gac tgg tat gaa atc aaa ctg tca aac ggc gat tcc gct tat				1445
Lys Gly Asp Trp Tyr Glu Ile Lys Leu Ser Asn Gly Asp Ser Ala Tyr	300	305	310	
gtc gca agc tgg gtc gtt cag act gtt gac cag gca ggc tca gcc gga				1493
Val Ala Ser Trp Val Val Gln Thr Val Asp Gln Ala Gly Ser Ala Gly	315	320	325	
gat tcg aaa agc gca gca ccg cct ttg gca aag cgg tca agc tcg gga				1541
Asp Ser Lys Ser Ala Ala Pro Pro Leu Ala Lys Arg Ser Ser Ser Gly	330	335	340	
ggc aca atc aaa aat aaa acg gtt gtc atc gat gcc gga cat gga gga				1589
Gly Thr Ile Lys Asn Lys Thr Val Val Ile Asp Ala Gly His Gly Gly	345	350	355	360
cat gac agc ggg aca atc gga acg cgg ggg acg ctc gaa aaa cgg ctg				1637
His Asp Ser Gly Thr Ile Gly Thr Arg Gly Thr Leu Glu Lys Arg Leu	365	370	375	
acc atc aaa acg gca acg ctt ctt gcc gcg aaa ctg aga gcc gat gcc				1685
Thr Ile Lys Thr Ala Thr Leu Leu Ala Ala Lys Leu Arg Ala Asp Gly	380	385	390	
gtc aac gtc tat atg acg cgg aat gac gat tct ttc gtc agc ctt cag				1733
Val Asn Val Tyr Met Thr Arg Asn Asp Asp Ser Phe Val Ser Leu Gln	395	400	405	
tcg cgg gtc gcg acc tct cat tac cga aac gcc gac gct ttt atc agc				1781
Ser Arg Val Ala Thr Ser His Tyr Arg Asn Ala Asp Ala Phe Ile Ser	410	415	420	
att cat tat gat agc ttt cca aat gcg tcc gtc agg gga aat acg gcc				1829
Ile His Tyr Asp Ser Phe Pro Asn Ala Ser Val Arg Gly Asn Thr Ala	425	430	435	440
tat tac tac agc ccg tcc aaa gac cgg aag ctc gca gca gac gtg cag				1877
Tyr Tyr Tyr Ser Pro Ser Lys Asp Arg Lys Leu Ala Ala Asp Val Gln	445	450	455	
tcc gag atc gaa agg cac tcg cct ctg cca agc cgc ggc gta cta ttc				1925
Ser Glu Ile Glu Arg His Ser Pro Leu Pro Ser Arg Gly Val Leu Phe				

10294.204.ST25.txt

460 465 470
 ggg gac tac ttc gta tta aga gaa aat aaa cag ccc gcc gca ttg ttt 1973
 Gly Asp Tyr Phe Val Leu Arg Glu Asn Lys Gln Pro Ala Ala Leu Phe
 475 480 485
 gaa ctc ggc tac ttg agc cat cct caa gaa gaa gcg gta gtc agc acg 2021
 Glu Leu Gly Tyr Leu Ser His Pro Gln Glu Glu Ala Val Val Ser Thr
 490 495 500
 aac gct tac aga gaa aga gtg aca gac ggc atc aga agc ggt cta gaa 2069
 Asn Ala Tyr Arg Glu Arg Val Thr Asp Gly Ile Arg Ser Gly Leu Glu
 505 510 515 520
 aac tat ttt gac taatttaaaa agctcccaat cgaggagcttt ttatgctttc 2121
 Asn Tyr Phe Asp
 gaatccataa taaacgtgac gggacccgaa tttgtcagct tgacatccat cattttctcca 2181
 aatcttccccg tttcgacagt gacgcctttt gcgcgaagca tgctgttcca ctcttcgtac 2241
 aattgaagcg cctgatcgagg ctttgccgct tttgtaaaat tcggccgtct tccttttttc 2301
 gtgtcgccgt acaaggtaaa ctgagaaacc gataaaacgg agccccgac atctaaaagc 2361
 gacaggttca tcttttcgcc ttcattcctca aaaattcgca gattgacaag cttctccgcc 2421
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 aggccgattt cgccgacagt ctcgcctcct accgaaacgc ttgcatctgt gacgcgctga 2541
 acaactaatc tcatgacgct tttcctccta attcatcacc ctg 2584
 <210> 102
 <211> 524
 <212> PRT
 <213> Bacillus licheniformis
 <400> 102
 Asn Met Lys Lys Arg Ala Val Leu Ile Leu Ser Met Met Leu Ala Ala
 1 5 10 15
 Gln Ala Ala Phe Tyr Thr Ser Ser Asn Thr Ala Ser Ala Ala Ile Gly
 20 25 30
 Glu Ala Val Ile Ala Thr Asp Glu Ile Asn Val Arg Ser Gly Pro Gly
 35 40 45
 Leu Ser His Glu Ile Val Ser Val Val Ser Arg Asn Glu Ser Tyr Pro
 50 55 60
 Ile Leu Glu Glu Arg Gly Asp Trp Val Gln Ile Gln Leu Asn Gly Gly
 65 70 75 80
 Gln Lys Gly Trp Val Val Ser Trp Leu Ile Lys Lys Lys Ser Gln Val
 85 90 95
 Ser Ser Gly Ser Asp Ser Ala Ser Gly Lys Val Thr Ser Ser Glu Ala
 100 105 110

10294.204.ST25.txt

Asn Leu Arg Ile Arg Lys Gly Pro Gly Thr Ser Tyr Glu Val Gln Gly
 115 120 125
 Val Phe Pro Glu Gly Glu Gln Ala Asp Leu Leu Lys Thr Asp Gly Lys
 130 135 140
 Trp Ile Lys Ile Ser Tyr Gln Asn Ile Thr Gly Trp Val Tyr Ser Asp
 145 150 155 160
 Tyr Val Asn Gln Gly Ser Gly Ala Lys Gln Ser Gln Ser Ser Ser Ser
 165 170 175
 His Ala Ser Ser Ser Lys Ser Gly Thr Val Gly Val Ser Thr Leu Asn
 180 185 190
 Val Arg Ser Thr Ala Ser His Gln Gly Arg Ile Ile Ala Thr Leu Gln
 195 200 205
 Arg Asn Ala Ser Val Thr Ile Leu Asn Glu Gln His Gly Trp Tyr Glu
 210 215 220
 Ile Glu Phe Asn Gly Gln Lys Gly Trp Ala Ala Ser His Tyr Ile Leu
 225 230 235 240
 Glu Gly Asn Lys Gln Asn Ser Gly Thr Ser Gly Thr Ser Ser Ser Ser
 245 250 255
 Glu Ala Lys Arg Gln Gly Thr Ile Val Tyr Glu Ser Thr Asn Val Arg
 260 265 270
 Ser Gly Ala Ser Thr Ser Ser Ala Ile Val Lys Arg Thr Gly Lys Gly
 275 280 285
 Glu Ser Tyr Pro Ile Val Ser Thr Lys Gly Asp Trp Tyr Glu Ile Lys
 290 295 300
 Leu Ser Asn Gly Asp Ser Ala Tyr Val Ala Ser Trp Val Val Gln Thr
 305 310 315 320
 Val Asp Gln Ala Gly Ser Ala Gly Asp Ser Lys Ser Ala Ala Pro Pro
 325 330 335
 Leu Ala Lys Arg Ser Ser Ser Gly Gly Thr Ile Lys Asn Lys Thr Val
 340 345 350
 Val Ile Asp Ala Gly His Gly Gly His Asp Ser Gly Thr Ile Gly Thr
 355 360 365
 Arg Gly Thr Leu Glu Lys Arg Leu Thr Ile Lys Thr Ala Thr Leu Leu
 370 375 380

10294.204.ST25.txt

Ala Ala Lys Leu Arg Ala Asp Gly Val Asn Val Tyr Met Thr Arg Asn
385 390 395 400

Asp Asp Ser Phe Val Ser Leu Gln Ser Arg Val Ala Thr Ser His Tyr
405 410 415

Arg Asn Ala Asp Ala Phe Ile Ser Ile His Tyr Asp Ser Phe Pro Asn
420 425 430

Ala Ser Val Arg Gly Asn Thr Ala Tyr Tyr Tyr Ser Pro Ser Lys Asp
435 440 445

Arg Lys Leu Ala Ala Asp Val Gln Ser Glu Ile Glu Arg His Ser Pro
450 455 460

Leu Pro Ser Arg Gly Val Leu Phe Gly Asp Tyr Phe Val Leu Arg Glu
465 470 475 480

Asn Lys Gln Pro Ala Ala Leu Phe Glu Leu Gly Tyr Leu Ser His Pro
485 490 495

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500 505 510

Asp Gly Ile Arg Ser Gly Leu Glu Asn Tyr Phe Asp
515 520

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<211> 1774
<212> DNA
<213> Bacillus licheniformis

<220>
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<222> (516)..(1271)

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aacttaagct acacagggcc tgataaacag gaaacattgg atactttagg aaaaattaaa 180
gatgcctata tgaaaggcga taaggcgctg ttctcaaaaa gagaagaagt cattgaaaag 240
aatattaagg cgcttgaaga cgaaacagtc agcgctgatt ccaaagttga caaacagcgg 300
tttttgtatg agcttgaaac aagcaagctt gatatgaagg ctgctgaaga aattgagccg 360
ttgatcgtgc ttgataacca ggctgccggc atgtcgcta agaaaagagc ggtgctgggc 420
gtactgatcg gtttagcgct gtcatttttc atcattgtca ttccggaagt ttccagagaa 480
cgttaaatth ttaattgggg atgtggatca ggacc atg acg agg caa aaa cct 533
Met Thr Arg Gln Lys Pro
1 5

10294.204.ST25.txt

tta atc tct gtc att acg cct tcc tat aac gcg gag gaa ttt atc gaa Leu Ile Ser Val Ile Thr Pro Ser Tyr Asn Ala Glu Glu Phe Ile Glu 10 15 20	581
aaa acc att aag tcc gtc tta aat cag acg ttt tcc gac tgg gaa atg Lys Thr Ile Lys Ser Val Leu Asn Gln Thr Phe Ser Asp Trp Glu Met 25 30 35	629
atc att gcc gat gat tgc tca aca gat ggg aca aga gac att ttg aag Ile Ile Ala Asp Asp Cys Ser Thr Asp Gly Thr Arg Asp Ile Leu Lys 40 45 50	677
cgc tat gaa gaa gat gat gag cgg atc cat gcc att ttt ctg aaa gag Arg Tyr Glu Glu Asp Asp Glu Arg Ile His Ala Ile Phe Leu Lys Glu 55 60 65 70	725
aat caa ggt gct gca gcg gcg cga aat gcg gcg ctc agc aaa gcc gaa Asn Gln Gly Ala Ala Ala Arg Asn Ala Ala Leu Ser Lys Ala Glu 75 80 85	773
ggg cgc tat gtc gcc ttt ttg gac agc gat gat gtt tgg aaa gca gaa Gly Arg Tyr Val Ala Phe Leu Asp Ser Asp Asp Val Trp Lys Ala Glu 90 95 100	821
aag ctg gat aag cag ctc gcc ttc atg aga aag cat cag cat gct ttc Lys Leu Asp Lys Gln Leu Ala Phe Met Arg Lys His Gln His Ala Phe 105 110 115	869
tca ttt acg gca tac gag ctg atc agc caa gac ggc gaa ccg ctt cat Ser Phe Thr Ala Tyr Glu Leu Ile Ser Gln Asp Gly Glu Pro Leu His 120 125 130	917
aaa acc att cat gca ccc gta agc ctt aca tat gat gat gta tta aaa Lys Thr Ile His Ala Pro Val Ser Leu Thr Tyr Asp Asp Val Leu Lys 135 140 145 150	965
aat acg atc atc ggc tgc ttg acg gtg atg att gac aga gaa caa acg Asn Thr Ile Ile Gly Cys Leu Thr Val Met Ile Asp Arg Glu Gln Thr 155 160 165	1013
ggt gat atc cgg atg ccg aat att aga acc cgc cag gat ttg gcg aca Gly Asp Ile Arg Met Pro Asn Ile Arg Thr Arg Gln Asp Leu Ala Thr 170 175 180	1061
tgg ctg tcc gta tta aag cgg ggg ttc aag gca tat gga ctg aac gaa Trp Leu Ser Val Leu Lys Arg Gly Phe Lys Ala Tyr Gly Leu Asn Glu 185 190 195	1109
ccc ctc gcg gaa tac cgc atc gtt gaa aca tcg atc tcc aga aac aag Pro Leu Ala Glu Tyr Arg Ile Val Glu Thr Ser Ile Ser Arg Asn Lys 200 205 210	1157
tgg aag gcg gcg cga aaa acc tgg tac gta tac agg gaa atc gaa cga Trp Lys Ala Ala Arg Lys Thr Trp Tyr Val Tyr Arg Glu Ile Glu Arg 215 220 225 230	1205
ctt cac ttg atg aaa gcg aca tgg tgc ttt ttc cat tac gct aag aac Leu His Leu Met Lys Ala Thr Trp Cys Phe Phe His Tyr Ala Lys Asn 235 240 245	1253
gca gta atg aaa aga tta taacggcatt gacagaaaag gtgattgaaa Ala Val Met Lys Arg Leu 250	1301
gtgaaagcag atcaattcat acacgtcata gtagcgacag gtgaatgggg gcaggatcag	1361
ctaagataca gaaggcaccg ccttgctgag tttttagcag gccgcaagga gacgaaggaa	1421

10294.204.ST25.txt

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gtcatttggg tttgtccgtc tgaaaatcct tcccgtgaga cttttacatt gcttgacaac 1481
ggaatcaagc aatttgcagt caaagatttt ttgaaaaaga aaatattcag gtttgcccgc 1541
tacaaagatg ttttctatca aagcaagctg aagccgctgc ttgaccggct gaaagaagac 1601
gttcagggag aaaaggtgtg cttatgggtac accttccccg gctttccgct gctgtcgtcg 1661
ctttatcaat gggatcaggt catctatgac tgcagcgacc tgtgggcggc cccgatcagc 1721
ggtagccaaa gccttgtctc aggattcagg caaaaggtca tttttgaagc tga 1774

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<210> 104
<211> 252
<212> PRT
<213> Bacillus licheniformis

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<400> 104

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Met Thr Arg Gln Lys Pro Leu Ile Ser Val Ile Thr Pro Ser Tyr Asn
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Ala Glu Glu Phe Ile Glu Lys Thr Ile Lys Ser Val Leu Asn Gln Thr
20          25          30

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Phe Ser Asp Trp Glu Met Ile Ile Ala Asp Asp Cys Ser Thr Asp Gly
35          40          45

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Thr Arg Asp Ile Leu Lys Arg Tyr Glu Glu Asp Asp Glu Arg Ile His
50          55          60

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Ala Ile Phe Leu Lys Glu Asn Gln Gly Ala Ala Ala Arg Asn Ala
65          70          75          80

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Ala Leu Ser Lys Ala Glu Gly Arg Tyr Val Ala Phe Leu Asp Ser Asp
85          90          95

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Asp Val Trp Lys Ala Glu Lys Leu Asp Lys Gln Leu Ala Phe Met Arg
100         105         110

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Lys His Gln His Ala Phe Ser Phe Thr Ala Tyr Glu Leu Ile Ser Gln
115         120         125

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Asp Gly Glu Pro Leu His Lys Thr Ile His Ala Pro Val Ser Leu Thr
130         135         140

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Tyr Asp Asp Val Leu Lys Asn Thr Ile Ile Gly Cys Leu Thr Val Met
145         150         155         160

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Ile Asp Arg Glu Gln Thr Gly Asp Ile Arg Met Pro Asn Ile Arg Thr
165         170         175

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Arg Gln Asp Leu Ala Thr Trp Leu Ser Val Leu Lys Arg Gly Phe Lys
180         185         190

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10294.204.ST25.txt

Ala Tyr Gly Leu Asn Glu Pro Leu Ala Glu Tyr Arg Ile Val Glu Thr
 195 200 205

Ser Ile Ser Arg Asn Lys Trp Lys Ala Ala Arg Lys Thr Trp Tyr Val
 210 215 220

Tyr Arg Glu Ile Glu Arg Leu His Leu Met Lys Ala Thr Trp Cys Phe
 225 230 235 240

Phe His Tyr Ala Lys Asn Ala Val Met Lys Arg Leu
 245 250

<210> 105
 <211> 1309
 <212> DNA
 <213> Bacillus licheniformis

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 <222> (485)..(808)

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 aatcaacacc gaaaatgaag gaactcccgg tcagatgaaa aaaatcgctc acacagtga 180
 gaaaaaggac gtcccgccct tattcgtgga gacaagcggt gacccgcgga gcatggaaag 240
 cctttcagcc gaaacgggcg tgccgattaa agcaaaagtc ttcaccgatt cgatcggaaa 300
 gcccggtga agcgggagat tcctattata agatgatgaa agaaaacctt gaccggatcc 360
 atcaaggcct cgccgaataa ccaatgaact gctgtacagg atgtacagca gtttttttct 420
 tatgtttttc cgatttttaa gcaggggtaca acgaaggga aacgaggaaa aaggagtgtg 480
 tttc gtg aaa tct gga tat gag gaa tgc atc aaa gcc tgc cga gaa tgt 529
 Val Lys Ser Gly Tyr Glu Glu Cys Ile Lys Ala Cys Arg Glu Cys
 1 5 10 15
 ctt gaa gcc tgc aac cac tgc ttt gac aaa tgt ctg atg gaa gaa gag 577
 Leu Glu Ala Cys Asn His Cys Phe Asp Lys Cys Leu Met Glu Glu Glu
 20 25 30
 gct ggg atg atg gcc gaa tgc atc cgt ctt gac cgg gaa tgc gcc gag 625
 Ala Gly Met Met Ala Glu Cys Ile Arg Leu Asp Arg Glu Cys Ala Glu
 35 40 45
 atg tgc ggt tac gca att caa gcc atg acg cgc aac agc ccg tat gcc 673
 Met Cys Gly Tyr Ala Ile Gln Ala Met Thr Arg Asn Ser Pro Tyr Ala
 50 55 60
 gaa gat att tgc cag ctt tgc gca aag gtt tgc gaa gct tgc gcc aat 721
 Glu Asp Ile Cys Gln Leu Cys Ala Lys Val Cys Glu Ala Cys Gly Asn
 65 70 75
 gaa tgc agc cag cac aag cat gac cac tgc caa ttt tgc gct gaa agc 769
 Glu Cys Ser Gln His Lys His Asp His Cys Gln Phe Cys Ala Glu Ser
 80 85 90 95

10294.204.ST25.txt

tgc ttt gca tgc gcg gaa gcg tgc aga aaa atg gct tct taacttgaaa 818
 Cys Phe Ala Cys Ala Glu Ala Cys Arg Lys Met Ala Ser
 100 105
 catccggccc tcgagccgga tatttttatg taggaaatgt ttattttttc tccttcccc 878
 tttctaaact gatacaatat gactataaaa gggggtttta tcatgaaaga cagcgtgttt 938
 caaatgactt ctgacacata tcaatctctc agcgattcag aacggcattt gctcgagtac 998
 atttatcagc acttagacgt catcgccact ttatcgattg taaaattaag cgaggatgca 1058
 aatgtttcaa cagccacgat tgtcaggtta atgaaaaaac tcggatatga cggctacact 1118
 tcttttaagt atgcattaaa agaaaaacac cacctcggac acgctccgct gatggatgat 1178
 atcgacagcc aaattaaaca ggccgtgcta aagaatgaaa gagaagttct ggatacgatt 1238
 aagatgcttg atatcgggtt gatcgaagat gccattcaaa aaatcagcaa tgccgaaaaa 1298
 gtttacatct t 1309

<210> 106
 <211> 108
 <212> PRT
 <213> Bacillus licheniformis

<400> 106

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 Glu Ala Cys Asn His Cys Phe Asp Lys Cys Leu Met Glu Glu Glu Ala
 20 25 30
 Gly Met Met Ala Glu Cys Ile Arg Leu Asp Arg Glu Cys Ala Glu Met
 35 40 45
 Cys Gly Tyr Ala Ile Gln Ala Met Thr Arg Asn Ser Pro Tyr Ala Glu
 50 55 60
 Asp Ile Cys Gln Leu Cys Ala Lys val Cys Glu Ala Cys Gly Asn Glu
 65 70 75 80
 Cys Ser Gln His Lys His Asp His Cys Gln Phe Cys Ala Glu Ser Cys
 85 90 95
 Phe Ala Cys Ala Glu Ala Cys Arg Lys Met Ala Ser
 100 105

<210> 107
 <211> 1561
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (284)..(1060)

10294.204.ST25.txt

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tccaaacagg aagtcaaagt ccgcgaagtt atgattgaag gcatcctttc gatcttgaa 180
ggccaggctc caaaagtcac tgaacaaaag cttttgatgt acgtttctcc aagcgaacgc 240
tccagcatcg tcatcccaga tggagacaaa ggggacagca gca atg gct aga aaa 295
Met Ala Arg Lys
1
aag aag cac aaa aaa gac cat gaa gaa cac gtg gat gag tct tgg ctc 343
Lys Lys His Lys Lys Asp His Glu Glu His Val Asp Glu Ser Trp Leu
5 10 15 20
atc cca tat gca gac ttg ctg aca ctg ctt ttg gcc ctg ttc atc gta 391
Ile Pro Tyr Ala Asp Leu Leu Thr Leu Leu Ala Leu Phe Ile Val
25 30 35
ctg ttt gcc atg agc tgc atc gac gcc aag aag ttc gat atg ctg tca 439
Leu Phe Ala Met Ser Ser Ile Asp Ala Lys Lys Phe Asp Met Leu Ser
40 45 50
aaa tca ttt aat gcc gta ttt acc ggc gga aca gga atg atg gat tat 487
Lys Ser Phe Asn Ala Val Phe Thr Gly Gly Thr Gly Met Met Asp Tyr
55 60 65
tcc agc ttc acc gag ccg aaa acg agc aca acc gaa gat gga aaa agc 535
Ser Ser Phe Thr Glu Pro Lys Thr Ser Thr Thr Glu Asp Gly Lys Ser
70 75 80
cct gac cag gca aaa gat ctc tcc gaa gct caa aaa gaa aaa gac aag 583
Pro Asp Gln Ala Lys Asp Leu Ser Glu Ala Gln Lys Glu Lys Asp Lys
85 90 95 100
cag tgc ctg aaa aaa att cag gag cag gtc aac cgg ttt att aaa gag 631
Gln Ser Leu Lys Lys Ile Gln Glu Gln Val Asn Arg Phe Ile Lys Glu
105 110 115
aag aat ctt caa aaa cag gtc aat acg aag ctg aca gac gag ggc ctc 679
Lys Asn Leu Gln Lys Gln Val Asn Thr Lys Leu Thr Asp Glu Gly Leu
120 125 130
ctc ctt tcc atc gag gat aat atc ttt ttc gat tcc gga aaa gcg gag 727
Leu Leu Ser Ile Glu Asp Asn Ile Phe Phe Asp Ser Gly Lys Ala Glu
135 140 145
atc cgc cag cag gac att ccg ctg gcc aag gaa gta tcc gac ctt ctc 775
Ile Arg Gln Gln Asp Ile Pro Leu Ala Lys Glu Val Ser Asp Leu Leu
150 155 160
gta ttg aac ccg ccc cgc aat atc gta atc agc ggg cat acg gac aat 823
Val Leu Asn Pro Pro Arg Asn Ile Val Ile Ser Gly His Thr Asp Asn
165 170 175 180
gtg ccg att cga aat tct caa ttt aaa tca aat tgg cat tta agc gtg 871
Val Pro Ile Arg Asn Ser Gln Phe Lys Ser Asn Trp His Leu Ser Val
185 190 195
atg cgg gct gtc aat ttc atg ggg ctt tta atc gaa aat cca aag ctt 919
Met Arg Ala Val Asn Phe Met Gly Leu Leu Ile Glu Asn Pro Lys Leu
200 205 210
gac gcc aag atc ttc agc gcg aaa ggc tac ggg gaa ttt aaa ccg atc 967
Asp Ala Lys Ile Phe Ser Ala Lys Gly Tyr Gly Glu Phe Lys Pro Ile
215 220 225

10294.204.ST25.txt

gct tca aat gac acc gaa gaa gga aga aga aaa aac aga cgc gtt gaa 1015
 Ala Ser Asn Asp Thr Glu Glu Gly Arg Arg Lys Asn Arg Arg Val Glu
 230 235 240
 atc ctt atc ctg ccg atc ggc cag gaa aat ctg aat aaa aaa gaa 1060
 Ile Leu Ile Leu Pro Ile Gly Gln Glu Asn Leu Asn Lys Lys Glu
 245 250 255
 taaggaagct gtcttttggc agcttcctta ctctttgccc ttataaatat ttcttgcatt 1120
 cagtcgcgact tttttcagca tttcgatgca ggcttctttc tcctcatcgc ttaatacgct 1180
 gatcatgttg tgcagctctt ctgcatgacc cggaaaaatc ttctcgagga gctcggtgcc 1240
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 cagctgcttt tgctcaagct tgtcaaccac atatgtaata ctcccgctcg ccagaagaat 1360
 cttatcccct atttgcgtgaa ggggctgac ccctttatga tagaggagtt ctaaaacggc 1420
 aaactcgggt ggattcagac catgatgatg aatatgttta ttcatatgat cattaatgga 1480
 tctgtacgct cgagataata caataaataa cttaaggac tgttcctggt ctctattact 1540
 catatcactc atctccaaag a 1561

<210> 108
 <211> 259
 <212> PRT
 <213> Bacillus licheniformis

<400> 108

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Glu Ser Trp Leu Ile Pro Tyr Ala Asp Leu Leu Thr Leu Leu Leu Ala
20 25 30

Leu Phe Ile Val Leu Phe Ala Met Ser Ser Ile Asp Ala Lys Lys Phe
35 40 45

Asp Met Leu Ser Lys Ser Phe Asn Ala Val Phe Thr Gly Gly Thr Gly
50 55 60

Met Met Asp Tyr Ser Ser Phe Thr Glu Pro Lys Thr Ser Thr Thr Glu
65 70 75 80

Asp Gly Lys Ser Pro Asp Gln Ala Lys Asp Leu Ser Glu Ala Gln Lys
85 90 95

Glu Lys Asp Lys Gln Ser Leu Lys Lys Ile Gln Glu Gln Val Asn Arg
100 105 110

Phe Ile Lys Glu Lys Asn Leu Gln Lys Gln Val Asn Thr Lys Leu Thr
115 120 125

Asp Glu Gly Leu Leu Leu Ser Ile Glu Asp Asn Ile Phe Phe Asp Ser
Page 196

10294.204.ST25.txt

130

135

140

Gly Lys Ala Glu Ile Arg Gln Gln Asp Ile Pro Leu Ala Lys Glu Val
 145 150 155 160

Ser Asp Leu Leu Val Leu Asn Pro Pro Arg Asn Ile Val Ile Ser Gly
 165 170 175

His Thr Asp Asn Val Pro Ile Arg Asn Ser Gln Phe Lys Ser Asn Trp
 180 185 190

His Leu Ser Val Met Arg Ala Val Asn Phe Met Gly Leu Leu Ile Glu
 195 200 205

Asn Pro Lys Leu Asp Ala Lys Ile Phe Ser Ala Lys Gly Tyr Gly Glu
 210 215 220

Phe Lys Pro Ile Ala Ser Asn Asp Thr Glu Glu Gly Arg Arg Lys Asn
 225 230 235 240

Arg Arg Val Glu Ile Leu Ile Leu Pro Ile Gly Gln Glu Asn Leu Asn
 245 250 255

Lys Lys Glu

<210> 109
 <211> 1735
 <212> DNA
 <213> Bacillus licheniformis

<220>
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 <222> (501)..(1232)

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 cccgaactca gcaagacaag agcaaaacaa ccctttggtc agcctgcctg tgccaaccga 180
 cgagctcgtc aagaatacag acgcagtcac cgtcactcat tcggacccgg atttctctcc 240
 tataaactag aagcctcatg ttgaaaaagt attttatatt gaaaaagaat tctatctggg 300
 acctcgccgg gagcaggaaa gaggatcact gaaacatcaa tgaattatat tgtaaaaaat 360
 cagaatttta tataaaatca aactttatca gtaaaaaaac tgtaacgaaa ttcgcatcaa 420
 tctgtcatag cgggtgacatt ttgctgtggt acgattttcc ctggttagttt caaaagggct 480
 aacaaggagg gatttaactt atg aag aag aca atc atg tcc ttg gct gca gcc 533
 Met Lys Lys Thr Ile Met Ser Leu Ala Ala Ala
 1 5 10
 gcg gct atg tcg gcg act gca ttc gga gcg act gcc tca gca aaa gaa 581
 Ala Ala Met Ser Ala Thr Ala Phe Gly Ala Thr Ala Ser Ala Lys Glu

10294.204.ST25.txt

15	20	25	
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gga atg aac ctc aag gac tta aaa aaa tgg aat cag ctt tca tca gat Gly Met Asn Leu Lys Asp Leu Lys Lys Trp Asn Gln Leu Ser Ser Asp 45 50 55			677
ctg att ttt cca ggt caa aag ctg aac att tct tct caa gaa gaa aaa Leu Ile Phe Pro Gly Gln Lys Leu Asn Ile Ser Ser Gln Glu Glu Lys 60 65 70 75			725
tct gaa gaa aag cag tac acc gtt cag cca ggg gac acg ctc tca aaa Ser Glu Glu Lys Gln Tyr Thr Val Gln Pro Gly Asp Thr Leu Ser Lys 80 85 90			773
atc gca aaa gag ttc ggt gtg act gta agc gat ctt caa aaa cgg aac Ile Ala Lys Glu Phe Gly Val Thr Val Ser Asp Leu Gln Lys Arg Asn 95 100 105			821
aac ctg aag tca gac ttg att att gca ggg caa acg att gca ata aac Asn Leu Lys Ser Asp Leu Ile Ile Ala Gly Gln Thr Ile Ala Ile Asn 110 115 120			869
gga gaa gcg gca gct gca gca gcg cct gtg aaa caa gag tcc gct cca Gly Glu Ala Ala Ala Ala Ala Pro Val Lys Gln Glu Ser Ala Pro 125 130 135			917
aaa caa aat gat cag cct gtc aac gta caa aag gaa atc aca gtg acc Lys Gln Asn Asp Gln Pro Val Asn Val Gln Lys Glu Ile Thr Val Thr 140 145 150 155			965
gca act gcg tat acg gca aat gac ggg ggc att tca ggc atc aca aaa Ala Thr Ala Tyr Thr Ala Asn Asp Gly Gly Ile Ser Gly Ile Thr Lys 160 165 170			1013
acg gga gtc gac ctg aat gcg aac cgc aat gcg aaa gtc atc gcg gtt Thr Gly Val Asp Leu Asn Ala Asn Arg Asn Ala Lys Val Ile Ala Val 175 180 185			1061
gat cca agc gtg att ccg ctc ggc acg aaa gta tat gtg gaa ggc tat Asp Pro Ser Val Ile Pro Leu Gly Thr Lys Val Tyr Val Glu Gly Tyr 190 195 200			1109
ggc gaa gcg acg gct gaa gac acc ggc ggc gcc att aaa ggc cat aaa Gly Glu Ala Thr Ala Glu Asp Thr Gly Gly Ala Ile Lys Gly His Lys 205 210 215			1157
ata gac gta ttt att cca gat aaa aaa gac gct ttc aat tgg ggc gtc Ile Asp Val Phe Ile Pro Asp Lys Lys Asp Ala Phe Asn Trp Gly Val 220 225 230 235			1205
aaa acc gta aag gtt aaa att tta aac tgatataaaa aatgcaggag Lys Thr Val Lys Val Lys Ile Leu Asn 240			1252
gcgttaattg cctcctgcat ttttttgtcg aacgatgttt atgctgcatg ctgttccgcg			1312
cgtctgcttt ttacaaaaac cgaaatcgca agagcggcgg ctgcaaaggc gatggctacg			1372
aaataaacca tatgaacgcc ttctgtcatg ccttgcattgt gcagctcctg acggctgcct			1432
ccggaagagt gcgcgataaa gcgattcgaa acggttgtca ggatcgtcgt atacaatgcc			1492
ggaccgattg cccctgaaac ttgattaact gtattcatta tcgccgaacc atgcgggtaa			1552

10294.204.ST25.txt

agcggtttgg gcacctgatt caaacccgagc gtcataatcg gagccattgt caacccgacg 1612
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 ttcgtaaaca gcgaaaggac ggcaatcaca atgatcaatc cggtgatcaa cagcggttta 1732
 aag 1735

<210> 110
 <211> 244
 <212> PRT
 <213> Bacillus licheniformis

<400> 110

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 Thr Ala Phe Gly Ala Thr Ala Ser Ala Lys Glu Ile Glu Val Gln Lys
 20 25 30
 Gly Asp Thr Leu Trp Gly Ile Ser Gln Asn Tyr Gly Met Asn Leu Lys
 35 40 45
 Asp Leu Lys Lys Trp Asn Gln Leu Ser Ser Asp Leu Ile Phe Pro Gly
 50 55 60
 Gln Lys Leu Asn Ile Ser Ser Gln Glu Glu Lys Ser Glu Glu Lys Gln
 65 70 75 80
 Tyr Thr Val Gln Pro Gly Asp Thr Leu Ser Lys Ile Ala Lys Glu Phe
 85 90 95
 Gly Val Thr Val Ser Asp Leu Gln Lys Arg Asn Asn Leu Lys Ser Asp
 100 105 110
 Leu Ile Ile Ala Gly Gln Thr Ile Ala Ile Asn Gly Glu Ala Ala Ala
 115 120 125
 Ala Ala Ala Pro Val Lys Gln Glu Ser Ala Pro Lys Gln Asn Asp Gln
 130 135 140
 Pro Val Asn Val Gln Lys Glu Ile Thr Val Thr Ala Thr Ala Tyr Thr
 145 150 155 160
 Ala Asn Asp Gly Gly Ile Ser Gly Ile Thr Lys Thr Gly Val Asp Leu
 165 170 175
 Asn Ala Asn Arg Asn Ala Lys Val Ile Ala Val Asp Pro Ser Val Ile
 180 185 190
 Pro Leu Gly Thr Lys Val Tyr Val Glu Gly Tyr Gly Glu Ala Thr Ala
 195 200 205

10294.204.ST25.txt
Glu Asp Thr Gly Gly Ala Ile Lys Gly His Lys Ile Asp Val Phe Ile
210 215 220

Pro₂₂₅ Asp Lys Lys Asp Ala₂₃₀ Phe Asn Trp Gly Val₂₃₅ Lys Thr Val Lys Val₂₄₀

Lys Ile Leu Asn

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<210> 111
<211> 1731
<212> DNA
<213> Bacillus licheniformis
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<220>
<221> CDS
<222> (507)..(1274)
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gcg cgc gaa aac cgg gtg ttg aag gct gaa ttt tca ctc ggg cgc ctg 629
Ala Arg Glu Asn Arg Val Leu Lys Ala Glu Phe Ser Leu Gly Arg Leu
30 35 40

aaa aag gaa ttg aat gtc ttt ttt att tca gat att cat agg cgg aca 677
Lys Lys Glu Leu Asn Val Phe Phe Ile Ser Asp Ile His Arg Arg Thr
45 50 55

gtc agc gaa gac att att tgt gaa gtg aaa gaa cgc ggg gtt cag ctc 725
Val Ser Glu Asp Ile Ile Cys Glu Val Lys Glu Arg Gly Val Gln Leu
60 65 70

gtc atc atc ggc ggc gac tta gca gag ggc ggc gtc cct tat acg aga 773
Val Ile Ile Gly Gly Asp Leu Ala Glu Gly Gly Val Pro Tyr Thr Arg
75 80 85

att gaa gaa aat atc aaa agg ctt tca agt ttg gga aaa acg tat ttt 821
ile Glu Glu Asn ile Lys Arg Leu Ser Ser Leu Gly Lys Thr Tyr Phe
90 95 100 105

gta tgg gga aat aac gat tat gaa gtt gat cag gaa agg ctg ctg gaa 869
Page 200

10294.204.ST25.txt

Val	Trp	Gly	Asn	Asn	Asp	Tyr	Glu	Val	Asp	Gln	Glu	Arg	Leu	Leu	Glu		
				110					115					120			
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Ile	Phe	Lys	Thr	Tyr	Gly	Val	Thr	Pro	Leu	Arg	Asn	Ala	Ser	Val	Leu		
			125					130					135				
cat	gac	cat	caa	gga	caa	act	gtc	aat	att	tgc	gga	gtg	gat	gac	atc		965
His	Asp	His	Gln	Gly	Gln	Thr	Val	Asn	Ile	Cys	Gly	Val	Asp	Asp	Ile		
			140				145					150					
aga	ctc	gaa	ttg	gat	gat	tac	ccg	gca	gct	ctc	ggc	ggc	gtg	cag	ccg		1013
Arg	Leu	Glu	Leu	Asp	Asp	Tyr	Pro	Ala	Ala	Leu	Gly	Gly	Val	Gln	Pro		
			155			160					165						
ggt	ttt	ccg	act	gtc	ctt	gtg	tca	cat	aat	ccg	gag	att	cat	cat	caa		1061
Gly	Phe	Pro	Thr	Val	Leu	Val	Ser	His	Asn	Pro	Glu	Ile	His	His	Gln		
					175					180					185		
ata	cag	gag	gcg	gac	ggt	att	gac	ctg	ata	ttg	agc	ggt	cat	acc	cac		1109
Ile	Gln	Glu	Ala	Asp	Gly	Ile	Asp	Leu	Ile	Leu	Ser	Gly	His	Thr	His		
				190					195					200			
gga	gga	cag	att	cgc	ttc	ggc	aga	ttc	ggg	ctc	tgt	gaa	atc	gga	gga		1157
Gly	Gly	Gln	Ile	Arg	Phe	Gly	Arg	Phe	Gly	Leu	Cys	Glu	Ile	Gly	Gly		
			205					210					215				
acc	ggc	act	gtt	ttc	aag	gct	ccg	tac	ttg	atc	agc	aac	ggc	tat	gga		1205
Thr	Gly	Thr	Val	Phe	Lys	Ala	Pro	Tyr	Leu	Ile	Ser	Asn	Gly	Tyr	Gly		
			220				225					230					
acg	tcg	aag	ctt	cct	gcg	ggg	atc	cta	ggc	gtg	ccc	gcg	atc	gcc	atg		1253
Thr	Ser	Lys	Leu	Pro	Ala	Gly	Ile	Leu	Gly	Val	Pro	Ala	Ile	Ala	Met		
			235			240					245						
gct	tat	gtc	gga	gag	gaa	ttt	gatccgcgag	ggctcggcaa	aatgatgggg								1304
Ala	Tyr	Val	Gly	Glu	Glu	Phe											
					255												
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agctatttgt	tttggatttt	gctgccccgg	ccgcagcact	ccgctaagcg	aaaaacaagt												1484
gtgaaaaaag	cgagcttggc	ctacggcgcc	gtcttgatga	acaaacggct	gctgtcaatc												1544
atttcacttg	gatttctatt	aatgggaagc	tttgttacgc	tgttcaatta	tatcgggttt												1604
cagttgatgg	gacctccgta	cagactctct	caaactgtca	tcgggttcat	ctttatcggt												1664
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ccgttgga																	1731

<210> 112
 <211> 256
 <212> PRT
 <213> Bacillus licheniformis

<400> 112

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 1 5 10 15

Ala Leu Val Trp Arg Met Ser Ala Ile Ala Arg Glu Asn Arg Val Leu
 Page 201

10294.204.ST25.txt

20

25

30

Lys Ala Glu Phe Ser Leu Gly Arg Leu Lys Lys Glu Leu Asn Val Phe
 35 40 45

Phe Ile Ser Asp Ile His Arg Arg Thr Val Ser Glu Asp Ile Ile Cys
 50 55 60

Glu Val Lys Glu Arg Gly Val Gln Leu Val Ile Ile Gly Gly Asp Leu
 65 70 75 80

Ala Glu Gly Gly Val Pro Tyr Thr Arg Ile Glu Glu Asn Ile Lys Arg
 85 90 95

Leu Ser Ser Leu Gly Lys Thr Tyr Phe Val Trp Gly Asn Asn Asp Tyr
 100 105 110

Glu Val Asp Gln Glu Arg Leu Leu Glu Ile Phe Lys Thr Tyr Gly Val
 115 120 125

Thr Pro Leu Arg Asn Ala Ser Val Leu His Asp His Gln Gly Gln Thr
 130 135 140

Val Asn Ile Cys Gly Val Asp Asp Ile Arg Leu Glu Leu Asp Asp Tyr
 145 150 155 160

Pro Ala Ala Leu Gly Gly Val Gln Pro Gly Phe Pro Thr Val Leu Val
 165 170 175

Ser His Asn Pro Glu Ile His His Gln Ile Gln Glu Ala Asp Gly Ile
 180 185 190

Asp Leu Ile Leu Ser Gly His Thr His Gly Gly Gln Ile Arg Phe Gly
 195 200 205

Arg Phe Gly Leu Cys Glu Ile Gly Gly Thr Gly Thr Val Phe Lys Ala
 210 215 220

Pro Tyr Leu Ile Ser Asn Gly Tyr Gly Thr Ser Lys Leu Pro Ala Gly
 225 230 235 240

Ile Leu Gly Val Pro Ala Ile Ala Met Ala Tyr Val Gly Glu Glu Phe
 245 250 255

<210> 113
 <211> 1722
 <212> DNA
 <213> Bacillus licheniformis

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 <222> (540)..(788)

10294.204.ST25.txt

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caagagcacg aacatgctct taaggattta gcaccattct gtcatagaca gcggttgccg      180
ggtttcacag ggccagtccc tccaccactc ttgataagga aaaccttttt atgcgatttt      240
ttaatagttt taatattaat actttttata aaaatgtcaa tgggttttaa aaaactcttc      300
gtttttttca ttttcttctt ctgcgggttaa actggagggc gtatcgaatc aatgtgtgaa      360
tttttcgtca ggacagccgt tcaaacagtc aacaagatgc tgaacaaaca gaataaatta      420
gaattttttt caatttttat ttccaaaaac agaaactttt tattgagttc accggtctat      480
aatgtgtacc tgatttcaaa atgggtatta taaaaaatga cagattaagg aggggttttt      539
atg aac aaa aaa aca gtg ttt aaa gcg ttc gga atg ttg atg aca ggg      587
Met Asn Lys Lys Thr Val Phe Lys Ala Phe Gly Met Leu Met Thr Gly
1 5 10 15
gta ttg ttt ttt gcg ctg tac agt gcg gcc gca ctt cct tct gca cac      635
Val Leu Phe Phe Ala Leu Tyr Ser Ala Ala Ala Leu Pro Ser Ala His
20 25 30
gcg gca aac gaa aaa aaa ccg acg gtc acg agc cat acg tac aaa aac      683
Ala Ala Asn Glu Lys Lys Pro Thr Val Thr Ser His Thr Tyr Lys Asn
35 40 45
att aag gct ttg aaa tac ccg caa gtt tca aat gta agc ccc aaa tct      731
Ile Lys Ala Leu Lys Tyr Pro Gln Val Ser Asn Val Ser Pro Lys Ser
50 55 60
ctc caa aac aag atc aac aaa gat ttt aaa cat tat att gag cag tcc      779
Leu Gln Asn Lys Ile Asn Lys Asp Phe Lys His Tyr Ile Glu Gln Ser
65 70 75 80
tac aaa gat tagtaaaaaa caagaaagac ggccaacagc acggatacca      828
Tyr Lys Asp

aacggattat caaacgtcct ttgaagtga ataccggacc ggccaaaagc tgagcatcct      888
gacaagcaat tacgtctatt ccggcggagc gcacggaaat acggcagtcc gctctttcaa      948
ctatgacctt gtctctaaaa aacgggtgta tttatccgac atcctaaata caaaatcgaa      1008
aatggataag acaaaaacat acattttaca ctatattcaa aaacacagcg acattttctt      1068
tccggatgtg aagaagaaag acatcgtcct cggtaaaaac acggccttct attacactaa      1128
cgacggcatt gcgatcgtct tccaacaata cgatgtcgcc ctttatgccg ccggaaatcc      1188
ggtcggttga gttccgaaaa cggtgtatca ataaataaca accgggggct tagtccttgt      1248
gcatcgcttg tgacccgaac ccgaaaaaac ggaagaagag ctgaatctga tcgtcgactt      1308
tggcgtaacg gtgaaagatg taacgattga acatccggtc tacggagact taacagcttc      1368
gatcagggtc agcacaagaa aagaagtcgc ggatttcgtc aaaaaaatct cttcgacaaa      1428
cgccgcttat ctgtctcagc tgacaaacgg catccatctc cacacattgg aggcagatga      1488
tgaagagaag atcgaacaag cttgcggcgc cctgcaaaaa gcgggcatcc tcattcccga      1548

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10294.204.ST25.txt

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gcgttgtagg caccgagcat tttcaccttg cagcccaaag cttcaagctc agctattgca 1668
cctggaatca gcacgtcatc cagggccatt tcaatatcaa taatgaagaa ataa 1722

<210> 114
<211> 83
<212> PRT
<213> Bacillus licheniformis

<400> 114

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1 5 10 15

Val Leu Phe Phe Ala Leu Tyr Ser Ala Ala Ala Leu Pro Ser Ala His
20 25 30

Ala Ala Asn Glu Lys Lys Pro Thr Val Thr Ser His Thr Tyr Lys Asn
35 40 45

Ile Lys Ala Leu Lys Tyr Pro Gln Val Ser Asn Val Ser Pro Lys Ser
50 55 60

Leu Gln Asn Lys Ile Asn Lys Asp Phe Lys His Tyr Ile Glu Gln Ser
65 70 75 80

Tyr Lys Asp

<210> 115
<211> 1705
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (507)..(1202)

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tagaaaaacta ccctgaaaaa gggcggcagg aaaaagtcgt tctccctct ctagtgcgca 180
gaaagggtac gaaagcaata tttaaagacg gcattttgga agtgatgttc ttaaaaaatg 240
aggactttta cctgtctgaa atcgacatca cgttttgaaa acggccagct tgaaaaagca 300
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tgcctgacat tcggccgcgc ctttaaattt tgacagtgtt agtcattatt ccttaaaaaag 420
tctctgtaac tatttcctct ttcggctgtt gtcgatttgt ccttataatg ataatgggtc 480
tcaatttata aaacaggagg atgtat atg aaa aag aaa atc agc ata ttg atc 533
Met Lys Lys Lys Ile Ser Ile Leu Ile
1 5

10294.204.ST25.txt

aca gca atg ttt ttg aca atc ctt tgt ttt tgc cct caa gct tcc gct 581
 Thr Ala Met Phe Leu Thr Ile Leu Cys Phe Ser Pro Gln Ala Ser Ala
 10 15 20 25
 gcg tac aac tca ctg cat acg ggc tat gcc act tat acg ggg tgc ggc 629
 Ala Tyr Asn Ser Leu His Thr Gly Tyr Ala Thr Tyr Thr Gly Ser Gly
 30 35 40
 tac tcc ggc ggc gca ttg ctt ttg gac cct att ccg tcc aat atg aag 677
 Tyr Ser Gly Gly Ala Leu Leu Leu Asp Pro Ile Pro Ser Asn Met Lys
 45 50 55
 atc acc gct tta aat ccg aca gat atg aat tac cgc ggt gtg aaa gct 725
 Ile Thr Ala Leu Asn Pro Thr Asp Met Asn Tyr Arg Gly Val Lys Ala
 60 65 70
 gct ctt gcc ggc gcc tat ctg cgg gtt gaa ggg ccg aaa gga aaa acg 773
 Ala Leu Ala Gly Ala Tyr Leu Arg Val Glu Gly Pro Lys Gly Lys Thr
 75 80 85
 acc gtc tat gtt acc gat ctg tat cct gaa gga gcg ccg gga gcc ctt 821
 Thr Val Tyr Val Thr Asp Leu Tyr Pro Glu Gly Ala Pro Gly Ala Leu
 90 95 100 105
 gac ctt tca ccg aac gct ttt cgc gag atc ggc gat atg aaa gac ggc 869
 Asp Leu Ser Pro Asn Ala Phe Arg Glu Ile Gly Asp Met Lys Asp Gly
 110 115 120
 aaa atc gac att aaa tgg cgt ata gtc aaa gcg ccg att acc ggc aat 917
 Lys Ile Asp Ile Lys Trp Arg Ile Val Lys Ala Pro Ile Thr Gly Asn
 125 130 135
 ttc act tac cgg atc aaa gaa ggc agc agc caa tgg tgg gcg gcg atc 965
 Phe Thr Tyr Arg Ile Lys Glu Gly Ser Ser Gln Trp Trp Ala Ala Ile
 140 145 150
 caa gtc aga aac cac aaa tat ccc gtc atg aaa atg gaa tat tac aaa 1013
 Gln Val Arg Asn His Lys Tyr Pro Val Met Lys Met Glu Tyr Tyr Lys
 155 160 165
 gac gga aag tgg atc aac atg gag aaa acg gat tac aac cat ttc gtc 1061
 Asp Gly Lys Trp Ile Asn Met Glu Lys Thr Asp Tyr Asn His Phe Val
 170 175 180 185
 agc acc aat ctc ggg aca agt ccg ctt aaa gtc agg atc aca gat atc 1109
 Ser Thr Asn Leu Gly Thr Ser Pro Leu Lys Val Arg Ile Thr Asp Ile
 190 195 200
 cga gga aaa gtc gtc aaa gac acg ata aaa aag ctt ccg gaa aac ggg 1157
 Arg Gly Lys Val Val Lys Asp Thr Ile Lys Lys Leu Pro Glu Asn Gly
 205 210 215
 acg tca agc gca tat acc gta ccg gga aaa gta cag ttc cct gac 1202
 Thr Ser Ser Ala Tyr Thr Val Pro Gly Lys Val Gln Phe Pro Asp
 220 225 230
 tgatcgatcc ggaaagaatg agacggcggc caaaggcgaa aagattcgca ggctttggcc 1262
 gccgcttcat attgacatcc ggcatttaga cgccagcaac aattggctta ttgatcaata 1322
 gcccggtcct gtcctctgt atggagctgc gcccggaaca cctccgtacg gaaaagcccc 1382
 aggagctgcc ccgtagccgt aataaggcgc gccgccgtaa ggtcccgggt atggcggcgg 1442
 gtaagcgtaa ggtcttgggt agttaaaaat cgcgcttccg agaaatccgc ccagcaatcc 1502
 gccgacaagc ggcgctccaa aacccagaa taacgggaat ctggccgggt atccggcagg 1562

10294.204.ST25.txt

acctgatctc gaataaagca tatgaggggtt cattggcttt taccctcctt tatgtctgcc 1622
 tatagtaaag gtattcataa agtcgggaaa cgtttgggct attcttcata aatcattttt 1682
 tttgtcattc cgccgtccac cgt 1705

<210> 116
 <211> 232
 <212> PRT
 <213> Bacillus licheniformis

<400> 116

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 20 25 30

Gly Tyr Ala Thr Tyr Thr Gly Ser Gly Tyr Ser Gly Gly Ala Leu Leu
 35 40 45

Leu Asp Pro Ile Pro Ser Asn Met Lys Ile Thr Ala Leu Asn Pro Thr
 50 55 60

Asp Met Asn Tyr Arg Gly Val Lys Ala Ala Leu Ala Gly Ala Tyr Leu
 65 70 75 80

Arg Val Glu Gly Pro Lys Gly Lys Thr Thr Val Tyr Val Thr Asp Leu
 85 90 95

Tyr Pro Glu Gly Ala Pro Gly Ala Leu Asp Leu Ser Pro Asn Ala Phe
 100 105 110

Arg Glu Ile Gly Asp Met Lys Asp Gly Lys Ile Asp Ile Lys Trp Arg
 115 120 125

Ile Val Lys Ala Pro Ile Thr Gly Asn Phe Thr Tyr Arg Ile Lys Glu
 130 135 140

Gly Ser Ser Gln Trp Trp Ala Ala Ile Gln Val Arg Asn His Lys Tyr
 145 150 155 160

Pro Val Met Lys Met Glu Tyr Tyr Lys Asp Gly Lys Trp Ile Asn Met
 165 170 175

Glu Lys Thr Asp Tyr Asn His Phe Val Ser Thr Asn Leu Gly Thr Ser
 180 185 190

Pro Leu Lys Val Arg Ile Thr Asp Ile Arg Gly Lys Val Val Lys Asp
 195 200 205

Thr Ile Lys Lys Leu Pro Glu Asn Gly Thr Ser Ser Ala Tyr Thr Val
 Page 206

215

220

<210> 117
<211> 1687
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501) .. (1184)

[illegible]

10294.204.ST25.txt

125	130	135	
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Ala Leu Asp Gln Leu Asp Asn Asn Gly Lys Asn Val Val Tyr Leu Leu			
140	145	150	
aca gac ggt gag gaa aca tgc gga ggc aat ccg gta aaa gtc gca aca			1013
Thr Asp Gly Glu Glu Thr Cys Gly Gly Asn Pro Val Lys Val Ala Thr			
	160	165	
gaa ctg cgc aaa tcc aat gcg gtt gtc aac gtg atc ggc ttt gat tat			1061
Glu Leu Arg Lys Ser Asn Ala Val Val Asn Val Ile Gly Phe Asp Tyr			
	175	180	
gaa gga gac ttc cac gga caa ttg acc agt atc gca gca gct ggc ggc			1109
Glu Gly Asp Phe His Gly Gln Leu Thr Ser Ile Ala Ala Ala Gly Gly			
	190	195	
ggt gaa tat ttc cag gca aaa act aaa aat gac atc aaa aga att ttt			1157
Gly Glu Tyr Phe Gln Ala Lys Thr Lys Asn Asp Ile Lys Arg Ile Phe			
	205	210	
act cag gaa gca att gag ctt tct aaa taaactggaa aaaagctgtg			1204
Thr Gln Glu Ala Ile Glu Leu Ser Lys			
	220	225	
gacatgtttc cgcagctttc cttttgtgat gaaaagattg tcaaaagtca agaaaaatac			1264
tttacaata ttaagttatt gtgtcagagc gttgaaccct gctgcgtcct ttggaggggt			1324
tatttgtcgt aacggtagct ttattgggat gaaatcggcc ttttagcaga cttttttgat			1384
aggtcttaag tgaatgcgtc gatcgattat cgtaaggatt atgaagaatt tgtgaatttg			1444
aaaaggagat ccggcctatt tatttctatc aagccttctt ttacgatgtt ggtggacttg			1504
atctcatgcg gaagatcggc ccgaaaaaac aaatgcggaa aggaaagtga gaaagttgaa			1564
aaagaggttt gctctgttga caacgttcac catgcttttg tcattggcgc cggcagcagc			1624
ttttgagggt gaaaacggaa atgcggacaa cagcaaaaaa gatgtcaatg ttgcagttgt			1684
gct			1687

<210> 118
 <211> 228
 <212> PRT
 <213> Bacillus licheniformis

<400> 118

Met Lys Lys Lys Met Thr Leu Gly Ile Leu Thr Ala Met Val Leu Ser
 1 5 10 15

Leu Gly Ser Pro Ala Phe Ala Ala Glu Lys Lys Gln Glu Val Thr Val
 20 25 30

Ala Glu Asp Ala Pro Asn Val Ala Ile Met Leu Asp Ala Ser Gly Ser
 35 40 45

Met Ala Lys Lys Ile Gly Gly Val Ser Lys Tyr Glu Leu Ala Lys Asn
 50 55 60

10294.204.ST25.txt

Glu Ala Phe Ser Phe Gly Ser Lys Leu Glu Asn Ala Asn Val Leu Met
65 70 75 80

Arg Val Phe Gly Ser Glu Gly Asn Asn Lys Asn Ser Gly Lys Val Gln
85 90 95

Ser Cys Asn Ala Ile Arg Gly Val Tyr Gly Phe Gln Thr Tyr Asp Glu
100 105 110

Gln Ser Phe Arg Asn Ser Leu Asn Gly Ile Gly Pro Thr Gly Trp Thr
115 120 125

Pro Ile Ala Asn Ala Leu Gln Asp Ala Lys Asn Ala Leu Asp Gln Leu
130 135 140

Asp Asn Asn Gly Lys Asn Val Val Tyr Leu Leu Thr Asp Gly Glu Glu
145 150 155 160

Thr Cys Gly Gly Asn Pro Val Lys Val Ala Thr Glu Leu Arg Lys Ser
165 170 175

Asn Ala Val Val Asn Val Ile Gly Phe Asp Tyr Glu Gly Asp Phe His
180 185 190

Gly Gln Leu Thr Ser Ile Ala Ala Ala Gly Gly Gly Glu Tyr Phe Gln
195 200 205

Ala Lys Thr Lys Asn Asp Ile Lys Arg Ile Phe Thr Gln Glu Ala Ile
210 215 220

Glu Leu Ser Lys
225

<210> 119
<211> 1428
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(944)

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tccgccggaa ggctgaacga actgatggaa gaagctcaga aagaagcgtt ttgcggtgcg 120
cttggcgagt atcatccgta tttttgggca tcaaagcttc atttttatat tacgtctgtt 180
ccgttttaca attttcctta tacgttcggc tacttgtttt cgcttggcatt ttacgcgcaa 240
gcgctgaaag aggggtgcggc atttgaagaa aaatatattg ctctcttaaa agatacagcc 300
tccatgtctg ttgaagaact ggccatgaag catctcggcg ccgatctgac gaagcgggat 360
ttctgggaag cggccattca gccggctgtc cgagatgcag aagcattttt agcgatgaca 420

[illegible]

<400> 120

Met Asn Gln Phe Arg Met Ala Val Ile Ala Leu Val Leu Ile Leu Met
Page 210

10294.204.ST25.txt

1 5 10 15
 Thr Gly Cys Gly Ser Ile Ala Glu Glu His Ala Glu Gly Lys Glu Ala
 20 25 30
 Val Pro Asp Asn Ala Pro Val Ser Asp Val Lys Ser Val Pro Tyr Ala
 35 40 45
 Ala Phe Ala Leu Glu Val Asn Tyr Gly His Gly Lys His Asn Thr Phe
 50 55 60
 Glu Ala Val Tyr Asp Lys Gln Glu Arg Glu Glu Ala Ser Ile Lys Asp
 65 70 75 80
 Tyr Leu Asn Gly Ala Asp Arg Glu Gly Glu Glu Ala Leu Asn Glu Met
 85 90 95
 Lys Met Val Leu Ser Glu Leu Ser Ile Ala Lys Ser Asp Pro Glu Gln
 100 105 110
 Asp Val Ile Ser Asn Val Leu Glu Ala Phe Asn Leu Asp Glu Gln Tyr
 115 120 125
 Asp Arg Phe Gln Leu Arg Val Lys Trp Pro Asp Gly Thr Ser Arg Ile
 130 135 140
 Tyr Asn Gly Lys
 145

<210> 121
 <211> 1589
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1109)

<400> 121
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 gcggagggtta cggacacgga agcgggtttg ctttaattgt tgttctgttc attctcttaa 180
 tcatcatcgg cgccagctgg ttcggcgggtg gatatggagg ctactaaaaa gttcgtttta 240
 aaagtcagca ataacttatg accttctcct ttttttacat gttctcctcc tgcttaccgt 300
 tgttgactcc atcatgaaag gctctttttt aaaaaagagc ctttttttaa tgcaatacag 360
 ataccgaacc tctcctgctg ctgaatgtta atagaaaatt aatgtttttt tcaaaaagag 420
 acatgatttt cattctatta atgctattat ttttccatcc tattaataaa taggaaaatt 480
 aagagagggga gtgttggttat atg ttt aaa act aag ttc aag aaa aca att ggg 533
 Met Phe Lys Thr Lys Phe Lys Lys Thr Ile Gly

10294.204.ST25.txt

1

5

10

att gga ctc gtt gcc gct gcc tgt ttg att tcc gcg tcg gcg gca agc 581
 Ile Gly Leu Val Ala Ala Ala Cys Leu Ile Ser Ala Ser Ala Ala Ser
 15 20 25

gct gcg tcg caa aat gaa agc gat gtt aaa gtg aaa ctg gac gat cag 629
 Ala Ala Ser Gln Asn Glu Ser Asp Val Lys Val Lys Leu Asp Asp Gln
 30 35 40

cag cgg aat caa tat acg gtc aaa tct ttc cac tac tta acc gtt gac 677
 Gln Arg Asn Gln Tyr Thr Val Lys Ser Phe His Tyr Leu Thr Val Asp
 45 50 55

gga aaa aat gtg gat tcg tcg gct caa gcc aac gcc aaa tcc gtc aga 725
 Gly Lys Asn Val Asp Ser Ser Ala Gln Ala Asn Ala Lys Ser Val Arg
 60 65 70 75

gat gtc aaa gta acc atg gtt ctg ccc aag cag aat aag aac ggc gat 773
 Asp Val Lys Val Thr Met Val Leu Pro Lys Gln Asn Lys Asn Gly Asp
 80 85 90

ttg ctt gcg tat gga ttt acg agc aag gtt act tta gaa gcc ttt atc 821
 Leu Leu Ala Tyr Gly Phe Thr Ser Lys Val Thr Leu Glu Ala Phe Ile
 95 100 105

gcg aaa gac aag cag agg ctt gag aag caa ttc aaa cct tct gcc agc 869
 Ala Lys Asp Lys Gln Arg Leu Glu Lys Gln Phe Lys Pro Ser Ala Ser
 110 115 120

ggt ccc tgc tgt acc gat ttc tat gaa tat aaa aat aaa ggc ggg cag 917
 Gly Pro Cys Cys Thr Asp Phe Tyr Glu Tyr Lys Asn Lys Gly Gly Gln
 125 130 135

tat att tac tgg aga gac gga ttt aaa aac ttg cca tcc agc tgg aat 965
 Tyr Ile Tyr Trp Arg Asp Gly Phe Lys Asn Leu Pro Ser Ser Trp Asn
 140 145 150 155

gac aga att tca tcg tta agt acg gcg tct cct tca tca agc tat tca 1013
 Asp Arg Ile Ser Ser Leu Ser Thr Ala Ser Pro Ser Ser Ser Tyr Ser
 160 165 170

acg acg ctg tgg gag cat act tca act caa gga tac ggc aaa ggc gtt 1061
 Thr Thr Leu Trp Glu His Thr Ser Thr Gln Gly Tyr Gly Lys Gly Val
 175 180 185

ttg ttt aga cat tcc gat tgg tac ggc act aat tcg agc tcg gca ccc 1109
 Leu Phe Arg His Ser Asp Trp Tyr Gly Thr Asn Ser Ser Ser Ala Pro
 190 195 200

tgataaatta cttttttttg cgatgccggt gttgttgatc gggtcatcat gaccgataca 1169

gctgatgaca tggatggtag tcatattccc cgaggagccgt ttaacatcag attctgcccgc 1229

ctgcttttaa aatgccttga gatctgtatc cgctttttgt tcgttcaggt gcaggagttt 1289

aacatacata tcatagatca gctgtttttgt cagttcagac atagtcaatg gacagtcctt 1349

tcttttttatt ttccggttaa caaaatatatt taatagtatta tttcaggatt tgtcaatatt 1409

atgataaggt gaaatcagat aacaaatgtg ttttgtttat catgaaacaa caccaaaaag 1469

gagaatcgct gatgaatatt gaaggaatag agatggaagt tcgctgcaca ggcgatgtat 1529

gttcagatgc ccttgaattt ttgagacgcc ataaccacga aaaaacagcc gaacattcga 1589

<210> 122

10294.204.ST25.txt

<211> 203
 <212> PRT
 <213> Bacillus licheniformis

<400> 122

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 1 5 10 15

Ala Ala Cys Leu Ile Ser Ala Ser Ala Ala Ser Ala Ala Ser Gln Asn
 20 25 30

Glu Ser Asp Val Lys Val Lys Leu Asp Asp Gln Gln Arg Asn Gln Tyr
 35 40 45

Thr Val Lys Ser Phe His Tyr Leu Thr Val Asp Gly Lys Asn Val Asp
 50 55 60

Ser Ser Ala Gln Ala Asn Ala Lys Ser Val Arg Asp Val Lys Val Thr
 65 70 75 80

Met Val Leu Pro Lys Gln Asn Lys Asn Gly Asp Leu Leu Ala Tyr Gly
 85 90 95

Phe Thr Ser Lys Val Thr Leu Glu Ala Phe Ile Ala Lys Asp Lys Gln
 100 105 110

Arg Leu Glu Lys Gln Phe Lys Pro Ser Ala Ser Gly Pro Cys Cys Thr
 115 120 125

Asp Phe Tyr Glu Tyr Lys Asn Lys Gly Gly Gln Tyr Ile Tyr Trp Arg
 130 135 140

Asp Gly Phe Lys Asn Leu Pro Ser Ser Trp Asn Asp Arg Ile Ser Ser
 145 150 155 160

Leu Ser Thr Ala Ser Pro Ser Ser Ser Tyr Ser Thr Thr Leu Trp Glu
 165 170 175

His Thr Ser Thr Gln Gly Tyr Gly Lys Gly Val Leu Phe Arg His Ser
 180 185 190

Asp Trp Tyr Gly Thr Asn Ser Ser Ser Ala Pro
 195 200

<210> 123
 <211> 1522
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1019)

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aagacgaaaa ggcgcgttttc gggttttgat acgtctgaaa gcagcgcctct tgaagtccgtt	180
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tccggcgagt caaacaccggc gaacacgaac gtccagccga aaatcgagac gagcatgatg	300
gttttccggc cgaacctgtc tgataagtac ccgccataaa agcttgccgc aattccgatc	360
agagagctcg ctgcaatgac agctcccgcga aagccggaag aggcgccctt cacttgtgtc	420
aaataaatg cttaaaaaagg gatgactcat gccgtgttcc tcatgcmcct taaggtaagg	480
caaaaaagaa ggtgatattg atg tac agc cga agc aag tt c aaa atc ggt tta Met Tyr Ser Arg Ser Lys Phe Lys Ile Gly Leu	533
	1 5 10
ttg ctt att gga agt ctg ctg gcc gcg ctc agc ttt cac ctg gag gcc Leu Leu ile Gly ser leu leu ala ala leu ser phe his leu glu ala	581
	15 20 25
ttg gcc gaa aag ccg gct aaa gtt caa atc cag ctt gaa aag gtt tat leu ala gl u lys pro ala lys val gl n ile gl n leu gl u lys val tyr	629
	30 35 40
ctg gac gga gac gtt gga att gag aat aaa gta gag gcc gct cgc aka leu asp gly asp val gly ile glu asn lys val gl u ala ala arg thr	677
	45 50 55
ctg gaa gac ttt aaa gct gct tat aaa ggg tgg cag ctc atc gat cag leu gl u asp phe lys ala ala tyr lys gly tr p gl n leu ile asp gl n	725
	60 65 70 75
aaa aag ggg ttt att ctg ttt cgc aaa cag gtg gac gac att tct ccc lys lys gly phe ile leu phe arg lys gl n val asp asp ile ser pro	773
	80 85 90
ctc agc aaa aca aac ggt tat atc gga gtg act gaa gat ggc gtg att leu ser lys thr asn gly tyr ile gly val thr gl u asp gly val ile	821
	95 100 105
tcg act ttt cac ggt cgc ccg ggc atc tta tca gaa ccc att caa tcg ser thr phe his gly arg pro gly ile leu ser gl u pro ile gl n ser	869
	110 115 120
ttt ttt cag att gat ata aag cgg ctg gaa agc cgg atg gcg gat gat phe phe gl n ile asp ile lys arg leu gl u ser arg met ala asp asp	917
	125 130 135
ctg cgc aaa ggg ata cca tac cgc acg aaa aag gaa ttt gaa cat gtc leu arg lys gly ile pro tyr arg thr lys lys gl u phe gl u his val	965
	140 145 150 155
att gaa gcc gta aaa tca tcc gga agc caa cat cat gta gaa gat atg ile gl u ala val lys ser ser gly ser gl n his his val gl u asp met	1013
	160 165 170
aag aca tgacgtgtt atgtcttttt tcagctgcag acagaagctt ttttagcgaa	1069
Lys Thr	
catatgttaa ctttttcatt ctagctttgc ctgttttgtg ttacaatgaa gagcagtcaa	1129
agagggtgaat gaacgttgat cgaattcgta aaagggacga ttgatttatgt atcgccccaa	1189

10294.204.ST25.txt

tatattgtca ttgaaaacgg cgggatcggc tatcagatct tcacgcaaaa tccgtttatt 1249
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 gcgctgtacg gcttttcgac aagggaagaa aaaatgctgt ttacgaaaat gctgaatgtt 1369
 acgggggatcg gcccaaaagg agcgcttgcg atcctcgctt ccggcgatcc gggagcggtg 1429
 attgaagcga tcgagaatga ggacgaagca tttctcgta aatttcccgg cgtaggcaaa 1489
 aaaacggcaa ggcagatcat ccttgacctg aaa 1522

<210> 124
 <211> 173
 <212> PRT
 <213> Bacillus licheniformis

<400> 124

Met Tyr Ser Arg Ser Lys Phe Lys Ile Gly Leu Leu Leu Ile Gly Ser
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Leu Leu Ala Ala Leu Ser Phe His Leu Glu Ala Leu Ala Glu Lys Pro
 20 25 30

Ala Lys Val Gln Ile Gln Leu Glu Lys Val Tyr Leu Asp Gly Asp Val
 35 40 45

Gly Ile Glu Asn Lys Val Glu Ala Ala Arg Thr Leu Glu Asp Phe Lys
 50 55 60

Ala Ala Tyr Lys Gly Trp Gln Leu Ile Asp Gln Lys Lys Gly Phe Ile
 65 70 75 80

Leu Phe Arg Lys Gln Val Asp Asp Ile Ser Pro Leu Ser Lys Thr Asn
 85 90 95

Gly Tyr Ile Gly Val Thr Glu Asp Gly Val Ile Ser Thr Phe His Gly
 100 105 110

Arg Pro Gly Ile Leu Ser Glu Pro Ile Gln Ser Phe Phe Gln Ile Asp
 115 120 125

Ile Lys Arg Leu Glu Ser Arg Met Ala Asp Asp Leu Arg Lys Gly Ile
 130 135 140

Pro Tyr Arg Thr Lys Lys Glu Phe Glu His Val Ile Glu Ala Val Lys
 145 150 155 160

Ser Ser Gly Ser Gln His His Val Glu Asp Met Lys Thr
 165 170

<210> 125
 <211> 1492
 <212> DNA

10294.204.ST25.txt

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(989)

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<400> 125
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cgtcattggtg atgtatcact ttgcagagcc gctgacctat ttatttttcg attcgggtcaa    120
ggcgtcgttt taccttaaaa tggtgtggcc gtatttttta ttccactttt ttgcgatgcc      180
ttttcaggcc tgtttaatcg gaatgggggtt ggccaaagat gctttttatc ataacgtttg    240
ggccagtgtc ttatcgtttt tgatgatgta tgttctcggg tccatgcaga ctttgcagat      300
gacggggatc attcttgcca tgaataccgg tatgattttg ctgacggcgc tgcattatgt      360
gacgatttgc aaggagctgg gcgtcacgct ttttttgaca aacaaatccc gatctccgag      420
aattgaaagc cgctgatgga tcctcttcat agtttttagct tttgcgggga agctaataatt    480
aaaaaagaag gggagttccc atg cga aga atc agt ctc att tac ccg ctc atc      533
                        1      5      10
                        Met Arg Arg Ile Ser Leu Ile Tyr Pro Leu Ile

ctg ctg ttt ttt acc ggg tta ttc gta ttt cag ccg cag gca tct gca      581
Leu Leu Phe Phe Thr Gly Leu Phe Val Phe Gln Pro Gln Ala Ser Ala
                        15      20      25

aaa caa gct tgc ccg gca gtc atg cag atg aac acg gtc gaa ggt cag      629
Lys Gln Ala Ser Pro Ala Val Met Gln Met Asn Thr Val Glu Gly Gln
                        30      35      40

cgc gtc gtc att ccc gcc gaa ggc cag aag acg atc gtt cat ttt tgg      677
Arg Val Val Ile Pro Ala Glu Gly Gln Lys Thr Ile Val His Phe Trp
                        45      50      55

acg acc tgg tgc ccg cca tgc cgt gaa gag ctt ccg cga ttc caa tcc      725
Thr Thr Trp Cys Pro Pro Cys Arg Glu Glu Leu Pro Arg Phe Gln Ser
                        60      65      70      75

tac tat gaa agc aag caa tcc ggc gtc aag ctc gtg acc gtt aat tta      773
Tyr Tyr Glu Ser Lys Gln Ser Gly Val Lys Leu Val Thr Val Asn Leu
                        80      85      90

ctg aat gcc gaa aag aac gaa cag aag gta aaa cag ttt att aaa gca      821
Leu Asn Ala Glu Lys Asn Glu Gln Lys Val Lys Gln Phe Ile Lys Ala
                        95      100      105

aac aag ctg aca ttt ccg atc gtt ttt gac aaa aag ggt gag atg atg      869
Asn Lys Leu Thr Phe Pro Ile Val Phe Asp Lys Lys Gly Glu Met Met
                        110      115      120

aaa gca tat aaa gtc atg aca att cct acg act ttt ttc ttt aat gaa      917
Lys Ala Tyr Lys Val Met Thr Ile Pro Thr Thr Phe Phe Phe Asn Glu
                        125      130      135

aaa gga gag ctg gag aaa acg ttt gtc ggc ccc att act gta gaa cag      965
Lys Gly Glu Leu Glu Lys Thr Phe Val Gly Pro Ile Thr Val Glu Gln
                        140      145      150      155

atg aag gaa tgg gca ggg aaa agc tgagccggga gttcagcttt ttttaaaatg    1019
Met Lys Glu Trp Ala Gly Lys Ser
                        160

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10294.204.ST25.txt

taaatgataa ttaatatcat aaagaaatta taataattat tatttgaaaa cgtaggatgt 1079
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 tatataaata aaataacttaa tgtttatgct gccgatgagg cggcaatttg ttttttaaga 1199
 aggaaattga cgatgaatta cattctcaat tagggaggat attggagatg caattagaga 1259
 tcgggaagca atcgcgacaa aaccgtcaca cgttgcaatt tgaaaattgg aggcagcacg 1319
 ggggaattgat agctgcgctt ttgtcgggtt tgttgattct tgcaggctgg ctgttgctcg 1379
 gcaatgaaac attgtccggtt gttctgttta ttttagcttt ttgtatcggc ggctttgcta 1439
 aagcgaaaga aggtatacaa gaaacgctgt cggaaaaaac gctgaatgtt gaa 1492

<210> 126
 <211> 163
 <212> PRT
 <213> Bacillus licheniformis
 <400> 126

Met Arg Arg Ile Ser Leu Ile Tyr Pro Leu Ile Leu Leu Phe Phe Thr
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 Gly Leu Phe Val Phe Gln Pro Gln Ala Ser Ala Lys Gln Ala Ser Pro
 20 25 30
 Ala Val Met Gln Met Asn Thr Val Glu Gly Gln Arg Val Val Ile Pro
 35 40 45
 Ala Glu Gly Gln Lys Thr Ile Val His Phe Trp Thr Thr Trp Cys Pro
 50 55 60
 Pro Cys Arg Glu Glu Leu Pro Arg Phe Gln Ser Tyr Tyr Glu Ser Lys
 65 70 75 80
 Gln Ser Gly Val Lys Leu Val Thr Val Asn Leu Leu Asn Ala Glu Lys
 85 90 95
 Asn Glu Gln Lys Val Lys Gln Phe Ile Lys Ala Asn Lys Leu Thr Phe
 100 105 110
 Pro Ile Val Phe Asp Lys Lys Gly Glu Met Met Lys Ala Tyr Lys Val
 115 120 125
 Met Thr Ile Pro Thr Thr Phe Phe Phe Asn Glu Lys Gly Glu Leu Glu
 130 135 140
 Lys Thr Phe Val Gly Pro Ile Thr Val Glu Gln Met Lys Glu Trp Ala
 145 150 155 160
 Gly Lys Ser

<210> 127
<211> 1477
<212> DNA
<213> *Bacillus licheniformis*

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<220>
<221> CDS
<222> (501) .. (974)
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[illegible]

10294.204.ST25.txt

Ser Ser Trp

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ggaaggttca cgttcggtgc attcgatc caagtgtatg gctcaatata aagcagatca 1134
tcctgatcag atgtaccgtt aaacacaacc cagtgcctaa aatggccgtc gcattgatag 1194
cgtacgcgaa tgccggcgag gctgtccgca atgacggcgg tgctgtttcc ttcttggtct 1254
tgctcagccg ccaatatatc atcaagcctt tcacccgctg ccatttttcc cgctttgaac 1314
tcctctgtca cccgatactc gccagtcggc agcatgcggt ctgtcagcgt ccaatgcttt 1374
gaggcaggaa gagtaaacag gcacttttct ttatcccctg attcgtttaa aggatagcgg 1434
aaagatgtgt gataccccaa tccgatcggc atcggatctt gac 1477

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<210> 128
 <211> 158
 <212> PRT
 <213> *Bacillus licheniformis*

<400> 128

Met Lys Gln Glu Tyr Lys Arg Pro Val Leu Phe Ile Ala Ser Leu Phe
 1 5 10 15

Met Ala Phe Cys Ala Val Tyr Phe Gly Gly Arg Leu Ile Gly Phe Tyr
 20 25 30

Met Ala Glu Tyr Pro Lys Trp Asn Gly Gln Ser Ala Asp Gly Asn Trp
 35 40 45

Glu Ala Val Ile Lys Lys Ile Asp Gly Arg Ala Leu Phe Gly Gly Glu
 50 55 60

Leu Tyr Trp Thr Gly Asp Arg Gly Lys Leu Asp Asp Thr Tyr Leu Glu
 65 70 75 80

Lys Leu Val Val Lys Phe Gly Asp Glu Ile Val Leu Asn Ala Gln Ile
 85 90 95

Glu Thr Pro Val Lys Asp Tyr Ala Gly Gly Lys Phe Pro Gly Gly Gly
 100 105 110

Ser Lys Glu Gln Ser Val Ser Phe Leu Glu Gly Leu Glu Glu Ala Glu
 115 120 125

Ile Ala Gly Arg Glu Val Thr Val Gln Leu Asp Trp Arg Glu Gly Lys
 130 135 140

Gln Ala Ser His Thr Gly Phe Thr Leu Asp Lys Ser Ser Trp
 145 150 155

<210> 129

10294.204.ST25.txt

<210> 130
 <211> 101
 <212> PRT
 <213> Bacillus licheniformis

<400> 130

Met Lys Arg Val Ile Val Leu Phe Ser Ile Leu Leu Ala Leu Phe Ile
 1 5 10 15

Val Tyr Tyr Asp Leu Lys Ser Gly Thr Ile Pro Gln Asn Ala Leu Pro
 20 25 30

Ala Ser Thr Met Ala Ala Glu Ala Pro Ala Ala Ser Leu Gln Tyr Lys
 35 40 45

Ser Val Thr Val Lys Pro Gly Gln Thr Val Phe Ser Ile Ile Gly Asn
 50 55 60

Ser Ala Val Pro Ala Asp Lys Ile Ala Glu Asp Phe Glu Glu Leu Asn
 65 70 75 80

Pro Asn Val Glu Ala Gly Arg Ile Gln Ala Gly Val Thr Tyr Lys Phe
 85 90 95

Pro Val Tyr Pro Asp
 100

<210> 131
 <211> 1381
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(878)

<400> 131
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 cgccatccct aaggcgccat ctatcagctg cgcaaataat cctatcaaga caaacacaat 180
 cagctttttc atgttggcct ccacttcaa ttggtttatt ttattgtta aatataatct 240
 atactatgcc tacctgtaaa gtgcgagttt tataaaatat aaattttttg tatttttcat 300
 cgacaccagc aaaaaagagc atatgcatgc aaaatgagcg cctatcccc ggtcttttgt 360
 cttaatgaaa gacagtttat ggatgctgct tgcaaaaaat gcatcgtgca gaaaaggcgt 420
 cggggagtaa cgccctattc gtttcattgg caatgatgat ataatcccc atgtaatgac 480
 ttcaaaagga ggctcaagcc atg aaa ttc agc aaa atc ggt gcc tta ctg ctc 533
 Met Lys Phe Ser Lys Ile Gly Ala Leu Leu
 1 5 10
 act ttg gcg tgt ttg ctt ttg cct ttt tct tcg gcg act gca gca ggt 581

10294.204.ST25.txt

Thr Leu Ala Cys Leu Leu Leu Pro Phe Ser Ser Ala Thr Ala Ala Gly
 15 20 25
 gcc ggt gta tgg gat aat atc ggc aca tac ggc atg acg tcg caa act 629
 Ala Gly Val Trp Asp Asn Ile Gly Thr Tyr Gly Met Thr Ser Gln Thr
 30 35 40
 ccg atc atc aaa tca agc gga ggg gaa ttt tat ttt cac aac aac agc 677
 Pro Ile Ile Lys Ser Ser Gly Gly Glu Phe Tyr Phe His Asn Asn Ser
 45 50 55
 ttt tac ggc ttt aca ttt acg ctg tat gaa gtt gac ggg gcg gga agc 725
 Phe Tyr Gly Phe Thr Phe Thr Leu Tyr Glu Val Asp Gly Ala Gly Ser
 60 65 70 75
 acg cct gaa atc gca aga aaa aat ttc tac gtc gga ccg aaa agc aac 773
 Thr Pro Glu Ile Ala Arg Lys Asn Phe Tyr Val Gly Pro Lys Ser Asn
 80 85 90
 agt ccg gcg atc gat gtc agc agt ttt gca gat ggt gcg aat aaa caa 821
 Ser Pro Ala Ile Asp Val Ser Ser Phe Ala Asp Gly Ala Asn Lys Gln
 95 100 105
 gca gaa ctc gtc ctg ttt aaa ggg aat gat aca tat atc acc gtt act 869
 Ala Glu Leu Val Leu Phe Lys Gly Asn Asp Thr Tyr Ile Thr Val Thr
 110 115 120
 tgt tat gat tgaatgtccc ataaacagca agcccgccgt ttacagccgg 918
 Cys Tyr Asp
 125
 cggggtttttt tgatcaagtt ccttccttat acctataggc acaaaaaagt gcctatatga 978
 cttaaaaagtg cgtacttccg ttttggtgtc ttctgttcca taatcataat tgatgttttg 1038
 tttgacattg ttctgtttat aatgaaaaga aaacggaggg atcaatgatg aacttggatt 1098
 tacgggggaaa aagagcggtg gtgaccggat cgacgtccgg aatcggcaaa gcgattgccg 1158
 cttcacttgc gaaagaaggt gcgtctgtca tcattaacgg acgccggcaa gaaaagggtca 1218
 accaaacaat agacgaattg aaaggccaat ttcccgaggc tgttcttcaa gcggcccctt 1278
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 ttctggtcaa taatttaggg atctttgaac cggcgggaata ttt 1381

<210> 132
 <211> 126
 <212> PRT
 <213> Bacillus licheniformis

<400> 132

Met Lys Phe Ser Lys Ile Gly Ala Leu Leu Leu Thr Leu Ala Cys Leu
 1 5 10 15

Leu Leu Pro Phe Ser Ser Ala Thr Ala Ala Gly Ala Gly Val Trp Asp
 20 25 30

Asn Ile Gly Thr Tyr Gly Met Thr Ser Gln Thr Pro Ile Ile Lys Ser
 35 40 45

Ser Gly Gly Glu Phe Tyr Phe His Asn Asn Ser Phe Tyr Gly Phe Thr
 Page 222

10294.204.ST25.txt
60

50

55

Phe Thr Leu Tyr Glu Val Asp Gly Ala Gly Ser Thr Pro Glu Ile Ala
65 70 75 80

Arg Lys Asn Phe Tyr Val Gly Pro Lys Ser Asn Ser Pro Ala Ile Asp
85 90 95

Val Ser Ser Phe Ala Asp Gly Ala Asn Lys Gln Ala Glu Leu Val Leu
100 105 110

Phe Lys Gly Asn Asp Thr Tyr Ile Thr Val Thr Cys Tyr Asp
115 120 125

<210> 133
<211> 1581
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (601)..(978)

<400> 133
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ggattgtgcg agttcctcca cattcggagt atttctgaat gatagagcca cacgggccac 120
gttctcactg gctaaccgga tcaaattgatc ttccaggagtc agcataatac atccagttca 180
ggtagataag atttgaattt ggtgacttgc ttttggttctt cttctttcat tttctgacta 240
atccaaactg gaaaaagcag gtcttttaac agattaggag gtttctgaca tgcaccattc 300
ggtcactaac cgaatgcagt aaaggacact gtgggtgcttg ccagccatta ggggtattgag 360
gaggtgatca aaatgctagg tgacagtatt tcgtcgaagt ggacaagtcg tgaccaaagc 420
acctcggatc gaggggttggc catggaggaa aaaattgatg tctggtgaca aagaggagtc 480
atgatcatgg caccgccaac gagggaaaaa actcttcccg catcgacacg gtatgtgggc 540
ggtgacaaac taacttatag agtaaattta ttagtcgaat gaaagaggag gaatgaaata 600
atg aaa aat cat ttg tat gag aaa aaa aag agg aaa cct ttg act cgg 648
Met Lys Asn His Leu Tyr Glu Lys Lys Lys Arg Lys Pro Leu Thr Arg
1 5 10 15
aca att aaa gcg acg ctc gcc gtg ttg aca atg tcc atc gct ttg gtg 696
Thr Ile Lys Ala Thr Leu Ala Val Leu Thr Met Ser Ile Ala Leu Val
20 25 30
gga ggc gct acg gtg cct tca ttt gca tgg gtg aat ccg ggt tat cac 744
Gly Gly Ala Thr Val Pro Ser Phe Ala Trp Val Asn Pro Gly Tyr His
35 40 45
tac cag tac cca tcg gaa ggt ggt aca tgg agg tat gga ttc gta aac 792
Tyr Gln Tyr Pro Ser Glu Gly Gly Thr Trp Arg Tyr Gly Phe Val Asn
50 55 60
gcc ggg ctc cgt tca gag tac aac cac ccg aca aag gtc cac ggc tcg 840
Ala Gly Leu Arg Ser Glu Tyr Asn His Pro Thr Lys Val His Gly Ser

10294.204.ST25.txt

65	70	75	80	
aca gtg caa aag ctc atc gat gga aaa gtg gat aaa acg aat aga agt				888
Thr Val Gln Lys Leu Ile Asp Gly Lys Val Asp Lys Thr Asn Arg Ser				
	85	90	95	
att gat acg gct gcg ggc cgc tac tct aat gcc tat gtc gga gcc ata				936
Ile Asp Thr Ala Ala Gly Arg Tyr Ser Asn Ala Tyr Val Gly Ala Ile				
	100	105	110	
aac tca cct ggt ctt aag ggt cgt tac tac tat cgc acc aac				978
Asn Ser Pro Gly Leu Lys Gly Arg Tyr Tyr Tyr Arg Thr Asn				
	115	120	125	
taatcaaagg gaaaacgggtt gctgtcaacg gggctagcat ggcaagaccc agaaaagttc				1038
tgggagatcc cgctttgcat aagcgtatta tagtggatga cgcgggcttt gttgtttaca				1098
cttcttgcac ctgctgacgg caatcatccc tatctatgaa atcgagattt cagcaggccg				1158
ttattttcga gagagttaaa tctatattca ttgtttttat tttggtaagg acataaccgga				1218
ttttaggttt ggattaccgg tcgagtttagc ttgtcttttc gccactacc gtgtc gatgc				1278
gggagcaatt taccagaagc acttaccgat tgatagtttt ttattccggt gattgcaaag				1338
tttcataaac tctgagaatt caataggggt aatacccccgc tttgaggggc gcggcatttt				1398
atgcgccccg agtattttatt cttaaaattt ttaaattaat gtatctatat aaaaaggaga				1458
tgctttcggg gtactgcaa agcatctcca caaaagatag tgcatactcg caggaaaaaa				1518
cataaaatgc aactaacatt tttttggaaa gcaatagggtt tatttaattt tgtagtttta				1578
tct				1581

<210> 134
 <211> 126
 <212> PRT
 <213> Bacillus licheniformis

<400> 134

Met Lys Asn His Leu Tyr Glu Lys Lys Lys Arg Lys Pro Leu Thr Arg
 1 5 10 15

Thr Ile Lys Ala Thr Leu Ala Val Leu Thr Met Ser Ile Ala Leu Val
 20 25 30

Gly Gly Ala Thr Val Pro Ser Phe Ala Trp Val Asn Pro Gly Tyr His
 35 40 45

Tyr Gln Tyr Pro Ser Glu Gly Gly Thr Trp Arg Tyr Gly Phe Val Asn
 50 55 60

Ala Gly Leu Arg Ser Glu Tyr Asn His Pro Thr Lys Val His Gly Ser
 65 70 75 80

Thr Val Gln Lys Leu Ile Asp Gly Lys Val Asp Lys Thr Asn Arg Ser
 85 90 95

10294.204.ST25.txt

Ile Asp Thr Ala Ala Gly Arg Tyr Ser Asn Ala Tyr Val Gly Ala Ile
 100 105 110

Asn Ser Pro Gly Leu Lys Gly Arg Tyr Tyr Tyr Arg Thr Asn
 115 120 125

<210> 135
 <211> 1357
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(854)

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 atgagcggat gacatatttt attcaagcga cacaatatat tgcgctgttt ctctccgtgt 120
 ttgacgcaaa agagaagatt tgcttttcga cgtctctaatt attttcaaac agcaccgctt 180
 cagccgctga aagcgcagcc tctgagattt cccagctcag ccgaacgggt tcatgatccg 240
 gcgaagttat ttttaaata tcggtacaaa acgaagaatc gcctcgaata ctatgttgaa 300
 aagggttttt cccgatgatt gtccttttca ccgcgcgccc tcccgttaag ccttgttatg 360
 tatctatcct attggaaatg gccccgcagg cgcaacgaaa ataaaattct tcgacaaaat 420
 ttttattttt tgcattaact ccttttgaag caagcgtttt tatggtataa aaaagaagga 480
 gaaaattaga attgaagggtg atg aac gtg gaa att gct atc att gcg ctg ctc 533
 Met Asn Val Glu Ile Ala Ile Ile Ala Leu Leu
 1 5 10
 gtt gtc agt att gcg ctg att gca ttc tca tat ttt caa aga gaa ccg 581
 Val Val Ser Ile Ala Leu Ile Ala Phe Ser Tyr Phe Gln Arg Glu Pro
 15 20 25
 atc aag gaa gtt gaa cag gag ttg gaa acc ctt cag ctg tcc gcc atg 629
 Ile Lys Glu Val Glu Gln Glu Leu Glu Thr Leu Gln Leu Ser Ala Met
 30 35 40
 cag gaa atc tat aaa ctg aaa aag aag atg acc gtg ctt gag gaa gag 677
 Gln Glu Ile Tyr Lys Leu Lys Lys Met Thr Val Leu Glu Glu Glu
 45 50 55
 ctc ctc gat tca aat gtg gtc gtc cgc aga ccg aat gcc gga atc agc 725
 Leu Leu Asp Ser Asn Val Val Val Arg Arg Pro Asn Ala Gly Ile Ser
 60 65 70 75
 cag cat att gcg aag cag att ctt tca aaa tat caa aac ggc atg tct 773
 Gln His Ile Ala Lys Gln Ile Leu Ser Lys Tyr Gln Asn Gly Met Ser
 80 85 90
 gta gac gcc atc gca aaa gct gag cac gta tct gtc gaa gat gtc aaa 821
 Val Asp Ala Ile Ala Lys Ala Glu His Val Ser Val Glu Asp Val Lys
 95 100 105
 gcg atc att aaa gac tat gag agg gtg ctt gta tgaccagaca gagtgtacaa 874
 Ala Ile Ile Lys Asp Tyr Glu Arg Val Leu Val
 110 115
 gcatttgccc ggagaatgga ttgtggctac cgccgttctt gcaagcgcatt tttatttgaa 934

10294.204.ST25.txt

cggataatac gacccgattt acctgtgcga tgcgaagatt ctccgtcagc atcagactgt 994
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 gattgatgat aaaatcaggc aggtggaggt tttctaaaaa cgctcttgag accgcctcac 1234
 cgtgcgcttc ctggttcata aagtttcccc agcgtccgat cgctgacca agcagaatgc 1294
 ttggagcagc gatatcagcc agcttccaaa acgaaagccc cttgactttc gcataaatga 1354
 ttc 1357

<210> 136
 <211> 118
 <212> PRT
 <213> Bacillus licheniformis

<400> 136

Met Asn Val Glu Ile Ala Ile Ile Ala Leu Leu Val Val Ser Ile Ala
1 5 10 15

Leu Ile Ala Phe Ser Tyr Phe Gln Arg Glu Pro Ile Lys Glu Val Glu
20 25 30

Gln Glu Leu Glu Thr Leu Gln Leu Ser Ala Met Gln Glu Ile Tyr Lys
35 40 45

Leu Lys Lys Lys Met Thr Val Leu Glu Glu Glu Leu Leu Asp Ser Asn
50 55 60

Val Val Val Arg Arg Pro Asn Ala Gly Ile Ser Gln His Ile Ala Lys
65 70 75 80

Gln Ile Leu Ser Lys Tyr Gln Asn Gly Met Ser Val Asp Ala Ile Ala
85 90 95

Lys Ala Glu His Val Ser Val Glu Asp Val Lys Ala Ile Ile Lys Asp
100 105 110

Tyr Glu Arg Val Leu Val
115

<210> 137
 <211> 1297
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(794)

<400> 137

10294.204.ST25.txt

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ttcttaaacg ttgatatgac gcagttttta cgaagattta accgtcgaat tttcgacctg      180
tttctaacga atagttttatc gtaattccga tgaatttttc gcccatattg cgatgaaatt      240
gtgctacgat ccgaaggggt taatacagta tttgaagggc ctcgttttta taaacgaggc      300
cgtttttttg cccgcaaattg tactgtttgc gatgtaagat caaaaagggtg aatcatttca      360
gcacagtgtg tattgtgtaa agtcattcta aaagcttatac tattgattcc gaaatattgt      420
aatttgatca ctttttgac atacctgcat gttatatgat gaaatagaaa tgaaataaat      480
ggaaaaggag ttgttttaaa atg aag gtc aat aaa tta tta act ggt acg act      533
                        Met Lys Val Asn Lys Leu Leu Thr Gly Thr Thr
                        1          5          10

ctg gct gtt ggt tta ctt att tct gca gcg ccg gta ttt gct gca tcg      581
Leu Ala Val Gly Leu Leu Ile Ser Ala Ala Pro Val Phe Ala Ala Ser
                        15          20          25

cat tca tct gag gtg att gca cat ccg act gct caa tat atc aat tgt      629
His Ser Ser Glu Val Ile Ala His Pro Thr Ala Gln Tyr Ile Asn Cys
                        30          35          40

cca agt gac ttg cca agc tca ttc aaa agc agt aaa tca tca aaa tgt      677
Pro Ser Asp Leu Pro Ser Ser Phe Lys Ser Ser Lys Ser Ser Lys Cys
                        45          50          55

gta aaa tca tct tct gga gtt ttc agt aac aaa ttt tct gat agc gat      725
Val Lys Ser Ser Ser Gly Val Phe Ser Asn Lys Phe Ser Asp Ser Asp
60          65          70          75

gga aca tgg tat ttc aaa ggg aaa ttt tac agt aat gtt ttt aat act      773
Gly Thr Trp Tyr Phe Lys Gly Lys Phe Tyr Ser Asn Val Phe Asn Thr
                        80          85          90

tgg gtt ggt ttt tat gaa gga tgaacaaaa aaggggggct ccccttttt      824
Trp Val Gly Phe Tyr Glu Gly

tttgttttcc ttttagtatc aagtaggaaa tagatggcgg agaattgtaa actcttcgaa      884
gagccgatct cgagttaaaa gtatgaaata agcgggtggt atgatgatct ttacgaaaac      944
agatcttcgc tatccggtga attttttcgg gccagggttg aggattaacc attacggatt      1004
gctcatcgta aacagcaatg caaaaatagg tgcaaaactgt gacattcatc aaggggttaa      1064
tatcggacaa aatcacgctc gccgcatgt tcccacaatc ggagacaatg tctggatcgg      1124
gccgggggca aagctctttg gcgacattca cattgctgac ggcatatcaa ttggcgcaaa      1184
cgccgtggtc aacaaatctt tcaactgagga aaatattaca atagccggca tgcttgccaa      1244
aaagattaaa gaggcgccgt caaataaaga ccggaagcaa gctgttcagc ggc      1297

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<210> 138
 <211> 98
 <212> PRT
 <213> Bacillus licheniformis
 <400> 138

10294.204.ST25.txt

Met Lys Val Asn Lys Leu Leu Thr Gly Thr Thr Leu Ala Val Gly Leu
 1 5 10 15

Leu Ile Ser Ala Ala Pro Val Phe Ala Ala Ser His Ser Ser Glu Val
 20 25 30

Ile Ala His Pro Thr Ala Gln Tyr Ile Asn Cys Pro Ser Asp Leu Pro
 35 40 45

Ser Ser Phe Lys Ser Ser Lys Ser Ser Lys Cys Val Lys Ser Ser Ser
 50 55 60

Gly Val Phe Ser Asn Lys Phe Ser Asp Ser Asp Gly Thr Trp Tyr Phe
 65 70 75 80

Lys Gly Lys Phe Tyr Ser Asn Val Phe Asn Thr Trp Val Gly Phe Tyr
 85 90 95

Glu Gly

<210> 139
 <211> 1261
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(836)

<400> 139
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 atgcggggcc ttacatcgct agactcgtcg agaactctct gcttgaagtg gatccgggag 180
 tcattgaagc cgctgaagca atgggagcga ctccgagaca gatcatcttc aggtttctga 240
 ttccagaagc gctcggttcg cttgtgctga gttttacggg ggcaacgggc ggattggctg 300
 gggcgctcggc gatggctggg gcgattggg caggcgggtct tggggatttg gcgatcacat 360
 acggctatca aagatttgac acgctgacga tgatcatcac ggttgcaatt ctcgtcatcg 420
 tagtgcaagg attgcagaca tccggaaacg ttctgtcaaa aaaattgaga agaagataga 480
 cagagaggga gacggctatt atg aaa aaa ttt gca tgt gtt gtg atc ttc ctg 533
 Met Lys Lys Phe Ala Cys Val Val Ile Phe Leu
 1 5 10
 ctg ctt gcg gca gtg atc gcg ggg tgc gcg gca gac tct gat gcg aaa 581
 Leu Leu Ala Ala Val Ile Ala Gly Cys Ala Ala Asp Ser Asp Ala Lys
 15 20 25
 acc att aaa atc ggc atc agc gga acg gat acg aga att tgg gac ttt 629
 Thr Ile Lys Ile Gly Ile Ser Gly Thr Asp Thr Arg Ile Trp Asp Phe
 30 35 40
 gtg aag aaa aaa gcc gaa aaa gaa ggc tta aag ctt gaa atc gtc aaa 677
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10294.204.ST25.txt

Val Lys Lys Lys Ala Glu Lys Glu Gly Leu Lys Leu Glu Ile Val Lys
 45 50 55
 tac tcc gac tat gtt cag cca aac cag gct ttg gcg agc ggc gac att 725
 Tyr Ser Asp Tyr Val Gln Pro Asn Gln Ala Leu Ala Ser Gly Asp Ile 75
 60 65 70
 gac cgc caa cgc ttt tca gac gat atc cta ctt tca tgc att caa aaa 773
 Asp Arg Gln Arg Phe Ser Asp Asp Ile Leu Leu Ser Cys Ile Gln Lys 90
 80 85
 gga acg caa cct tta att atc gcc ggt cgg cac aac gac acc agg tcg 821
 Gly Thr Gln Pro Leu Ile Ile Ala Gly Arg His Asn Asp Thr Arg Ser 105
 95 100
 ggg ggg gga gga aga ataaataaac acggggccctt ttgggtgata agtccccggc 876
 Gly Gly Gly Gly Arg 110
 attacaagcc cgaccattcc cattgctgat ccgcgttttt cttttgggaa aatcaataaa 936
 agcaccgtct gcatcaatgg catcataatg ccggcgccag ccgcctgcac gacgcgcccc 996
 gcaatcagcg ccggaaagct gaatgacaag gcgcagatca gcgtgccggc cgtaaataaa 1056
 gacattgccg ccatgaacag ctttctcgtt gtgaattttt caattaaaaa agccgtaact 1116
 ggaatcatga tcccattcac gagcataaaa acggtcgtca gccattgggc aagccccggc 1176
 gtaatgttta agtcctcat aatcggaggc agagccctga tgaatcccct aatgattttg 1236
 gtaaaaatca ttaagttaag gtgga 1261

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 <212> PRT
 <213> Bacillus licheniformis

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 20 25 30
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 35 40 45
 Glu Lys Glu Gly Leu Lys Leu Glu Ile Val Lys Tyr Ser Asp Tyr Val
 50 55 60
 Gln Pro Asn Gln Ala Leu Ala Ser Gly Asp Ile Asp Arg Gln Arg Phe
 65 70 75 80
 Ser Asp Asp Ile Leu Leu Ser Cys Ile Gln Lys Gly Thr Gln Pro Leu
 85 90 95
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 100 105 110

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<210> 141
<211> 1426
<212> DNA
<213> Bacillus licheniformis
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<220>
<221> CDS
<222> (507) .. (923)
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10294.204.ST25.txt

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 ctttatctaa aggctctacc cttagtatct aactaacacc tgcattgcaca gaaatcggag 1093
 tggctttgtg catgcaccga catcggagtg ggtctgtgca tgcaccgata tcggagagac 1153
 tctgtgcatg caccgatatc ggagtggctc tgtgcatgca ccgatatcgg agtggctctg 1213
 tgcattgcacc gatattcggag tggctctgtg catgcaccga tatcggagtg gctctcatgc 1273
 acgtgttgat gaatgcggcc catgtacgtg ttgatgaatg cggcccatgt acgtgttgat 1333
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 attcttatca ggggaccca acgggattct tat 1426

<210> 142
 <211> 139
 <212> PRT
 <213> Bacillus licheniformis
 <400> 142

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 20 25 30
 Thr Asp Val His Thr Cys Ala Leu Leu Glu Val Cys Ser Phe Ala Glu
 35 40 45
 His Ser Thr Ala Gln Ile Val Tyr Ile Leu Pro Pro Glu Gln Ala Phe
 50 55 60
 Ile Asp Leu Phe Ser Asp Pro Thr Gly Arg Phe Val Phe His Pro Arg
 65 70 75 80
 Ser Tyr Pro Gly Arg Cys Pro Ser Pro Ser Pro Gly Ser Ala Phe Ser
 85 90 95
 Lys Phe Ser Gly Phe Ala Tyr Leu Met Pro Met Val Ser Arg Ser Arg
 100 105 110
 Pro Tyr Ala Val Val Leu Arg Tyr Phe Lys Cys Leu Pro Gly Ser Pro
 115 120 125
 Arg Pro Thr Pro Pro Asn Lys Arg Gly Leu Pro
 130 135

<210> 143
 <211> 1513
 <212> DNA
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<220>
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10294.204.ST25.txt

<222> (496)..(1035)

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 aacaatgccc agtcaggagg tgatgaatga tgccatggat gtttttagtg atttccggaa 180
 tcgaagaggt tattgccgcc atcgctatga aatatgtaga cggcacaaga aaaaaatggc 240
 cgattatcgt catgggtgtg gggtttggct tgtctttttt ctgcctttca aaagcaatgc 300
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 cggcagtcag tttatttttg ttttaaggagc gtattcgtgc tccgcagctc atctcgcttg 420
 gctttattat aatcgggggtg atcggcctgc gccttacatc atcttaaatt ttaatttgca 480
 ttggaggttg ctgat atg att aat cag ctt aaa ttg cgt ccg ctt gaa aga 531
 Met Ile Asn Gln Leu Lys Leu Arg Pro Leu Glu Arg
 1 5 10
 gaa gac ctt ccg ttt gtc cac cgt ctt aac aac gat gcg aaa att atg 579
 Glu Asp Leu Pro Phe Val His Arg Leu Asn Asn Asp Ala Lys Ile Met
 15 20 25
 tca tat tgg ttt gaa gaa ccg tac gag act ttt gtt gag ctg cag gat 627
 Ser Tyr Trp Phe Glu Glu Pro Tyr Glu Thr Phe Val Glu Leu Gln Asp
 30 35 40
 tta ttt gac aaa cac att cac gac caa agc gag cgg cgc ttt atc ata 675
 Leu Phe Asp Lys His Ile His Asp Gln Ser Glu Arg Arg Phe Ile Ile
 45 50 55 60
 gag aaa gag act gag atg atc gga ttg gta gag ctg gtc gaa att gat 723
 Glu Lys Glu Thr Glu Met Ile Gly Leu Val Glu Leu Val Glu Ile Asp
 65 70 75
 tat att cac agg cgg gcg gag ttt caa atc ata att gat ccc gag cat 771
 Tyr Ile His Arg Arg Ala Glu Phe Gln Ile Ile Ile Asp Pro Glu His
 80 85 90
 caa ggg aac ggt tat tcg tca agc gca aca tat ttg gca atg aac tac 819
 Gln Gly Asn Gly Tyr Ser Ser Ser Ala Thr Tyr Leu Ala Met Asn Tyr
 95 100 105
 gca ttt tcc gtc ttg aac ttg cac aaa ttg tat ttg atc gtc gac gaa 867
 Ala Phe Ser Val Leu Asn Leu His Lys Leu Tyr Leu Ile Val Asp Glu
 110 115 120
 gat aat gca aaa gcg att cac ttg tat aaa aag gca ggg ttc act atc 915
 Asp Asn Ala Lys Ala Ile His Leu Tyr Lys Lys Ala Gly Phe Thr Ile
 125 130 135 140
 gag agc gag ctg cag gat gaa ttt ttc gtc gac ggc tat tat cgt aac 963
 Glu Ser Glu Leu Gln Asp Glu Phe Phe Val Asp Gly Tyr Tyr Arg Asn
 145 150 155
 gcc att aga atg tgc att ttt cag gat gag ttt tta tca ctt aaa aaa 1011
 Ala Ile Arg Met Cys Ile Phe Gln Asp Glu Phe Leu Ser Leu Lys Lys
 160 165 170
 agc aaa gag gaa ggc atg cag gga taaataaaag agatggcggc gccatctcct 1065
 Ser Lys Glu Glu Gly Met Gln Gly
 175 180
 gcatgctttt ttaatttttc acaccttaatt gctctttggc tttggcggga atatcgtctt 1125

10294.204.ST25.txt

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 caaaaccggc cagttcatat ttgaagacgg agtattcctc gccgtcgtca aatttcgacg 1305
 tgtcttcctc cccgtttcca gtaatgtgaa cataatattc gtccgtcccc acacggttta 1365
 agttacatcc gcttaaaaaat gcggcaaata tgatcatcag gctgatccat ggaatatggg 1425
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 aaaaaaattg aataacgtga catgaaca 1513

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 <211> 180
 <212> PRT
 <213> Bacillus licheniformis

<400> 144

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Glu Glu Pro Tyr Glu Thr Phe Val Glu Leu Gln Asp Leu Phe Asp Lys
35 40 45

His Ile His Asp Gln Ser Glu Arg Arg Phe Ile Ile Glu Lys Glu Thr
50 55 60

Glu Met Ile Gly Leu Val Glu Leu Val Glu Ile Asp Tyr Ile His Arg
65 70 75 80

Arg Ala Glu Phe Gln Ile Ile Ile Asp Pro Glu His Gln Gly Asn Gly
85 90 95

Tyr Ser Ser Ser Ala Thr Tyr Leu Ala Met Asn Tyr Ala Phe Ser Val
100 105 110

Leu Asn Leu His Lys Leu Tyr Leu Ile Val Asp Glu Asp Asn Ala Lys
115 120 125

Ala Ile His Leu Tyr Lys Lys Ala Gly Phe Thr Ile Glu Ser Glu Leu
130 135 140

Gln Asp Glu Phe Phe Val Asp Gly Tyr Tyr Arg Asn Ala Ile Arg Met
145 150 155 160

Cys Ile Phe Gln Asp Glu Phe Leu Ser Leu Lys Lys Ser Lys Glu Glu
165 170 175

Gly Met Gln Gly

180

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<221> CDS  
<222> (503) .. (1264)
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10294.204.ST25.txt

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 Pro Pro Thr Gly Gln Phe Asn Lys Asp Val Leu Asp Val Ala Lys Gln 170
 155 160 165

tac ggc tac acc gtt gtt cat tat agt att aac tcg gat gac tgg acg 1060
 Tyr Gly Tyr Thr Val Val His Tyr Ser Ile Asn Ser Asp Asp Trp Thr 185
 175 180

aac ccg ggg gtt caa aag atc gtc caa aac gta aat gga acg gta aac 1108
 Asn Pro Gly Val Gln Lys Ile Val Gln Asn Val Asn Gly Thr Val Asn 200
 190 195

gcc ggt gac atc gtg ctc ttt cac gct tca gat tcc gcc aaa caa aca 1156
 Ala Gly Asp Ile Val Leu Phe His Ala Ser Asp Ser Ala Lys Gln Thr 215
 205 210

aaa gaa gcc ctg cca gag atc gtg cac cat ctc aga agc aag ggg ctc 1204
 Lys Glu Ala Leu Pro Glu Ile Val His His Leu Arg Ser Lys Gly Leu 230
 220 225

aaa aac gta aca gtc agc gaa tta atc gca aat acg gat gca aaa tct 1252
 Lys Asn Val Thr Val Ser Glu Leu Ile Ala Asn Thr Asp Ala Lys Ser 250
 235 240 245

tca gaa gta aag tagcagccgg tctaagcgcg tgcctgaaat tttggcagca 1304
 Ser Glu Val Lys

ttaaaagctg aaaagcgttg caggctaata aaggaagcag cattaaatag agccagtcct 1364

cttcattgac ccttaacgcc gggaaccact ccatcacagt aaaaacaaac attagaaata 1424

atgcggaaac gaacgttttt ttagaggact gtttttgctt tgcataagcg gccgcaatgc 1484

ctaccgccaa aataaagagc ggcagccaaa tgtacggaat gatggagcct ccatcttttt 1544

caaaaaacag aaagcgcaag taaaccaagt caaacgcgac aaatataatc aaaaacagct 1604

gaatcgaatt ccacaaagaa tgagatctga aaatttccag tgcaaagcgg tgaatcgтта 1664

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<210> 146

<211> 254

<212> PRT

<213> Bacillus licheniformis

<400> 146

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 20 25 30

Asn Leu Leu Pro Leu Pro Val Phe Ser Thr Glu Gly Gly Ala Lys Ala
 35 40 45

Val Tyr Arg Gly Asp Ser Asp Thr Asn Glu Val Ala Leu Thr Phe Asn
 50 55 60

10294.204.ST25.txt

Ile Ser Trp Gly Asp Gln Lys Ala Met Pro Ile Leu Asp Thr Leu Lys
65 70 75 80

Ala Asn Gly Ile Lys Asp Ala Thr Phe Phe Leu Ser Ala Ser Trp Ala
85 90 95

Glu Arg His Pro Asp Val Val Glu Arg Ile Arg Lys Asp Gly His Gln
100 105 110

Ile Gly Ser Met Gly Tyr Ala Tyr Lys Asn Tyr Ser Gln Met Lys Lys
115 120 125

Ser Glu Ile Lys Lys Asp Leu Ala Lys Ala Arg His Ser Phe Gln Lys
130 135 140

Leu Gly Leu Asp Asp Leu Thr Leu Leu Arg Pro Pro Thr Gly Gln Phe
145 150 155 160

Asn Lys Asp Val Leu Asp Val Ala Lys Gln Tyr Gly Tyr Thr Val Val
165 170 175

His Tyr Ser Ile Asn Ser Asp Asp Trp Thr Asn Pro Gly Val Gln Lys
180 185 190

Ile Val Gln Asn Val Asn Gly Thr Val Asn Ala Gly Asp Ile Val Leu
195 200 205

Phe His Ala Ser Asp Ser Ala Lys Gln Thr Lys Glu Ala Leu Pro Glu
210 215 220

Ile Val His His Leu Arg Ser Lys Gly Leu Lys Asn Val Thr Val Ser
225 230 235 240

Glu Leu Ile Ala Asn Thr Asp Ala Lys Ser Ser Glu Val Lys
245 250

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<211> 1855
<212> DNA
<213> Bacillus licheniformis

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acacgaggaa gacgcggaat aaggaggaac atagtgacgc aggggtgaacg gtagggaggg 180
tggcaaatag tagtatgata tttgaaagac ggggtcccgt cgaatcggt gaaaaacaaa 240

10294.204.ST25.txt

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 gccaaagggat ctttttttgt ttatcaggaa atttatgaaa attaaagact gctgaaacat 420
 aatcttaaca gtgcgaacct atactttggc aagagaagag caaaagggga gtggatgat 479
 gtg tca gct tta ttc aaa aaa ttg atg tta tct tca ttg atc ggg gtt 527
 Val Ser Ala Leu Phe Lys Lys Leu Met Leu Ser Ser Leu Ile Gly Val 15
 1 5 10
 tcc atc ggg tca gcg ctg ttt gca ccg aat gcg ggt gca caa gag ccg 575
 Ser Ile Gly Ser Ala Leu Phe Ala Pro Asn Ala Gly Ala Gln Glu Pro 20 25 30
 gcg gtg aag cct aaa aaa gtg gat gtc att gca cac aga ggc gct tcg 623
 Ala Val Lys Pro Lys Lys Val Asp Val Ile Ala His Arg Gly Ala Ser 35 40 45
 gga tat gcg ccg gaa aac acg atg gct gct ttt gat aaa gcg ctt cag 671
 Gly Tyr Ala Pro Glu Asn Thr Met Ala Ala Phe Asp Lys Ala Leu Gln 50 55 60
 atg aaa gca gat tat atc gag ctg gat gtt caa atg tcc aaa gac ggg 719
 Met Lys Ala Asp Tyr Ile Glu Leu Asp Val Gln Met Ser Lys Asp Gly 65 70 75 80
 gag ctt gtc atc att cac gat acg acc gta aac cgt acg aca gat att 767
 Glu Leu Val Ile Ile His Asp Thr Thr Val Asn Arg Thr Thr Asp Ile 85 90 95
 gac tca gtg ctg ccg gtt gcc gta aag gat ttg acg ctt gcc gag ctg 815
 Asp Ser Val Leu Pro Val Ala Val Lys Asp Leu Thr Leu Ala Glu Leu 100 105 110
 cgc aag ctt gat gcc ggc agc ttc ttc ggt ccg cag ttc gca gga gag 863
 Arg Lys Leu Asp Ala Gly Ser Phe Phe Gly Pro Gln Phe Ala Gly Glu 115 120 125
 cgc att ccg aca ttt gaa gaa gtg ctt gac cgg tat aaa ggg aag gtc 911
 Arg Ile Pro Thr Phe Glu Glu Val Leu Asp Arg Tyr Lys Gly Lys Val 130 135 140
 gga atg ctg atc gaa ttg aaa gag cct gca cgc tat ccg gga atc gaa 959
 Gly Met Leu Ile Glu Leu Lys Glu Pro Ala Arg Tyr Pro Gly Ile Glu 145 150 155 160
 gga aaa gtg tca gca gca ttg aaa gag cgg aga atg gat aag cct aaa 1007
 Gly Lys Val Ser Ala Ala Leu Lys Glu Arg Arg Met Asp Lys Pro Lys 165 170 175
 aac gga aaa atc att gta caa tcg ttt gat ttt aac tct gtc tat aaa 1055
 Asn Gly Lys Ile Ile Val Gln Ser Phe Asp Phe Asn Ser Val Tyr Lys 180 185 190
 att cat cag ctg ctt cca tcg atg ccg aca ggt gtc ttg acg tca aaa 1103
 Ile His Gln Leu Leu Pro Ser Met Pro Thr Gly Val Leu Thr Ser Lys 195 200 205
 gcg gcg gac tta aca gat gca aag ctt aag gaa ttt tcc ggc tat gcc 1151
 Ala Ala Asp Leu Thr Asp Ala Lys Leu Lys Glu Phe Ser Gly Tyr Ala 210 215 220
 aaa tac gtg aac gcc aac ttg aaa aat gtg gcc gct gat cct acg ctt 1199
 Lys Tyr Val Asn Ala Asn Leu Lys Asn Val Ala Ala Asp Pro Thr Leu 225 230 235 240

10294.204.ST25.txt

gtg ccg aga att cat gcg ctc ggc atg aag ata cgc cct tgg acc gtc 1247
Val Pro Arg Ile His Ala Leu Gly Met Lys Ile Arg Pro Trp Thr Val 255
245 250

cgc tcc cgc gat gaa gtg cct ccg cta ttt agg ccc gcg tgg aac ggg 1295
Arg Ser Arg Asp Glu Val Pro Pro Leu Phe Arg Pro Ala Trp Asn Gly 270
260 265

att gtg aca aac ttt ccc gac tat tgt tcc aaa aaa gta cgg gag ccc 1343
Ile Val Thr Asn Phe Pro Asp Tyr Cys Ser Lys Lys Val Arg Glu Pro 285
275 280

caa taaaaaaccc tgaagtttgc tttgaagggc tttttaattt aaaaataaaa 1396
Gln

atggggctta aaacaaaaaa ggttaacggt aacgggttta tcgttcccc cgattttttt 1456

tgggacacct gggaaaaacg ggtataaacc tttgggggcc ctttttgggg gccttaaaaa 1516

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aacaatggaa gaggaaaacc tgcaggcccg catcgtctca ttcagcgttg atcccgaaaa 1756

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<212> PRT
<213> Bacillus licheniformis
<400> 148

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35 40 45

Gly Tyr Ala Pro Glu Asn Thr Met Ala Ala Phe Asp Lys Ala Leu Gln
50 55 60

Met Lys Ala Asp Tyr Ile Glu Leu Asp Val Gln Met Ser Lys Asp Gly
65 70 75 80

Glu Leu Val Ile Ile His Asp Thr Thr Val Asn Arg Thr Thr Asp Ile
85 90 95

Asp Ser Val Leu Pro Val Ala Val Lys Asp Leu Thr Leu Ala Glu Leu
100 105 110

10294.204.ST25.txt

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 115 120 125

Arg Ile Pro Thr Phe Glu Glu Val Leu Asp Arg Tyr Lys Gly Lys Val
 130 135 140

Gly Met Leu Ile Glu Leu Lys Glu Pro Ala Arg Tyr Pro Gly Ile Glu
 145 150 155 160

Gly Lys Val Ser Ala Ala Leu Lys Glu Arg Arg Met Asp Lys Pro Lys
 165 170 175

Asn Gly Lys Ile Ile Val Gln Ser Phe Asp Phe Asn Ser Val Tyr Lys
 180 185 190

Ile His Gln Leu Leu Pro Ser Met Pro Thr Gly Val Leu Thr Ser Lys
 195 200 205

Ala Ala Asp Leu Thr Asp Ala Lys Leu Lys Glu Phe Ser Gly Tyr Ala
 210 215 220

Lys Tyr Val Asn Ala Asn Leu Lys Asn Val Ala Ala Asp Pro Thr Leu
 225 230 235 240

Val Pro Arg Ile His Ala Leu Gly Met Lys Ile Arg Pro Trp Thr Val
 245 250 255

Arg Ser Arg Asp Glu Val Pro Pro Leu Phe Arg Pro Ala Trp Asn Gly
 260 265 270

Ile Val Thr Asn Phe Pro Asp Tyr Cys Ser Lys Lys Val Arg Glu Pro
 275 280 285

Gln

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 <213> Bacillus licheniformis

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 gaagggatgc tccctcttga cgaatggttc aattttgcag gcggtaatga aaactaccgg 180
 gtatgggagg ctttagagga cggcaagcct gtcggcggtt tcatgggttg agttgaggag 240

10294.204.ST25.txt

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gccggaattg aagaggataa caagagggtgc ttagcgtgct tccgatccgt cgggtattca 420
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taaataagga gcataagaag atg aac ttg atc aaa tgg att ttg ttt tcc gtt 533
Met Asn Leu Ile Lys Trp Ile Leu Phe Ser Val
1 5 10
att tca ttc gcc ttt ttt cag ccg gca cca gcc gct cta tta aaa gaa 581
Ile Ser Phe Ala Phe Phe Gln Pro Ala Pro Ala Ala Leu Leu Lys Glu
15 20 25
aag gac gac tat act att ctt gtt tat atg att ggt tct gac atg gaa 629
Lys Asp Asp Tyr Thr Ile Leu Val Tyr Met Ile Gly Ser Asp Met Glu
30 35 40
agc gat ttt cat atg gca agc gat gac att cag gaa atg atg gat gcg 677
Ser Asp Phe His Met Ala Ser Asp Asp Ile Gln Glu Met Met Asp Ala
45 50 55
ggg tca tct tca aac gtc aat gtc gtt ctt cag aca gga gga gca aaa 725
Gly Ser Ser Ser Asn Val Asn Val Val Leu Gln Thr Gly Gly Ala Lys
60 65 70 75
aaa tgg gcg aac ccg tcg atc agt cac aag gtg aat cag agg tgg aaa 773
Lys Trp Ala Asn Pro Ser Ile Ser His Lys Val Asn Gln Arg Trp Lys
80 85 90
gtt gaa cat cag aag ctg gtg ccc ctc gaa aat gtc ggg aag aaa aat 821
Val Glu His Gln Lys Leu Val Pro Leu Glu Asn Val Gly Lys Lys Asn
95 100 105
atg gac agt ccc ggc tcc gtc aca gat ttt atc aca tgg gga gtc aaa 869
Met Asp Ser Pro Gly Ser Val Thr Asp Phe Ile Thr Trp Gly Val Lys
110 115 120
aca tat ccg gct aaa aaa tat gta ttg atc ttt tgg ggg cat ggg ctt 917
Thr Tyr Pro Ala Lys Lys Tyr Val Leu Ile Phe Trp Gly His Gly Leu
125 130 135
ggc tca gtt gac ggc tac ggg gga gac gaa aac ttc ggc aat aag aaa 965
Gly Ser Val Asp Gly Tyr Gly Gly Asp Glu Asn Phe Gly Asn Lys Lys
140 145 150 155
atg aaa ata agc gag ctg cag tcg gga atc aaa acg gcc tat gaa cat 1013
Met Lys Ile Ser Glu Leu Gln Ser Gly Ile Lys Thr Ala Tyr Glu His
160 165 170
acg aag caa aag ttt gat tta atc ggt ttt gac aac tgc aaa atg gcc 1061
Thr Lys Gln Lys Phe Asp Leu Ile Gly Phe Asp Asn Cys Lys Met Ala
175 180 185
ggg att gaa acg gca tat gcc ttg agg gat tat ggt aag tac atg ctg 1109
Gly Ile Glu Thr Ala Tyr Ala Leu Arg Asp Tyr Gly Lys Tyr Met Leu
190 195 200
gct tca gtc gac tat acg aat caa aac ggc tgg gat tat aaa agg gcg 1157
Ala Ser Val Asp Tyr Thr Asn Gln Asn Gly Trp Asp Tyr Lys Arg Ala
205 210 215
ctg cag tct gta caa gac gac cct tca atc gat ccg aaa gag ctt ggc 1205
Leu Gln Ser Val Gln Asp Asp Pro Ser Ile Asp Pro Lys Glu Leu Gly
220 225 230 235

10294.204.ST25.txt

agg gaa atc gct gca ggc tac gta cag cag tca aaa gaa aac ggt gaa 1253
 Arg Glu Ile Ala Ala Gly Tyr Val Gln Gln Ser Lys Glu Asn Gly Glu 250
 240 245
 aca gaa gac ctg cag cag tct tta att caa ttg aac cgt gtc aaa gac 1301
 Thr Glu Asp Leu Gln Gln Ser Leu Ile Gln Leu Asn Arg Val Lys Asp 265
 255 260
 gct gtc gat gcc ctc gac aga ttg agc gta aac atg aac ctg gca ttg 1349
 Ala Val Asp Ala Leu Asp Arg Leu Ser Val Asn Met Asn Leu Ala Leu 280
 270 275
 aaa gag cct gac gga aag cgc ctg ctc cac tac gcg cgt ctc gct gct 1397
 Lys Glu Pro Asp Gly Lys Arg Leu Leu His Tyr Ala Arg Leu Ala Ala 295
 285 290
 gaa gat tat gca gat gaa tcg gat atg gtt gat ttg gcg gat ttg tca 1445
 Glu Asp Tyr Ala Asp Glu Ser Asp Met Val Asp Leu Ala Asp Leu Ser 310
 300 305 315
 agc ttg atc ggt cag cag atc gga gcc gag aaa gaa gca aaa gag gtc 1493
 Ser Leu Ile Gly Gln Gln Ile Gly Ala Glu Lys Glu Ala Lys Glu Val 330
 320 325 330
 gta aaa tcc gtc aag aag gct gtc atc atg aac atc aaa tct ccg gag 1541
 Val Lys Ser Val Lys Lys Ala Val Ile Met Asn Ile Lys Ser Pro Glu 345
 335 340 345
 cat cca aga gga agc ggc atg tcc gtt tat tat ccg gcc aga gac aac 1589
 His Pro Arg Gly Ser Gly Met Ser Val Tyr Tyr Pro Ala Arg Asp Asn 360
 350 355 360
 cat aag cgg ttt gcg gaa aaa tcg aaa ata tac cgc ctg ctt gac ttc 1637
 His Lys Arg Phe Ala Glu Lys Ser Lys Ile Tyr Arg Leu Leu Asp Phe 375
 365 370 375
 agc agc cgg tat caa aca ttc atc aaa gat tac tcg cat tca aca ttt 1685
 Ser Ser Arg Tyr Gln Thr Phe Ile Lys Asp Tyr Ser His Ser Thr Phe 395
 380 385 390 395
 aac ttt gat cta tagttgcgtt taacagcaaa aaagcgccgg cggaataacc 1737
 Asn Phe Asp Leu
 ggcaacttttt ttatcggtc atgtgcttcc ggatcaatgg aagtcgtag atgatgaaag 1797
 cggcgacatg ggcatgaca acgttgagaa taaagagtgc gatcatgaga gagtgtcctg 1857
 taggagaaag gctgctggtc atatagaaaa agaagaatac ccacattaaa atgatggcg 1917
 gaatagaaga aattgcgacc tttttgttgt ccagccataa aaataaagga gtggcgcttg 1977
 caatcagcaa gtaagcgaaa aacatatcca tgcgttttca gcccctttcg ataatgatag 2037
 cgctgtcaaa aaaagcgga tgaacatca atttgttcta attggagaat attttgtgaa 2097
 cattctgtta catttattat accacgttct tcgaaaaatg atacatactg gaaagcattt 2157
 tccgctccaa ctatcggtc aattttcacg gtgattcagt tag 2200
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 <211> 399
 <212> PRT
 <213> Bacillus licheniformis
 <400> 150

10294.204.ST25.txt

Met Asn Leu Ile Lys Trp Ile Leu Phe Ser Val Ile Ser Phe Ala Phe
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 Phe Gln Pro Ala Pro Ala Ala Leu Leu Lys Glu Lys Asp Asp Tyr Thr
 20 25 30
 Ile Leu Val Tyr Met Ile Gly Ser Asp Met Glu Ser Asp Phe His Met
 35 40 45
 Ala Ser Asp Asp Ile Gln Glu Met Met Asp Ala Gly Ser Ser Ser Asn
 50 55 60
 Val Asn Val Val Leu Gln Thr Gly Gly Ala Lys Lys Trp Ala Asn Pro
 65 70 75 80
 Ser Ile Ser His Lys Val Asn Gln Arg Trp Lys Val Glu His Gln Lys
 85 90 95
 Leu Val Pro Leu Glu Asn Val Gly Lys Lys Asn Met Asp Ser Pro Gly
 100 105 110
 Ser Val Thr Asp Phe Ile Thr Trp Gly Val Lys Thr Tyr Pro Ala Lys
 115 120 125
 Lys Tyr Val Leu Ile Phe Trp Gly His Gly Leu Gly Ser Val Asp Gly
 130 135 140
 Tyr Gly Gly Asp Glu Asn Phe Gly Asn Lys Lys Met Lys Ile Ser Glu
 145 150 155 160
 Leu Gln Ser Gly Ile Lys Thr Ala Tyr Glu His Thr Lys Gln Lys Phe
 165 170 175
 Asp Leu Ile Gly Phe Asp Asn Cys Lys Met Ala Gly Ile Glu Thr Ala
 180 185 190
 Tyr Ala Leu Arg Asp Tyr Gly Lys Tyr Met Leu Ala Ser Val Asp Tyr
 195 200 205
 Thr Asn Gln Asn Gly Trp Asp Tyr Lys Arg Ala Leu Gln Ser Val Gln
 210 215 220
 Asp Asp Pro Ser Ile Asp Pro Lys Glu Leu Gly Arg Glu Ile Ala Ala
 225 230 235 240
 Gly Tyr Val Gln Gln Ser Lys Glu Asn Gly Glu Thr Glu Asp Leu Gln
 245 250 255
 Gln Ser Leu Ile Gln Leu Asn Arg Val Lys Asp Ala Val Asp Ala Leu
 260 265 270

ttc tcc aag gct gag cct tat ctg tca aag gtc gtg cag tat gaa ggc 629
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Phe Ser Lys Ala Glu Pro Tyr Leu Ser Lys Val Val Gln Tyr Glu Gly
 30 35 40

gtg aac aac atg aaa atc ggc gaa tgg atc gag aca ttt aag ccg 674
 Val Asn Asn Met Lys Ile Gly Glu Trp Ile Glu Thr Phe Lys Pro
 45 50 55

taattcacgc taaaatctcc cttttttcgc ctaatacatg atacaatcct ataaggagta 734
 ccagatagca aggagaggaa ttatggaaaa gaaattatgc attgcaatag acggccctgc 794
 ggcagccgga aaaagcaccg tggcgaaaat cgtggccaga aaaaagtcgt atatttatat 854
 tgatacgggt gccatgtaca gggcgattac gtatctagcg ctggaaaagg gcgttgattt 914
 aaacgacgaa gcggcgctga cggccttggt aaaagaatct gccatcgatc tcacggtttc 974
 gcctgaagga gagcagaagg tttatatcgc aggcgaagat gtaacagagg cgatccgcac 1034
 ggatagcgtg agcaaccaag tctccatcgt cgccaaatac gccgggatcc gcgaagaaat 1094
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 cggaaccac gttctc 1170

<210> 152
 <211> 58
 <212> PRT
 <213> Bacillus licheniformis

<400> 152

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Val Ile Leu Ile Ser Val Gln Leu Leu Phe His Phe Ser Lys Ala Glu
 20 25 30

Pro Tyr Leu Ser Lys Val Val Gln Tyr Glu Gly Val Asn Asn Met Lys
 35 40 45

Ile Gly Glu Trp Ile Glu Thr Phe Lys Pro
 50 55

<210> 153
 <211> 1435
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(932)

<400> 153
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 cgtcttcatc aaaaccggcc agttcatatt tgaagacgga gtattcctcg ccgtcgtcaa 180
 atttcgacgt gtcttcctcc ccgtttccag taatgtgaac ataatatctg tccgtcccca 240

cacggttttaa	gttacatccg	cttaaaaaatg	cggcaaatat	gatcatcagg	ctgatccatg		300									
gaatatgggt	ttttcacttt	ttctcctcat	ttatggtttc	tgtgtaaatg	ataagattca		360									
ttgtctgata	aaaaaattga	ataacgtgac	atgaacatta	cacttttgta	agggatcgtt		420									
ttagcacacg	caggcaaatt	aaattttcaat	atccttttta	ttcaataaag	tttataatat		480									
ggaaaaaagg	aggggcgcca	atg	aaa	aaa	atc	gta	tgt	ttg	atg	gtg	ttt	tca		533		
		Met	Lys	Lys	Ile	Val	Cys	Leu	Met	Val	Phe	Ser				
		1				5					10					
atc	atg	acg	gcc	ttc	ggg	att	cac	atc	cag	cct	gct	gaa	gct	gcg	gtt	581
Ile	Met	Thr	Ala	Phe	Gly	Ile	His	Ile	Gln	Pro	Ala	Glu	Ala	Ala	Val	
			15					20					25			
ata	aaa	gat	gag	aaa	aag	atg	acc	atg	aca	atg	act	gaa	gat	cat	gtg	629
Ile	Lys	Asp	Glu	Lys	Lys	Met	Thr	Met	Thr	Met	Thr	Glu	Asp	His	Val	
		30					35					40				
gga	ttt	ttt	atg	gcg	gac	agc	acc	aat	gta	aat	tac	tac	ccg	aca	tgg	677
Gly	Phe	Phe	Met	Ala	Asp	Ser	Thr	Asn	Val	Asn	Tyr	Tyr	Pro	Thr	Trp	
	45					50					55					
ctg	tat	tac	aag	ctt	acg	att	ttt	aac	gcg	gaa	ggc	tgc	aca	ctc	aac	725
Leu	Tyr	Tyr	Lys	Leu	Thr	Ile	Phe	Asn	Ala	Glu	Gly	Cys	Thr	Leu	Asn	
					65					70					75	
atc	aag	ctg	cag	aga	atc	acg	tta	aca	gga	cat	gcg	gtc	act	tta	agc	773
Ile	Lys	Leu	Gln	Arg	Ile	Thr	Leu	Thr	Gly	His	Ala	Val	Thr	Leu	Ser	
				80					85					90		
gag	aaa	gag	tat	acg	gga	aat	cat	ctt	cat	tta	agt	gct	gca	gat	aaa	821
Glu	Lys	Glu	Tyr	Thr	Gly	Asn	His	Leu	His	Leu	Ser	Ala	Ala	Asp	Lys	
			95					100					105			
gtg	agc	ggg	tcg	ccg	cac	cga	aat	cat	ttc	ttg	gat	atc	aca	aaa	gtg	869
Val	Ser	Gly	Ser	Pro	His	Arg	Asn	His	Phe	Leu	Asp	Ile	Thr	Lys	Val	
		110					115					120				
tcg	ggg	tgc	ggg	gat	gtt	gga	atc	aca	ggg	ttt	tac	ggc	ttt	gag	cac	917
Ser	Gly	Cys	Gly	Asp	Val	Gly	Ile	Thr	Gly	Phe	Tyr	Gly	Phe	Glu	His	
	125					130					135					
caa	atg	ccg	ggc	tac	taattgatat			agaaagcgcg			ggagggggact			tttcagagt		972
Gln	Met	Pro	Gly	Tyr												

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10294.204.ST25.txt

<213> Bacillus licheniformis

<400> 154

Met Lys Lys Ile Val Cys Leu Met Val Phe Ser Ile Met Thr Ala Phe
 1 5 10 15

Gly Ile His Ile Gln Pro Ala Glu Ala Ala Val Ile Lys Asp Glu Lys
 20 25 30

Lys Met Thr Met Thr Met Thr Glu Asp His Val Gly Phe Phe Met Ala
 35 40 45

Asp Ser Thr Asn Val Asn Tyr Tyr Pro Thr Trp Leu Tyr Tyr Lys Leu
 50 55 60

Thr Ile Phe Asn Ala Glu Gly Cys Thr Leu Asn Ile Lys Leu Gln Arg
 65 70 75 80

Ile Thr Leu Thr Gly His Ala Val Thr Leu Ser Glu Lys Glu Tyr Thr
 85 90 95

Gly Asn His Leu His Leu Ser Ala Ala Asp Lys Val Ser Gly Ser Pro
 100 105 110

His Arg Asn His Phe Leu Asp Ile Thr Lys Val Ser Gly Cys Gly Asp
 115 120 125

Val Gly Ile Thr Gly Phe Tyr Gly Phe Glu His Gln Met Pro Gly Tyr
 130 135 140

<210> 155

<211> 1768

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1265)

<400> 155

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 acggcctatt tggcaggcta catcgctgaa aaatataatt acgatgatga agagcttttt 180
 ccgcgggcga aaagcaaaat cagcggctac atcgagtcac atatcgattc caccctgtcc 240
 ggggtacagct cagtcgatgt gaaaacgaaa cacgtcgata cacaaaaagt gaaaagcttg 300
 tatgtgcttt tgcccgtctg gatgggtcaat tacaactaca aacaaaagga ttacatcttt 360
 gccatgaacg gacaaacggg aaaagtcgtc ggcaagccgc cgatcagctc atttaaagaa 420
 aaaatgtggt tcagcgggct ggccgtctcc atatttgcac tctggaaaat cattgctgct 480
 gtaatgggag gcggggcgtg atg aga agt tta ttg aga agc gcg atg atc tta 533

10294.204.ST25.txt

Met Arg Ser Leu Leu Arg Ser Ala Met Ile Leu
1 5 10

tgt atg att ttc ctt gtc ttc atc cct ata gcc tcc ggt gcg gca gcc Cys Met Ile Phe 15 Leu Val Phe Ile Pro Ile Ala Ser Gly Ala Ala Ala	581
tct gaa cag aag cgg ttt gtt tat gat gaa gcc ggg ctt ctg acc aaa Ser Glu Gln Lys Arg Phe Val Tyr Asp Glu Ala Gly Leu Leu Thr Lys	629
cag gaa atc gag aag ctg gaa acg ctg gca gcc aaa ttg ggc gcc gaa Gln Glu Ile Glu Lys Leu Glu Thr Leu Ala Ala Lys Leu Gly Ala Glu	677
cgg gag acc gac ttt atc att gtg acg acc aat gat aca aac ggc cgc Arg Glu Thr Asp Phe Ile Ile Val Thr Thr Asn Asp Thr Asn Gly Arg	725
gat gta aag aaa tat gcg gag gac ttc tat gac gaa aaa gcg ccc ggc Asp Val Lys Lys Tyr Ala Glu Asp Phe Tyr Asp Glu Lys Ala Pro Gly	773
tac cag aag aag cac gga aat gca gcc gta tta acg gta gat atg gag Tyr Gln Lys Lys His Gly Asn Ala Ala Val Leu Thr Val Asp Met Glu	821
cat aga gaa gtc tat ctt gcc ggc ttt aaa aag gct gaa gaa tat ttg His Arg Glu Val Tyr Leu Ala Gly Phe Lys Lys Ala Glu Glu Tyr Leu	869
aat gac gcc agg ctg gac aaa att aga gaa aaa atc acg ccg gat ata Asn Asp Ala Arg Leu Asp Lys Ile Arg Glu Lys Ile Thr Pro Asp Ile	917
tcc gac aag cat tat gag gcc gca ttc gaa atg ttt atg aag gcg gcg Ser Asp Lys His Tyr Glu Ala Ala Phe Glu Met Phe Met Lys Ala Ala	965
cat gat gat atg gag aag aaa ccg tgg gcg gac agc atc ttt ttt aag His Asp Asp Met Glu Lys Lys Pro Trp Ala Asp Ser Ile Phe Phe Lys	1013
acg tgg ttt caa ttg ctt gtt tcg gca gtc atc gcg gga att gcc gtc Thr Trp Phe Gln Leu Leu Val Ser Ala Val Ile Ala Gly Ile Ala Val	1061
gcc att atg aaa tac aat tca ggc ggc aaa gtg aca gta agt gca agc Ala Ile Met Lys Tyr Asn Ser Gly Gly Lys Val Thr Val Ser Ala Ser	1109
act tat atg aac ggt gat acg tcc gga gtg atc aga aat aat gac gaa Thr Tyr Met Asn Gly Asp Thr Ser Gly Val Ile Arg Asn Asn Asp Glu	1157
tac atc aga acg acc gtc aca aaa cag aga aaa ccg tcc aat aat aaa Tyr Ile Arg Thr Thr Val Thr Lys Gln Arg Lys Pro Ser Asn Asn Lys	1205
agc tca ggc ggc gga acg acg agc gga ggc cat tcg cac agc ggc agc Ser Ser Gly Gly Gly Thr Thr Ser Gly Gly His Ser His Ser Gly Ser	1253
cgg gga agc ttt tagaaaggga aaggaagagc ttaaattggtg ttttttagaa Arg Gly Ser Phe 255	1305
atcaatttgc aaatgtagta gagtgggatg aatttcgcga tgatatgatt ttctataaat	1365

10294.204.ST25.txt

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ggaacaaccg cgaaatcaaa aaggggagcc ggctgatcat tcgccccggt caggatgccg 1425
tcttttttaa caacggaaaa attgaaggca ttttccagga tgagggcgac tatgatattg 1485
aatccgaaat tattcctttt ttatccactt taaaagggtt taaatttggc tttaacagcg 1545
ggatgcgcgc cgaagtcctg tttgtcaaca cgaaggaatt taccgtcaag tgggggacga 1605
agaatgccat caatatcccg gctgcaggac ttccgggcgg catgccgatc agggcgaaacg 1665
gaagatttaa ctttaagggtg aatgattatg tcgcattaat cgataaaatt gccggtgtga 1725
aagatcagta tgttgtggaa gatatcaaaa tacggatcac atc 1768

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<210> 156
<211> 255
<212> PRT
<213> Bacillus licheniformis
<400> 156

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Val Phe Ile Pro Ile Ala Ser Gly Ala Ala Ala Ser Glu Gln Lys Arg
20 25 30

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Phe Val Tyr Asp Glu Ala Gly Leu Leu Thr Lys Gln Glu Ile Glu Lys
35 40 45

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Leu Glu Thr Leu Ala Ala Lys Leu Gly Ala Glu Arg Glu Thr Asp Phe
50 55 60

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Ile Ile Val Thr Thr Asn Asp Thr Asn Gly Arg Asp Val Lys Lys Tyr
65 70 75 80

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Ala Glu Asp Phe Tyr Asp Glu Lys Ala Pro Gly Tyr Gln Lys Lys His
85 90 95

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Gly Asn Ala Ala Val Leu Thr Val Asp Met Glu His Arg Glu Val Tyr
100 105 110

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Leu Ala Gly Phe Lys Lys Ala Glu Glu Tyr Leu Asn Asp Ala Arg Leu
115 120 125

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Asp Lys Ile Arg Glu Lys Ile Thr Pro Asp Ile Ser Asp Lys His Tyr
130 135 140

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Glu Ala Ala Phe Glu Met Phe Met Lys Ala Ala His Asp Asp Met Glu
145 150 155 160

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Lys Lys Pro Trp Ala Asp Ser Ile Phe Phe Lys Thr Trp Phe Gln Leu
165 170 175

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Leu Val Ser Ala Val Ile Ala Gly Ile Ala Val Ala Ile Met Lys Tyr

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180

10294.204.ST25.txt
185

190

Asn Ser Gly Gly Lys Val Thr Val Ser Ala Ser Thr Tyr Met Asn Gly
195 200 205

Asp Thr Ser Gly Val Ile Arg Asn Asn Asp Glu Tyr Ile Arg Thr Thr
210 215 220

Val Thr Lys Gln Arg Lys Pro Ser Asn Asn Lys Ser Ser Gly Gly Gly
225 230 235 240

Thr Thr Ser Gly Gly His Ser His Ser Gly Ser Arg Gly Ser Phe
245 250 255

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<211> 1688
<212> DNA
<213> Bacillus licheniformis

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<222> (501)..(1652)

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gtctatcatc gatgcataga agaatttttt acaccgaaaa aagatacttg gtacgaagac 180
agcagagcgg cctacacggg aaaaaacgcc atttgctttc acgaaccagc gccggcctca 240
ttaaaaaatt tgatggcttc gcttgaaaca ggatatcaat cgatgagaga agaattggaa 300
tactatgcga ctgactatcg aatgaagatg gttcagccga gatcatagct taaatgaacc 360
gtgagccgga actccccctt tcatgaaagg ggggttttta tcttgcttta gatttttctc 420
gggaaatcat ccaattggtg ttcataacaa aaagacaagc gcataaactt gtacaaacaa 480
ccacaaggac gtgagaaaaa atg cgc ttt ttt cta aaa caa gcg gca gca gcc 533
Met Arg Phe Phe Leu Lys Gln Ala Ala Ala Ala
1 5 10
atc atg ata tgc tct ctt tta tgc tct tca tac gaa acc gct caa gca 581
Ile Met Ile Cys Ser Leu Leu Cys Ser Ser Tyr Glu Thr Ala Gln Ala
15 20 25
cag ccc tcc ctt cat atc agc gca aaa agc gcg att gtc atg gac ggg 629
Gln Pro Ser Leu His Ile Ser Ala Lys Ser Ala Ile Val Met Asp Gly
30 35 40
caa tcc gga cgg gtt ttg ttt gca aag gat gag cat gaa aaa cgg cgc 677
Gln Ser Gly Arg Val Leu Phe Ala Lys Asp Glu His Glu Lys Arg Arg
45 50 55
att gca agc att acg aag att atg aca gcc att ttg gcc gtg gaa tcg 725
Ile Ala Ser Ile Thr Lys Ile Met Thr Ala Ile Leu Ala Val Glu Ser
60 65 70 75
ggc aaa ttg gat gag acg gtc acg gtc agc gac aga gcg gtc agg aca 773
Gly Lys Leu Asp Glu Thr Val Thr Val Ser Asp Arg Ala Val Arg Thr

10294.204.ST25.txt																
80								85		90						
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Glu	Gly	Ser	Ser	Ile	Tyr	Leu	Thr	Ser	Gly	Gln	Lys	Val	Lys	Leu	Lys	
			95					100					105			
gac	ctt	gtt	tac	ggt	ttg	atg	ctg	aga	tcg	gga	aat	gat	gca	gcc	gtt	869
Asp	Leu	Val	Tyr	Gly	Leu	Met	Leu	Arg	Ser	Gly	Asn	Asp	Ala	Ala	Val	
		110					115					120				
gcg	att	gcc	gaa	cat	gtg	ggc	gga	agc	ctg	gaa	ggc	ttt	gtc	tac	atg	917
Ala	Ile	Ala	Glu	His	Val	Gly	Gly	Ser	Leu	Glu	Gly	Phe	Val	Tyr	Met	
	125					130					135					
atg	aat	caa	aaa	gcg	gcc	gag	ctc	ggc	atg	gaa	aac	acc	ctg	ttc	cgc	965
Met	Asn	Gln	Lys	Ala	Ala	Glu	Leu	Gly	Met	Glu	Asn	Thr	Leu	Phe	Arg	
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aat	ccg	cac	gga	ctt	gat	gac	cac	cct	gat	cac	tat	tcc	tcg	gcc	tat	1013
Asn	Pro	His	Gly	Leu	Asp	Asp	His	Pro	Asp	His	Tyr	Ser	Ser	Ala	Tyr	
				160					165					170		
gat	atg	gcg	ctt	tta	aca	aaa	tat	gcg	atg	agc	aat	gaa	acg	tac	aaa	1061
Asp	Met	Ala	Leu	Leu	Thr	Lys	Tyr	Ala	Met	Ser	Asn	Glu	Thr	Tyr	Lys	
			175					180					185			
aaa	atc	gcc	gga	acg	aaa	cgc	tat	aaa	gca	gaa	acg	atg	caa	ggc	atc	1109
Lys	Ile	Ala	Gly	Thr	Lys	Arg	Tyr	Lys	Ala	Glu	Thr	Met	Gln	Gly	Ile	
		190					195					200				
tgg	gag	aat	aaa	aac	aag	ctt	tta	aca	ggg	ctt	tac	aaa	tac	agt	aca	1157
Trp	Glu	Asn	Lys	Asn	Lys	Leu	Leu	Thr	Gly	Leu	Tyr	Lys	Tyr	Ser	Thr	
	205					210					215					
ggc	ggg	aag	acg	gga	tat	aca	agg	ctt	gca	aag	cgg	acg	ctc	gtc	tcc	1205
Gly	Gly	Lys	Thr	Gly	Tyr	Thr	Arg	Leu	Ala	Lys	Arg	Thr	Leu	Val	Ser	
220					225					230					235	
att	tca	tcg	aaa	gac	gga	acc	gat	ttg	atc	gcc	gtc	aca	atc	aat	gcc	1253
Ile	Ser	Ser	Lys	Asp	Gly	Thr	Asp	Leu	Ile	Ala	Val	Thr	Ile	Asn	Ala	
				240					245					250		
cct	gac	gac	tgg	aat	gat	cat	atg	aac	atg	ttc	aac	tat	gta	ttc	ggc	1301
Pro	Asp	Asp	Trp	Asn	Asp	His	Met	Asn	Met	Phe	Asn	Tyr	Val	Phe	Gly	
			255					260					265			
cag	tac	aaa	aca	tat	atc	atc	gcc	aaa	aaa	ggc	gag	att	ccg	aaa	tta	1349
Gln	Tyr	Lys	Thr	Tyr	Ile	Ile	Ala	Lys	Lys	Gly	Glu	Ile	Pro	Lys	Leu	
		270					275					280				
aaa	gac	tct	ttt	tac	gga	cat	aca	gct	ttt	att	aaa	cgg	gat	gtc	aca	1397
Lys	Asp	Ser	Phe	Tyr	Gly	His	Thr	Ala	Phe	Ile	Lys	Arg	Asp	Val	Thr	
	285					290					295					
tat	ctt	tta	aac	gaa	gag	gaa	aaa	gaa	gat	gtg	aag	gtt	gat	atc	gag	1445
Tyr	Leu	Leu	Asn	Glu	Glu	Glu	Lys	Glu	Asp	Val	Lys	Val	Asp	Ile	Glu	
300					305					310					315	
ctt	ctt	gaa	ccg	aaa	aaa	tca	tgg	cgt	aaa	aac	aaa	aaa	gaa	atc	ccg	1493
Leu	Leu	Glu	Pro	Lys	Lys	Ser	Trp	Arg	Lys	Asn	Lys	Lys	Glu	Ile	Pro	
				320					325					330		
gac	atc	atc	gga	gaa	atg	aac	gtc	atg	ttc	gac	gga	aaa	acg	att	gca	1541
Asp	Ile	Ile	Gly	Glu	Met	Asn	Val	Met	Phe	Asp	Gly	Lys	Thr	Ile	Ala	
			335					340					345			
agc	gta	ccg	atc	tat	tat	gaa	aac	gag	cga	aac	aaa	aat	ccg	aaa	aaa	1589
Ser	Val	Pro	Ile	Tyr	Tyr	Glu	Asn	Glu	Arg	Asn	Lys	Asn	Pro	Lys	Lys	

10294.204.ST25.txt

350

355

360

tcg ttt ttc gag acc ttt caa tcc gta ttc caa aaa gcg gcg ggc ggt 1637
 Ser Phe Phe Glu Thr Phe Gln Ser Val Phe Gln Lys Ala Ala Gly Gly
 365 370 375

tca tca tgg tca ata taatctgggt cggcttaacg gtgatcggta tgggtg 1688
 Ser Ser Trp Ser Ile
 380

<210> 158
 <211> 384
 <212> PRT
 <213> Bacillus licheniformis

<400> 158

Met Arg Phe Phe Leu Lys Gln Ala Ala Ala Ala Ile Met Ile Cys Ser
 1 5 10 15

Leu Leu Cys Ser Ser Tyr Glu Thr Ala Gln Ala Gln Pro Ser Leu His
 20 25 30

Ile Ser Ala Lys Ser Ala Ile Val Met Asp Gly Gln Ser Gly Arg Val
 35 40 45

Leu Phe Ala Lys Asp Glu His Glu Lys Arg Arg Ile Ala Ser Ile Thr
 50 55 60

Lys Ile Met Thr Ala Ile Leu Ala Val Glu Ser Gly Lys Leu Asp Glu
 65 70 75 80

Thr Val Thr Val Ser Asp Arg Ala Val Arg Thr Glu Gly Ser Ser Ile
 85 90 95

Tyr Leu Thr Ser Gly Gln Lys Val Lys Leu Lys Asp Leu Val Tyr Gly
 100 105 110

Leu Met Leu Arg Ser Gly Asn Asp Ala Ala Val Ala Ile Ala Glu His
 115 120 125

Val Gly Gly Ser Leu Glu Gly Phe Val Tyr Met Met Asn Gln Lys Ala
 130 135 140

Ala Glu Leu Gly Met Glu Asn Thr Leu Phe Arg Asn Pro His Gly Leu
 145 150 155 160

Asp Asp His Pro Asp His Tyr Ser Ser Ala Tyr Asp Met Ala Leu Leu
 165 170 175

Thr Lys Tyr Ala Met Ser Asn Glu Thr Tyr Lys Lys Ile Ala Gly Thr
 180 185 190

Lys Arg Tyr Lys Ala Glu Thr Met Gln Gly Ile Trp Glu Asn Lys Asn
 195 200 205

10294.204.ST25.txt

Lys Leu Leu Thr Gly Leu Tyr Lys Tyr Ser Thr Gly Gly Lys Thr Gly
 210 215 220

Tyr Thr Arg Leu Ala Lys Arg Thr Leu Val Ser Ile Ser Ser Lys Asp
 225 230 235 240

Gly Thr Asp Leu Ile Ala Val Thr Ile Asn Ala Pro Asp Asp Trp Asn
 245 250 255

Asp His Met Asn Met Phe Asn Tyr Val Phe Gly Gln Tyr Lys Thr Tyr
 260 265 270

Ile Ile Ala Lys Lys Gly Glu Ile Pro Lys Leu Lys Asp Ser Phe Tyr
 275 280 285

Gly His Thr Ala Phe Ile Lys Arg Asp Val Thr Tyr Leu Leu Asn Glu
 290 295 300

Glu Glu Lys Glu Asp Val Lys Val Asp Ile Glu Leu Leu Glu Pro Lys
 305 310 315 320

Lys Ser Trp Arg Lys Asn Lys Lys Glu Ile Pro Asp Ile Ile Gly Glu
 325 330 335

Met Asn Val Met Phe Asp Gly Lys Thr Ile Ala Ser Val Pro Ile Tyr
 340 345 350

Tyr Glu Asn Glu Arg Asn Lys Asn Pro Lys Lys Ser Phe Phe Glu Thr
 355 360 365

Phe Gln Ser Val Phe Gln Lys Ala Ala Gly Gly Ser Ser Trp Ser Ile
 370 375 380

<210> 159
 <211> 1617
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1118)

<400> 159
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 cctgctgctg cggcttgctt tacagccccg ggtattaaag ataaggtacg ggggtgaaaa 120
 aattcagcgg gtgaggtggt cgacatgagg aaaggagtca tccttggttct gttcgctatg 180
 ctgttatttg caggctgcgg cacaacgcag cataatgggc aaagcgggtga tgagagccga 240
 aaaggaacag gcgaggaaac gctcgtgaaa gaaggcacct ttgtcggttt ggcggaccag 300
 cataccgtcg ccgtaatat tgacggcaaa gaaacgatgt ttcaggtccc tcccgaaaaa 360

[illegible]

10294.204.ST25.txt

catgatgaaa agcttgacag gacgacttca ctgaaaggggt atgtgaaaga tcttacatat 1458
 gaggaaataa aacatggaga cgcaagccac cgttttgccg aaaaaaccgg ttctgtccct 1518
 gtgccgaccc ttgaagaagt gtttgagtgg gcggcagatg ctgaatttct tcttaatggt 1578
 gaattgaaaa acagcattat ccgctatgaa gggatggaa 1617

<210> 160
 <211> 206
 <212> PRT
 <213> Bacillus licheniformis

<400> 160

Val Lys Leu Leu Ile Lys Ser Phe Val Leu Leu Leu Phe Ser Phe Met
 1 5 10 15

Ala Ala Phe Pro Ala Ala Phe Ala Ala Glu Pro Leu Ser Gly Lys Thr
 20 25 30

Val Tyr Val Asp Ala Gly His Gly Gly Glu Asp Ser Gly Ala Val Gly
 35 40 45

Asn Gly Leu Leu Glu Lys Asp Val Asn Leu Glu Val Ala Met Leu Ile
 50 55 60

Asp Glu Lys Leu Lys Glu Glu Gly Ala Asp Thr Val Ala Ser Arg Thr
 65 70 75 80

Asp Asp Thr Phe Leu Thr Leu Glu Asp Arg Val Ala Lys Ala Ser Lys
 85 90 95

Asn Ala Ser Asp Leu Phe Ile Ser Ile His Ala Asn Ser Ala Val Pro
 100 105 110

Glu Ala Ser Gly Thr Glu Thr Tyr Phe Asp Ser Thr Tyr Gln Ala Ala
 115 120 125

Asp Ser Glu Arg Leu Ala Ser Asp Ile Gln Glu Arg Leu Pro Asp Ala
 130 135 140

Leu Gly Thr Arg Asp Arg Gly Val Lys Glu Ser Gly Phe Tyr Val Ile
 145 150 155 160

Lys Asn Ser Gln Met Pro Ser Val Leu Val Glu Leu Gly Phe Ile Thr
 165 170 175

Asn Lys Thr Asp Ala Asp Lys Leu Glu Ser Pro Glu Tyr Gln Glu Lys
 180 185 190

Ala Ala Asp Ala Ile Ala Asp Ala Val Val Ser Tyr Tyr Glu
 195 200 205

10294.204.ST25.txt

<210> 161
 <211> 1803
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (165)..(1487)

<400> 161
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 catatatgga atcgaaaaag aatgctcggc tatgaaatat ttaggatgga gcatgtcggg 120
 cattcctcct tgagagcggtt ttcttaacaa acgggaggga tcgt atg aaa aag tta 176
 Met Lys Lys Leu
 1
 tgt tgc ctg atc ttg gtc ttg gtt ttt tcc gcg ggc tgt act cag caa 224
 Cys Cys Leu Ile Leu Val Leu Val Phe Ser Ala Gly Cys Thr Gln Gln
 5 10 15 20
 aag gca tca acg gaa gag gac ggg gcg ctt gaa atc aat tgg ctc gta 272
 Lys Ala Ser Thr Glu Glu Asp Gly Ala Leu Glu Ile Asn Trp Leu Val
 25 30 35
 ccg ctc cac aca ccg cag cct ccg aaa gag aag gcg ctt gac atc att 320
 Pro Leu His Thr Pro Gln Pro Pro Lys Glu Lys Ala Leu Asp Ile Ile
 40 45 50
 gaa gac aaa acg aat aca aag ctg aag ctc atc tgg gtt ccg gat tca 368
 Glu Asp Lys Thr Asn Thr Lys Leu Lys Leu Ile Trp Val Pro Asp Ser
 55 60 65
 aca aaa gaa gag cgg atc aat aca acc ctt gca agc gga aac atg cct 416
 Thr Lys Glu Glu Arg Ile Asn Thr Thr Leu Ala Ser Gly Asn Met Pro
 70 75 80
 aaa gta atg aca ttg cct gat ctt gaa gat tca gcg gtt gtc agc gcg 464
 Lys Val Met Thr Leu Pro Asp Leu Glu Asp Ser Ala Val Val Ser Ala
 85 90 95 100
 ctg cgc tcg gga atg ttc tgg gaa atc gga ccg tat ttc aaa gac tat 512
 Leu Arg Ser Gly Met Phe Trp Glu Ile Gly Pro Tyr Phe Lys Asp Tyr
 105 110 115
 ccg aat tta aga aaa ctt gat aaa act ata ttg aaa aat att tcg gtt 560
 Pro Asn Leu Arg Lys Leu Asp Lys Thr Ile Leu Lys Asn Ile Ser Val
 120 125 130
 gat ggc aaa gtt tac ggg att tat aga gaa agg ccg atg gcc agg cag 608
 Asp Gly Lys Val Tyr Gly Ile Tyr Arg Glu Arg Pro Met Ala Arg Gln
 135 140 145
 gga gtc gtg att cgg aaa gac tgg ctc gac aat ctc gga ttg gaa atg 656
 Gly Val Val Ile Arg Lys Asp Trp Leu Asp Asn Leu Gly Leu Glu Met
 150 155 160
 ccg gaa acc gtt gat gac ctt tat aaa ata gcg aaa gca ttt aca gaa 704
 Pro Glu Thr Val Asp Asp Leu Tyr Lys Ile Ala Lys Ala Phe Thr Glu
 165 170 175 180
 cag gac ccc gat caa aac gga aaa gac gac acg ttc ggt ctc gcc gac 752
 Gln Asp Pro Asp Gln Asn Gly Lys Asp Asp Thr Phe Gly Leu Ala Asp
 185 190 195

10294.204.ST25.txt																
cgc Arg	aat Asn	gat Asp	ctc Leu 200	acc Thr	ttc Phe	gga Gly	gcg Ala	ttt Phe 205	aaa Lys	acc Thr	ctg Leu	gct Ala	tcg Ser 210	tac Tyr	ttt Phe	800
ggc Gly	gcg Ala	ccg Pro 215	aac Asn	gaa Glu	tgg Trp	gga Gly	acg Thr 220	gac Asp	gaa Glu	gac Asp	gga Gly	aat Asn 225	ctc Leu	ttc Phe	ccc Pro	848
tat Tyr	ttt Phe 230	aag Lys	cat His	gag Glu	gcc Ala	tat Tyr 235	aaa Lys	gac Asp	gca Ala	atg Met	gca Ala 240	tac Tyr	atg Met	aaa Lys	aag Lys	896
ctt Leu 245	tat Tyr	gaa Glu	gaa Glu	ggc Gly	ctg Leu 250	atg Met	aac Asn	agg Arg	gac Asp	ttt Phe 255	gcg Ala	gtg Val	aca Thr	agc Ser	aaa Lys 260	944
acg Thr	cag Gln	cag Gln	cag Gln	gat Asp 265	tta Leu	gtg Val	att Ile	cag Gln	ggg Gly 270	aaa Lys	gcg Ala	gga Gly	atc Ile	tat Tyr 275	atc Ile	992
ggc Gly	gcg Ala	atg Met	agc Ser 280	gat Asp	gcc Ala	atg Met	aac Asn	ttg Leu 285	cgt Arg	gat Asp	cag Gln	gga Gly	ctc Leu 290	gct Ala	ttg Leu	1040
aac Asn	ccc Pro	ggc Gly 295	ttt Phe	cag Gln	ctt Leu	gat Asp	atc Ile 300	gca Ala	aac Asn	cgg Arg	atc Ile	aag Lys 305	ggc Gly	ccc Pro	gac Asp	1088
ggc Gly	aag Lys 310	gag Glu	cgc Arg	aca Thr	tgg Trp	gcg Ala 315	ctc Leu	ggc Gly	ggg Gly	cat His	ggc Gly 320	ggg Gly	atg Met	ttc Phe	gcc Ala	1136
att Ile 325	tcg Ser	aaa Lys	tca Ser	agc Ser	gtc Val 330	aag Lys	act Thr	gaa Glu	aaa Lys	gag Glu 335	gtc Val	aga Arg	aaa Lys	atc Ile	ctc Leu 340	1184
gca Ala	ttt Phe	ttt Phe	gac Asp	aga Arg 345	atc Ile	gct Ala	gaa Glu	gaa Glu	gac Asp 350	ctc Leu	aac Asn	aat Asn	ttg Leu	atg Met 355	ttg Leu	1232
tat Tyr	gga Gly	ata Ile	gaa Glu 360	ggc Gly	gta Val	cac His	tat Tyr	gaa Glu 365	aag Lys	aaa Lys	ggg Gly	ggg Gly	agc Ser 370	ggc Gly	tat Tyr	1280
ttt Phe	cga Arg	aag Lys 375	cag Gln	gaa Glu	aac Asn	tac Tyr	cat His 380	ctg Leu	tgg Trp	gaa Glu	gcg Ala	gaa Glu 385	att Ile	cag Gln	ccg Pro	1328
tta Leu	aac Asn 390	cag Gln	ctg Leu	att Ile	ggc Gly	gtc Val 395	aat Asn	aaa Lys	caa Gln	gct Ala	tta Leu 400	aaa Lys	agc Ser	gct Ala	gaa Glu	1376
gat Asp 405	ccg Pro	ctc Leu	cgc Arg	gcc Ala	aaa Lys 410	aat Asn	gaa Glu	aag Lys	ctt Leu	gag Glu 415	gag Glu	gac Asp	aac Asn	cgg Arg	gca Ala 420	1424
atc Ile	gca Ala	gtc Val	cag Gln	aat Asn 425	ccg Pro	gcc Ala	gaa Glu	ccg Pro	tgt Cys 430	att Ile	ctg Leu	ccg Pro	cac His	aga Arg 435	tgg Trp	1472
aca Thr	ggg Gly	gaa Glu	cag Gln 440	aat Asn	tgaagaaaat cattgatgac gccacatttc aattttattct											1527
cggggaaatc aatgaaaaag ctttgaccag gcagtcctga aatgggagaa gcatggcggc																1587
ggaaagatca tgaagaact gaatgaagat ctgaaaaaag caaactaaac agaaaaccct																1647

10294.204.ST25.txt

ttccattttt ttgaaaagga aagggtttt catcgattc gctccaagtt cattttcttt 1707
 aaattctgca aaataaaca tataattcca tcataggacg aaaaggagga agcgatatgc 1767
 agactgccgt tatatatgca cacccaaatt caaaca 1803

<210> 162
 <211> 441
 <212> PRT
 <213> Bacillus licheniformis

<400> 162

Met Lys Lys Leu Cys Cys Leu Ile Leu Val Leu Val Phe Ser Ala Gly
 1 5 10 15

Cys Thr Gln Gln Lys Ala Ser Thr Glu Glu Asp Gly Ala Leu Glu Ile
 20 25 30

Asn Trp Leu Val Pro Leu His Thr Pro Gln Pro Pro Lys Glu Lys Ala
 35 40 45

Leu Asp Ile Ile Glu Asp Lys Thr Asn Thr Lys Leu Lys Leu Ile Trp
 50 55 60

Val Pro Asp Ser Thr Lys Glu Glu Arg Ile Asn Thr Thr Leu Ala Ser
 65 70 75 80

Gly Asn Met Pro Lys Val Met Thr Leu Pro Asp Leu Glu Asp Ser Ala
 85 90 95

Val Val Ser Ala Leu Arg Ser Gly Met Phe Trp Glu Ile Gly Pro Tyr
 100 105 110

Phe Lys Asp Tyr Pro Asn Leu Arg Lys Leu Asp Lys Thr Ile Leu Lys
 115 120 125

Asn Ile Ser Val Asp Gly Lys Val Tyr Gly Ile Tyr Arg Glu Arg Pro
 130 135 140

Met Ala Arg Gln Gly Val Val Ile Arg Lys Asp Trp Leu Asp Asn Leu
 145 150 155 160

Gly Leu Glu Met Pro Glu Thr Val Asp Asp Leu Tyr Lys Ile Ala Lys
 165 170 175

Ala Phe Thr Glu Gln Asp Pro Asp Gln Asn Gly Lys Asp Asp Thr Phe
 180 185 190

Gly Leu Ala Asp Arg Asn Asp Leu Thr Phe Gly Ala Phe Lys Thr Leu
 195 200 205

Ala Ser Tyr Phe Gly Ala Pro Asn Glu Trp Gly Thr Asp Glu Asp Gly
 210 215 220

10294.204.ST25.txt

Asn Leu Phe Pro Tyr Phe Lys His Glu Ala Tyr Lys Asp Ala Met Ala
225 230 235 240

Tyr Met Lys Lys Leu Tyr Glu Glu Gly Leu Met Asn Arg Asp Phe Ala
245 250 255

Val Thr Ser Lys Thr Gln Gln Gln Asp Leu Val Ile Gln Gly Lys Ala
260 265 270

Gly Ile Tyr Ile Gly Ala Met Ser Asp Ala Met Asn Leu Arg Asp Gln
275 280 285

Gly Leu Ala Leu Asn Pro Gly Phe Gln Leu Asp Ile Ala Asn Arg Ile
290 295 300

Lys Gly Pro Asp Gly Lys Glu Arg Thr Trp Ala Leu Gly Gly His Gly
305 310 315 320

Gly Met Phe Ala Ile Ser Lys Ser Ser Val Lys Thr Glu Lys Glu Val
325 330 335

Arg Lys Ile Leu Ala Phe Phe Asp Arg Ile Ala Glu Glu Asp Leu Asn
340 345 350

Asn Leu Met Leu Tyr Gly Ile Glu Gly Val His Tyr Glu Lys Lys Gly
355 360 365

Gly Ser Gly Tyr Phe Arg Lys Gln Glu Asn Tyr His Leu Trp Glu Ala
370 375 380

Glu Ile Gln Pro Leu Asn Gln Leu Ile Gly Val Asn Lys Gln Ala Leu
385 390 395 400

Lys Ser Ala Glu Asp Pro Leu Arg Ala Lys Asn Glu Lys Leu Glu Glu
405 410 415

Asp Asn Arg Ala Ile Ala Val Gln Asn Pro Ala Glu Pro Cys Ile Leu
420 425 430

Pro His Arg Trp Thr Gly Glu Gln Asn
435 440

<210> 163
<211> 1400
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(983)

10294.204.ST25.txt

<400> 163

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cttttacact gcaaaaaaaaa aaaactatgt aaaaaccata tagaattata tctaatttga      180
tgtgaaatca caatattttct cgggaaaata acatacacta acgcctagaa tcgataatta      240
gtaaaactct ttaaagtatt aatatgttac aaaagcttta ttctccagcc ttaaactttg      300
actaatgaaa cgcathtaggt gtacgataaa aagtcgatgt gaggtgagat aaggtgtcaa      360
ggcgctttttg aaattgaagc atctgctgga taaagtgggtg caatagcatg taagctgccg      420
gcatgaaacc ggcagcattt ttttaagcgtc cgacgggaag tctttttttg attaaatttc      480
atggtttagcg agtgaaaaat atg tca aca ata tta tgg ctt gtg agc ttc acg      533
                      Met Ser Thr Ile Leu Trp Leu Val Ser Phe Thr
                      1           5           10

ctc cac ggt ata ttg att tat ttc gtc atc att ttg aat acg agg ctc      581
Leu His Gly Ile Leu Ile Tyr Phe Val Ile Ile Leu Asn Thr Arg Leu
                      15           20           25

agc gct ttc aag gca gcg gag aaa gag caa aaa cag ctt ttg gaa gaa      629
Ser Ala Phe Lys Ala Ala Glu Lys Glu Gln Lys Gln Leu Leu Glu Glu
                      30           35           40

acc gag aat aca ttg acc gct ttt ttg atg gag tta aaa gac gaa aat      677
Thr Glu Asn Thr Leu Thr Ala Phe Leu Met Glu Leu Lys Asp Glu Asn
                      45           50           55

gaa aaa ctc gtt caa gag att cgg gcg aat gcc gaa aaa gag ccg caa      725
Glu Lys Leu Val Gln Glu Ile Arg Ala Asn Ala Glu Lys Glu Pro Gln
60                      65                      70                      75

aga ccg gaa aca cag cct gaa att ccc gct caa acc ccc gtc ctt ccg      773
Arg Pro Glu Thr Gln Pro Glu Ile Pro Ala Gln Thr Pro Val Leu Pro
                      80                      85                      90

gaa gcg gac gaa tcg cgc gat ctg ccg ctt cac atc gaa gcg atg atc      821
Glu Ala Asp Glu Ser Arg Asp Leu Pro Leu His Ile Glu Ala Met Ile
                      95           100           105

aat gag gtg gag cag gaa gag gat gag ctc aat caa aag gag cag gaa      869
Asn Glu Val Glu Gln Glu Glu Asp Glu Leu Asn Gln Lys Glu Gln Glu
                      110           115           120

gca tcc ata tcc tat gaa gaa gaa gct ctc gca tta gaa aaa cat ggg      917
Ala Ser Ile Ser Tyr Glu Glu Glu Ala Leu Ala Leu Glu Lys His Gly
                      125           130           135

gac tgg ggg aaa gaa ttt ttt cat aaa aca ggc ccc aaa atg ggg ggg      965
Asp Trp Gly Lys Glu Phe Phe His Lys Thr Gly Pro Lys Met Gly Gly
140                      145                      150                      155

ggt ggt gtt cca gtc tct taaagaaaaa aaaaattcaa cctctcttct      1013
Gly Gly Val Pro Val Ser
                      160

ttgggggaggg gggggggggga aaaaataagg tggttggtaga gggggggagga attttttttt      1073
aaaggaaacc ctcatgggga gggagatgtg ctttaaacga gggaggggagc gaggaaatgg      1133
cactggttcc ataggatgaa acgcgcggga ttgtctccag aaaacagggga gaccccgga      1193
aaggagcggg gcagccaatt catcactttt taagttttcaa agcctcagca aatttggggg      1253

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10294.204.ST25.txt

ttaaaaattc acacggaatt ggttgggagg gaataaggag agtttaaaaa cccgccaatt 1313
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 atgggggggat atggtttcgg actcgaa 1400

<210> 164
 <211> 161
 <212> PRT
 <213> Bacillus licheniformis
 <400> 164

Met Ser Thr Ile Leu Trp Leu Val Ser Phe Thr Leu His Gly Ile Leu
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 Ile Tyr Phe Val Ile Ile Leu Asn Thr Arg Leu Ser Ala Phe Lys Ala
 20 25 30
 Ala Glu Lys Glu Gln Lys Gln Leu Leu Glu Glu Thr Glu Asn Thr Leu
 35 40 45
 Thr Ala Phe Leu Met Glu Leu Lys Asp Glu Asn Glu Lys Leu Val Gln
 50 55 60
 Glu Ile Arg Ala Asn Ala Glu Lys Glu Pro Gln Arg Pro Glu Thr Gln
 65 70 75 80
 Pro Glu Ile Pro Ala Gln Thr Pro Val Leu Pro Glu Ala Asp Glu Ser
 85 90 95
 Arg Asp Leu Pro Leu His Ile Glu Ala Met Ile Asn Glu Val Glu Gln
 100 105 110
 Glu Glu Asp Glu Leu Asn Gln Lys Glu Gln Glu Ala Ser Ile Ser Tyr
 115 120 125
 Glu Glu Glu Ala Leu Ala Leu Glu Lys His Gly Asp Trp Gly Lys Glu
 130 135 140
 Phe Phe His Lys Thr Gly Pro Lys Met Gly Gly Gly Gly Val Pro Val
 145 150 155 160
 Ser

<210> 165
 <211> 2644
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (502)..(2142)

10294.204.ST25.txt

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caccgggggca tgtttcgctt ttccggcagt cggacagaac cttgatcgca ggggacgccg 60
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gaccgccggc ttatttcaca atggattgga caaaagcagc agattcgggtt cggaagctgg 180
caggattaaa accggctgca ttattgacgg gacacgggtgt accgatgaaa ggaagcgatt 240
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tatgctgcgc ttaaaacatt cagccaggct gaatgttttt ttatagggaa aaactaacca 360
ttttacatgt gatgatggcc gtccattggt ctaaattccg gatgttgatg tataccaaag 420
gaatcatttt ctgaaatttt agacaaaata tgttgatatt tcatttataa tgcaggatg 480
cctgaaagga gctgagaaaa g atg aaa att caa aaa agg gtc caa gct ttg 531
Met Lys Ile Gln Lys Arg Val Gln Ala Leu
1 5 10
ctg gca act tcg gca atg ttt gca gga ctg atg ctg tcc gat gcg gtg 579
Leu Ala Thr Ser Ala Met Phe Ala Gly Leu Met Leu Ser Asp Ala Val
15 20 25
tac gct gcg gaa acc cct tac tat gga aag aac tat act cag cca gag 627
Tyr Ala Ala Glu Thr Pro Tyr Tyr Gly Lys Asn Tyr Thr Gln Pro Glu
30 35 40
caa gtg tca tca tta tat ccg gag cct gaa gaa aca ttc tca acc cct 675
Gln Val Ser Ser Leu Tyr Pro Glu Pro Glu Glu Thr Phe Ser Thr Pro
45 50 55
gct ttt gta aaa gaa ggg gaa gcc ttt acg aca caa gaa gaa atg atg 723
Ala Phe Val Lys Glu Gly Glu Ala Phe Thr Thr Gln Glu Glu Met Met
60 65 70
aag ttt ata acc agt ctg aca aag aaa agc ccg aat gtc aaa atc ggg 771
Lys Phe Ile Thr Ser Leu Thr Lys Lys Ser Pro Asn Val Lys Ile Gly
75 80 85 90
aat atc ggt ttt tca att gaa aaa aga aat att cct gtg ctt tac ttc 819
Asn Ile Gly Phe Ser Ile Glu Lys Arg Asn Ile Pro Val Leu Tyr Phe
95 100 105
aca aag gac aag caa ata cgt tcc ata tca aaa aaa cca acc gtc tgg 867
Thr Lys Asp Lys Gln Ile Arg Ser Ile Ser Lys Lys Pro Thr Val Trp
110 115 120
ctg caa gga cag ata cat gga aat gag ccg gca gcg gga gaa tct gct 915
Leu Gln Gly Gln Ile His Gly Asn Glu Pro Ala Ala Gly Glu Ser Ala
125 130 135
ctg gcg ata gct gaa aaa ctg gcc gga ccg tat ggc gac aaa gtg ttg 963
Leu Ala Ile Ala Glu Lys Leu Ala Gly Pro Tyr Gly Asp Lys Val Leu
140 145 150
gac aag atc aat gtc atc gtt gtt ccg cggt gtc aat cct gac gga tca 1011
Asp Lys Ile Asn Val Ile Val Val Pro Arg Val Asn Pro Asp Gly Ser
155 160 165 170
tat cag ttc aac aga cgg ctg gcg aac gga atc gac gga aac agg gat 1059
Tyr Gln Phe Asn Arg Arg Leu Ala Asn Gly Ile Asp Gly Asn Arg Asp
175 180 185
cat gtc aag ctc gag tct cca gaa gtg cgc gcc att cac caa gaa ttc 1107
His Val Lys Leu Glu Ser Pro Glu Val Arg Ala Ile His Gln Glu Phe

10294.204.ST25.txt

190	195	200	
aat aag tat tcg cct gaa gtc gtt atc gat gcc cat gaa tac ggt gtc Asn Lys Tyr Ser Pro Glu Val Val Ile Asp Ala His Glu Tyr Gly Val 205 210 215			1155
ggc caa aac gaa ttt cag agc ata ggc gaa aaa ggg tca tta aaa tac Gly Gln Asn Glu Phe Gln Ser Ile Gly Glu Lys Gly Ser Leu Lys Tyr 220 225 230			1203
cat gat att tta att tta tca gga aaa aat tta aac att ccc aag tcg His Asp Ile Leu Ile Leu Ser Gly Lys Asn Leu Asn Ile Pro Lys Ser 235 240 245 250			1251
atc agg cat gcg tcc gac agc ctt tat gtg aac ggc gtc aga gct aaa Ile Arg His Ala Ser Asp Ser Leu Tyr Val Asn Gly Val Arg Ala Lys 255 260 265			1299
ctt gat gaa aaa gga ttt tct aat gat gct tat tat acg aca gga aaa Leu Asp Glu Lys Gly Phe Ser Asn Asp Ala Tyr Tyr Thr Thr Gly Lys 270 275 280			1347
agc aag gac gga aaa atc gaa atc tat gaa ggc ggt aca gaa gcg aga Ser Lys Asp Gly Lys Ile Glu Ile Tyr Glu Gly Gly Thr Glu Ala Arg 285 290 295			1395
atc ggg cgt aat gca ttc gcc ctc cag cct gcc ctt tcc ttc ctg gtg Ile Gly Arg Asn Ala Phe Ala Leu Gln Pro Ala Leu Ser Phe Leu Val 300 305 310			1443
gaa agc agg gga ata gac atc gga cgc gaa aat ttt gca aga aga gtc Glu Ser Arg Gly Ile Asp Ile Gly Arg Glu Asn Phe Ala Arg Arg Val 315 320 325 330			1491
gcg gct cag gtt gct aca cat gag acg atc atc gac acg aca gtg aag Ala Ala Gln Val Ala Thr His Glu Thr Ile Ile Asp Thr Thr Val Lys 335 340 345			1539
cat gca gcc gag atc aag cgc ctt gtc tcc aaa gaa aaa tta aag ctg His Ala Ala Glu Ile Lys Arg Leu Val Ser Lys Glu Lys Leu Lys Leu 350 355 360			1587
ata caa aac ggc gct aaa gtg agc gat aaa gac caa gtg gtc atc aac Ile Gln Asn Gly Ala Lys Val Ser Asp Lys Asp Gln Val Val Ile Asn 365 370 375			1635
agt gag ttt gca ggc ccg ttt aaa gac acg ctt aaa gtc gct gat att Ser Glu Phe Ala Gly Pro Phe Lys Asp Thr Leu Lys Val Ala Asp Ile 380 385 390			1683
gcc tca gga caa gca gtt gac gtt cct gtc caa tat tac agc gcc tca Ala Ser Gly Gln Ala Val Asp Val Pro Val Gln Tyr Tyr Ser Ala Ser 395 400 405 410			1731
gag gcc gtt cct gtg ctg tca aga act cgg ccg acc gct tac ctt gtc Glu Ala Val Pro Val Leu Ser Arg Thr Arg Pro Thr Ala Tyr Leu Val 415 420 425			1779
ctt ccg ggc cat caa gat atc gaa cag aag ctg aag gat cag gga tta Leu Pro Gly His Gln Asp Ile Glu Gln Lys Leu Lys Asp Gln Gly Leu 430 435 440			1827
aag agc gtg aca ctg gct ttc aaa caa aaa ctc acc gct gaa gcg tat Lys Ser Val Thr Leu Ala Phe Lys Gln Lys Leu Thr Ala Glu Ala Tyr 445 450 455			1875
gag gtt tta tcg aaa gaa aca gcg gga gaa tct gag ggc cgg cca gtg Glu Val Leu Ser Lys Glu Thr Ala Gly Glu Ser Glu Gly Arg Pro Val 460 465 470 475 480			1923

10294.204.ST25.txt

460

465

470

atc aag gta gaa acg aag ctc aaa aaa cag aaa aaa gag ttt cct aaa 1971
 Ile Lys Val Glu Thr Lys Leu Lys Lys Gln Lys Lys Glu Phe Pro Lys
 475 480 485 490

gga aca aaa atc tat ttt aca gct cag cag caa agc aat ctg ctg tca 2019
 Gly Thr Lys Ile Tyr Phe Thr Ala Gln Gln Gln Ser Asn Leu Leu Ser
 495 500 505

atc gca ctt gag ccg gag tcg gtt gac agt tat gta agc aca ggt tac 2067
 Ile Ala Leu Glu Pro Glu Ser Val Asp Ser Tyr Val Ser Thr Gly Tyr
 510 515 520

att cct tct caa aaa ggc aaa gag ctg ccg gtt tac cgc ttc atg ctg 2115
 Ile Pro Ser Gln Lys Gly Lys Glu Leu Pro Val Tyr Arg Phe Met Leu
 525 530 535

aac acc aaa acg ctt aat ttt aag gaa taatcaccag gcatccgtct 2162
 Asn Thr Lys Thr Leu Asn Phe Lys Glu
 540 545

ttgacggatg ctttttagcg gttttttggt ttttcataca taattgtttt aaactgagat 2222

cgaacacat acaataaata tcagtctgaa atctggaagg agagaatccg gttggaatca 2282

catgaagaat tatggaggga agccaaggcc ttcacgcagc tctgctacgg ggaactgtcg 2342

aagtccgaag aagaaacaag gatgcgctta cataaaatag ataaagaaat cagagaaacc 2402

ggaagctata cacatacatt agaagaaatc gaacatggag ccagaatggc gtggagaaac 2462

agcagccgct gcatcggcag gctgttttgg cactctctta ctgtcatcga tcaaagaggc 2522

gttcaaaccg aggagaggt gcgggatgcg cttttccacc atattcagct tgcaacaaac 2582

ggagggaaaa tcagaccgtt cattacggtt ttcccccccg aacaaaacgg acacagcgaa 2642

gt 2644

<210> 166

<211> 547

<212> PRT

<213> Bacillus licheniformis

<400> 166

Met Lys Ile Gln Lys Arg Val Gln Ala Leu Leu Ala Thr Ser Ala Met
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Phe Ala Gly Leu Met Leu Ser Asp Ala Val Tyr Ala Ala Glu Thr Pro
 20 25 30

Tyr Tyr Gly Lys Asn Tyr Thr Gln Pro Glu Gln Val Ser Ser Leu Tyr
 35 40 45

Pro Glu Pro Glu Glu Thr Phe Ser Thr Pro Ala Phe Val Lys Glu Gly
 50 55 60

Glu Ala Phe Thr Thr Gln Glu Glu Met Met Lys Phe Ile Thr Ser Leu
 65 70 75 80

10294.204.ST25.txt

Thr Lys Lys Ser Pro Asn Val Lys Ile Gly Asn Ile Gly Phe Ser Ile
 85 90 95

Glu Lys Arg Asn Ile Pro Val Leu Tyr Phe Thr Lys Asp Lys Gln Ile
 100 105 110

Arg Ser Ile Ser Lys Lys Pro Thr Val Trp Leu Gln Gly Gln Ile His
 115 120 125

Gly Asn Glu Pro Ala Ala Gly Glu Ser Ala Leu Ala Ile Ala Glu Lys
 130 135 140

Leu Ala Gly Pro Tyr Gly Asp Lys Val Leu Asp Lys Ile Asn Val Ile
 145 150 155 160

Val Val Pro Arg Val Asn Pro Asp Gly Ser Tyr Gln Phe Asn Arg Arg
 165 170 175

Leu Ala Asn Gly Ile Asp Gly Asn Arg Asp His Val Lys Leu Glu Ser
 180 185 190

Pro Glu Val Arg Ala Ile His Gln Glu Phe Asn Lys Tyr Ser Pro Glu
 195 200 205

Val Val Ile Asp Ala His Glu Tyr Gly Val Gly Gln Asn Glu Phe Gln
 210 215 220

Ser Ile Gly Glu Lys Gly Ser Leu Lys Tyr His Asp Ile Leu Ile Leu
 225 230 235 240

Ser Gly Lys Asn Leu Asn Ile Pro Lys Ser Ile Arg His Ala Ser Asp
 245 250 255

Ser Leu Tyr Val Asn Gly Val Arg Ala Lys Leu Asp Glu Lys Gly Phe
 260 265 270

Ser Asn Asp Ala Tyr Tyr Thr Thr Gly Lys Ser Lys Asp Gly Lys Ile
 275 280 285

Glu Ile Tyr Glu Gly Gly Thr Glu Ala Arg Ile Gly Arg Asn Ala Phe
 290 295 300

Ala Leu Gln Pro Ala Leu Ser Phe Leu Val Glu Ser Arg Gly Ile Asp
 305 310 315 320

Ile Gly Arg Glu Asn Phe Ala Arg Arg Val Ala Ala Gln Val Ala Thr
 325 330 335

His Glu Thr Ile Ile Asp Thr Thr Val Lys His Ala Ala Glu Ile Lys
 340 345 350

10294.204.ST25.txt

Arg Leu Val Ser Lys Glu Lys Leu Lys Leu Ile Gln Asn Gly Ala Lys
 355 360 365

Val Ser Asp Lys Asp Gln Val Val Ile Asn Ser Glu Phe Ala Gly Pro
 370 375 380

Phe Lys Asp Thr Leu Lys Val Ala Asp Ile Ala Ser Gly Gln Ala Val
 385 390 395 400

Asp Val Pro Val Gln Tyr Tyr Ser Ala Ser Glu Ala Val Pro Val Leu
 405 410 415

Ser Arg Thr Arg Pro Thr Ala Tyr Leu Val Leu Pro Gly His Gln Asp
 420 425 430

Ile Glu Gln Lys Leu Lys Asp Gln Gly Leu Lys Ser Val Thr Leu Ala
 435 440 445

Phe Lys Gln Lys Leu Thr Ala Glu Ala Tyr Glu Val Leu Ser Lys Glu
 450 455 460

Thr Ala Gly Glu Ser Glu Gly Arg Pro Val Ile Lys Val Glu Thr Lys
 465 470 475 480

Leu Lys Lys Gln Lys Lys Glu Phe Pro Lys Gly Thr Lys Ile Tyr Phe
 485 490 495

Thr Ala Gln Gln Gln Ser Asn Leu Leu Ser Ile Ala Leu Glu Pro Glu
 500 505 510

Ser Val Asp Ser Tyr Val Ser Thr Gly Tyr Ile Pro Ser Gln Lys Gly
 515 520 525

Lys Glu Leu Pro Val Tyr Arg Phe Met Leu Asn Thr Lys Thr Leu Asn
 530 535 540

Phe Lys Glu
 545

<210> 167
 <211> 2146
 <212> DNA
 <213> Bacillus licheniformis

<220>
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 <222> (501)..(1643)

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 aagacaaaac taaagggaaa gatacaaaag ataaagaaac gtctgcgagt gagcagaacg 120
 gagaggttgt cacagaggaa tcatcgggtg atgaagattt attcacaaca taccgcatgg 180

10294.204.ST25.txt

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aatggacga tcagcgcagc agggagaggg aggaattaac cgaaatcgtc agaagcgata 240
aagcgacggc aaaagaaaaa agcgaagctt acgacaagat gacagagctc agcgaagctg 300
aaggaacgga aaagaccctt gaaaccctca tcaaaacaaa aggctattaa gacgccttgg 360
tcaacgccga cggcgataaa gtcaatatta cgggtgaaggc gaaggagcac tcgaaagccg 420
cctgcaccga gtttacatctt cctcaaatga tagttttcat tgatttgcta gtataagtgt 480
tatcaaaagg aggttaatat atg aac ttt tac aaa acg ctc gcc tta tca act 533
                        Met Asn Phe Tyr Lys Thr Leu Ala Leu Ser Thr
                        1           5           10

ctt gcg gca tcc tta ttg tct ccc tca tgg agc att ctc ccc cgt gcc 581
Leu Ala Ala Ser Leu Leu Ser Pro Ser Trp Ser Ile Leu Pro Arg Ala
                        15           20           25

gaa gct tca gct tat aag gac ttc tcg gtg act gcc gat gca gag aca 629
Glu Ala Ser Ala Tyr Lys Asp Phe Ser Val Thr Ala Asp Ala Glu Thr
                        30           35           40

gag ccg gtg gat acc cct gac gac gcg gca gat gac ccg gcg att tgg 677
Glu Pro Val Asp Thr Pro Asp Asp Ala Ala Asp Asp Pro Ala Ile Trp
                        45           50           55

gtt cat ccg aag cag cct gaa aaa agc cgg ctg atc aca aca aat aaa 725
Val His Pro Lys Gln Pro Glu Lys Ser Arg Leu Ile Thr Thr Asn Lys
                        60           65           70           75

aaa tct ggc ttg atc gtt tac gat tta aac gga aaa cag ctg gca gcc 773
Lys Ser Gly Leu Ile Val Tyr Asp Leu Asn Gly Lys Gln Leu Ala Ala
                        80           85           90

tat ccg ttt ggc aaa tta aac aac gtc gat ctc cgc tac aat ttt ccg 821
Tyr Pro Phe Gly Lys Leu Asn Asn Val Asp Leu Arg Tyr Asn Phe Pro
                        95           100           105

ctc gat ggc aaa aaa att gat att gcc ggg gcc tca aac ccg tca gac 869
Leu Asp Gly Lys Lys Ile Asp Ile Ala Gly Ala Ser Asn Arg Ser Asp
                        110           115           120

ggc aaa aac acg gtt gaa ata tac gcc ttt gac ggc gaa aaa aac aag 917
Gly Lys Asn Thr Val Glu Ile Tyr Ala Phe Asp Gly Glu Lys Asn Lys
                        125           130           135

ctg aaa aac atc gtc aat cct caa aaa cct att caa acc gat att gag 965
Leu Lys Asn Ile Val Asn Pro Gln Lys Pro Ile Gln Thr Asp Ile Glu
                        140           145           150           155

gag gtg tat ggt ttc agc ctg tat cac agc cag aaa acc ggc aag ttc 1013
Glu Val Tyr Gly Phe Ser Leu Tyr His Ser Gln Lys Thr Gly Lys Phe
                        160           165           170

tac gcc atg gtg acc gga aag aac gga gaa ttc gag caa tac gaa ctg 1061
Tyr Ala Met Val Thr Gly Lys Asn Gly Glu Phe Glu Gln Tyr Glu Leu
                        175           180           185

ttt gac aac gga aaa gga caa gtc gaa ggc aaa aag gtc cgc tca ttc 1109
Phe Asp Asn Gly Lys Gly Gln Val Glu Gly Lys Lys Val Arg Ser Phe
                        190           195           200

aaa atg agc tct caa aca gaa ggg ctt gca gca gat gat gaa tac ggc 1157
Lys Met Ser Ser Gln Thr Glu Gly Leu Ala Ala Asp Asp Glu Tyr Gly
                        205           210           215

aaa atg tac atc gct gaa gaa gac gct gcg att tgg tct ttc agc gcc 1205

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10294.204.ST25.txt

Lys Met Tyr Ile Ala Glu Glu Asp Ala Ala Ile Trp Ser Phe Ser Ala
 220 225 230 235
 gag cca aac ggc gga gat aaa gga aaa att gtc gat cgc gca ggc gga 1253
 Glu Pro Asn Gly Gly Asp Lys Gly Lys Ile Val Asp Arg Ala Gly Gly
 240 245 250
 ccg cat tta acc gct gat att gaa ggg ctg acg att tac tac gga gaa 1301
 Pro His Leu Thr Ala Asp Ile Glu Gly Leu Thr Ile Tyr Tyr Gly Glu
 255 260 265
 gac ggc gaa gga tat ttg atc gcg tcc agt cag ggc gat aac cgt tat 1349
 Asp Gly Glu Gly Tyr Leu Ile Ala Ser Ser Gln Gly Asp Asn Arg Tyr
 270 275 280
 gcc atc tat gac cgg cgc ggg aaa aac gac tat gtc gcc gat ttt tca 1397
 Ala Ile Tyr Asp Arg Arg Gly Lys Asn Asp Tyr Val Ala Asp Phe Ser
 285 290 295
 att gat gac ggt aaa gaa atc gac ggg aca agc gat acc gat gga atc 1445
 Ile Asp Asp Gly Lys Glu Ile Asp Gly Thr Ser Asp Thr Asp Gly Ile
 300 305 310 315
 gac gtc atc ggc ttc ggc ctc ggc aaa aaa tat cca tac ggc atc ttt 1493
 Asp Val Ile Gly Phe Gly Leu Gly Lys Lys Tyr Pro Tyr Gly Ile Phe
 320 325 330
 gtc gcc caa gac ggc gaa aat acg gaa aat gga cag cca gcc aat cag 1541
 Val Ala Gln Asp Gly Glu Asn Thr Glu Asn Gly Gln Pro Ala Asn Gln
 335 340 345
 aac ttc aaa att gtc tcc tgg gaa aaa att gct gac gcg ctg gac gac 1589
 Asn Phe Lys Ile Val Ser Trp Glu Lys Ile Ala Asp Ala Leu Asp Asp
 350 355 360
 aag cct gat atc gat gat cag gtc aat ccc cga aaa ctg aaa aaa cga 1637
 Lys Pro Asp Ile Asp Asp Gln Val Asn Pro Arg Lys Leu Lys Lys Arg
 365 370 375
 gcc aaa taacgacgga tccgcgggaa atgcccgcg atttttcaca ttcctttatg 1693
 Ala Lys 380
 ttaagataac tattaatgga gggatggat tgcgtttaaa tctctatgcc gtagtgttta 1753
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 cgtacacttc tgctgtcatc ttcctgcttg ctgctgcata ttgcacgaag cgtcggcctg 1873
 aaaagtaagg cttcctatgc cttatggctt ctccgtaaaa tgctcgttcc gtaaggcggc 1933
 agtttgagcg cgcctttttt ccgggttccc tttaaaacgt ccgtatttgt ttcctccgga 1993
 agcgagacac ttctgttttc cgctgtaaaa ttcacacga aaatataatc gtggcgggccg 2053
 tctgtgcgga gctgggcggt gacgcctttc gggagctctg tatcgagcac tttggcaatc 2113
 ccgcactctt caatgagcct ggatataaac gcc 2146

<210> 168

<211> 381

<212> PRT

<213> Bacillus licheniformis

<400> 168

Met Asn Phe Tyr Lys Thr Leu Ala Leu Ser Thr Leu Ala Ala Ser Leu

10294.204.ST25.txt

1 5 10 15
 Leu Ser Pro Ser Trp Ser Ile Leu Pro Arg Ala Glu Ala Ser Ala Tyr
 20 25 30
 Lys Asp Phe Ser Val Thr Ala Asp Ala Glu Thr Glu Pro Val Asp Thr
 35 40 45
 Pro Asp Asp Ala Ala Asp Asp Pro Ala Ile Trp Val His Pro Lys Gln
 50 55 60
 Pro Glu Lys Ser Arg Leu Ile Thr Thr Asn Lys Lys Ser Gly Leu Ile
 65 70 75 80
 Val Tyr Asp Leu Asn Gly Lys Gln Leu Ala Ala Tyr Pro Phe Gly Lys
 85 90 95
 Leu Asn Asn Val Asp Leu Arg Tyr Asn Phe Pro Leu Asp Gly Lys Lys
 100 105 110
 Ile Asp Ile Ala Gly Ala Ser Asn Arg Ser Asp Gly Lys Asn Thr Val
 115 120 125
 Glu Ile Tyr Ala Phe Asp Gly Glu Lys Asn Lys Leu Lys Asn Ile Val
 130 135 140
 Asn Pro Gln Lys Pro Ile Gln Thr Asp Ile Glu Glu Val Tyr Gly Phe
 145 150 155 160
 Ser Leu Tyr His Ser Gln Lys Thr Gly Lys Phe Tyr Ala Met Val Thr
 165 170 175
 Gly Lys Asn Gly Glu Phe Glu Gln Tyr Glu Leu Phe Asp Asn Gly Lys
 180 185 190
 Gly Gln Val Glu Gly Lys Lys Val Arg Ser Phe Lys Met Ser Ser Gln
 195 200 205
 Thr Glu Gly Leu Ala Ala Asp Asp Glu Tyr Gly Lys Met Tyr Ile Ala
 210 215 220
 Glu Glu Asp Ala Ala Ile Trp Ser Phe Ser Ala Glu Pro Asn Gly Gly
 225 230 235 240
 Asp Lys Gly Lys Ile Val Asp Arg Ala Gly Gly Pro His Leu Thr Ala
 245 250 255
 Asp Ile Glu Gly Leu Thr Ile Tyr Tyr Gly Glu Asp Gly Glu Gly Tyr
 260 265 270
 Leu Ile Ala Ser Ser Gln Gly Asp Asn Arg Tyr Ala Ile Tyr Asp Arg
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10294.204.ST25.txt
280 285

Arg Gly Lys Asn Asp Tyr Val Ala Asp Phe Ser Ile Asp Asp Gly Lys
290 295 300

Glu Ile Asp Gly Thr Ser Asp Thr Asp Gly Ile Asp Val Ile Gly Phe
305 310 315 320

Gly Leu Gly Lys Lys Tyr Pro Tyr Gly Ile Phe Val Ala Gln Asp Gly
325 330 335

Glu Asn Thr Glu Asn Gly Gln Pro Ala Asn Gln Asn Phe Lys Ile Val
340 345 350

Ser Trp Glu Lys Ile Ala Asp Ala Leu Asp Asp Lys Pro Asp Ile Asp
355 360 365

Asp Gln Val Asn Pro Arg Lys Leu Lys Lys Arg Ala Lys
370 375 380

<210> 169
<211> 1301
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(803)

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ctgttcgcgt gtactgcgtt ccctaatacga cgtggaacca cgtgctgaac agtggactat 180
ctctcgctct ctccataacc tggcttatcc ttcgcgcgcg gtcttaaaac atgctctcct 240
ataagcagct ttgggtaatg tctgcttatt ccatcaccct cgcaaccgtg ttttttgcaa 300
ttatggacgc gctggaggcg gtggttccaa gtcagttcct cctgaactgg tttgtgaact 360
ttatcatgct gtttctcgcc attaaagaaa cgccggcttc taaagcagcg aggtaaagcg 420
ggcaggagca aatttggtgt catgttggaag gagggacaag cgtaacataa taaaaaatgc 480
acgaaatggg gacaaatcag atg aaa cgt gtc att gtg ctg ttt tcg att ttg 533
Met Lys Arg Val Ile Val Leu Phe Ser Ile Leu
1 5 10
ctc gcc ctg ttc att gtt tat tat gac ttg aaa tca ggc acc atc cct 581
Leu Ala Leu Phe Ile Val Tyr Tyr Asp Leu Lys Ser Gly Thr Ile Pro
15 20 25
caa aac gcc tta ccg gct tca acc atg gca gcg gaa gct ccg gct gca 629
Gln Asn Ala Leu Pro Ala Ser Thr Met Ala Ala Glu Ala Pro Ala Ala
30 35 40
agc ctg caa tat aag tcc gtt acg gta aag ccc gga caa acg gta ttt 677
Ser Leu Gln Tyr Lys Ser Val Thr Val Lys Pro Gly Gln Thr Val Phe
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10294.204.ST25.txt

45

50

55

tca atc atc ggg aac agc gcc gtt ccg gct gac aaa ata gcc gaa gat 725
 Ser Ile Ile Gly Asn Ser Ala Val Pro Ala Asp Lys Ile Ala Glu Asp 75
 60 65 70
 ttt gaa gag ttg aat ccg aat gtt gag gcg ggc cgc att caa gca ggt 773
 Phe Glu Glu Leu Asn Pro Asn Val Glu Ala Gly Arg Ile Gln Ala Gly 90
 80 85
 gtc acc tac aag ttt ccc gtt tat cct gat taagcggttaa tttcttgtca 823
 Val Thr Tyr Lys Phe Pro Val Tyr Pro Asp 100
 95
 gtttcatgaa cgggctgtta caataagact tgtaaacgat ttggtataag aaaaggagca 883
 accgcctccg aattatactt aaggagcgaa ttcaagtgag tgaaatcaca catcgtacaa 943
 aaacgcgtcc cgtaaagtgt ggacctttaa caataggcgg caataacgaa gtcgtcattc 1003
 aaagcatgac aacaacgaaa acacatgacg ttgaagcaac cgtcgccgaa atcaacagac 1063
 tcgcggaagc aggatgtcaa atcgtccgcg tcgcctgtcc tgatgaacgg gtcgccgacg 1123
 ccattccaga gatcaaaaag cggatatcca tccctcttgt cgtggatatt catttcaact 1183
 ataaattggc attaaaagcg atcgaaggcg gagccgataa aatccgcatc aatccgggta 1243
 acatcggccg ccgcgaaaag gttgaagcgg tcgtcaacgc agcgaaggaa aagggcat 1301

<210> 170
 <211> 101
 <212> PRT
 <213> Bacillus licheniformis

<400> 170

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 20 25 30
 Ala Ser Thr Met Ala Ala Glu Ala Pro Ala Ala Ser Leu Gln Tyr Lys
 35 40 45
 Ser Val Thr Val Lys Pro Gly Gln Thr Val Phe Ser Ile Ile Gly Asn
 50 55 60
 Ser Ala Val Pro Ala Asp Lys Ile Ala Glu Asp Phe Glu Glu Leu Asn
 65 70 75 80
 Pro Asn Val Glu Ala Gly Arg Ile Gln Ala Gly Val Thr Tyr Lys Phe
 85 90 95
 Pro Val Tyr Pro Asp
 100

<210> 171
 <211> 1627

10294.204.ST25.txt

<212> DNA
 <213> *Bacillus licheniformis*

<220>
 <221> CDS
 <222> (501)..(1124)

<400> 171
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 ggtatttcagc tgacgaaaaa cgtgtttaag catgacggag catggatatt tcagcctgag 180
 tacatcggca aaaattggag ctggcgccct tattttctcg agaatatcat gaggatgaga 240
 acgatgagaa aagggttttt cagcgatttg tacagcgata tcgaaacggg ggaaatgatc 300
 agaacgtttt cctatccgat ggatgaagaa ttgtatctgt tcattgacct gtcctactca 360
 tatttatacg aacaagacgg attaatTTAA gcggcgccct ttcgccgctt tttctttttg 420
 aaaaaatgaa tcccagagg tttgtttcgc gtatataaag gaaaatgtga aaatataaat 480
 gctaaaaagg ggtggatcat atg aag aac gtt tgg tca tcc tta ctg tgc gcg 533
 Met Lys Asn Val Trp Ser Ser Leu Leu Cys Ala
 1 5 10
 ctt ctg gct gcg gct ctt gta ttc ttc tgc gcg gat ttt gcc aaa gcc 581
 Leu Leu Ala Ala Ala Leu Val Phe Phe Cys Ala Asp Phe Ala Lys Ala
 15 20 25
 gga gaa aaa ccg aca aga gca tcg tta ttt gag acc ctt caa tcc gta 629
 Gly Glu Lys Pro Thr Arg Ala Ser Leu Phe Glu Thr Leu Gln Ser Val
 30 35 40
 tcg gac gtc cat ttt cag ctg acc gaa aag gaa aga acg aaa aca gac 677
 Ser Asp Val His Phe Gln Leu Thr Glu Lys Glu Arg Thr Lys Thr Asp
 45 50 55
 atg ata tcc ctc ttg gaa cct tat atg gag cac gcc atg gca gtg aag 725
 Met Ile Ser Leu Leu Glu Pro Tyr Met Glu His Ala Met Ala Val Lys
 60 65 70 75
 tat gta gag gcg aac gcc ttt cct gaa caa gcg ggg tgg att ttt tac 773
 Tyr Val Glu Ala Asn Ala Phe Pro Glu Gln Ala Gly Trp Ile Phe Tyr
 80 85 90
 ggg aca gac gcg cct gaa gtt gca atc cct ttc ttc agc tat ggc gga 821
 Gly Thr Asp Ala Pro Glu Val Ala Ile Pro Phe Phe Ser Tyr Gly Gly
 95 100 105
 gac aca aaa gtg gcg ggg aaa gac gga agc tat acc gta tat gaa ttt 869
 Asp Thr Lys Val Ala Gly Lys Asp Gly Ser Tyr Thr Val Tyr Glu Phe
 110 115 120
 gtt gga gat caa aac gac ggc cct gtt tca tat caa aaa aat tat cag 917
 Val Gly Asp Gln Asn Asp Gly Pro Val Ser Tyr Gln Lys Asn Tyr Gln
 125 130 135
 acg gtg acg ctg aag aat acc ggc ggc agc ttc aaa gta acg gat atc 965
 Thr Val Thr Leu Lys Asn Thr Gly Gly Ser Phe Lys Val Thr Asp Ile
 140 145 150 155
 ggc caa tct gat aca aaa ccg gct gga gaa gaa ata atg tcc aaa caa 1013
 Gly Gln Ser Asp Thr Lys Pro Ala Gly Glu Glu Ile Met Ser Lys Gln
 160 165 170

10294.204.ST25.txt

ccg gat gaa aaa gaa aca agc tcg aat ttt gcg gat aaa ggg gaa gga 1061
 Pro Asp Glu Lys Glu Thr Ser Ser Asn Phe Ala Asp Lys Gly Glu Gly
 175 180 185
 gac cag gct gca ttt ccg ctt ttt gcc acc gat gtt aac tgg aca ttg 1109
 Asp Gln Ala Ala Phe Pro Leu Phe Ala Thr Asp Val Asn Trp Thr Leu
 190 195 200
 gcc gga att ttc agc tagcaaaaga atttaaagaa aatcattgac aatgatactg 1164
 Ala Gly Ile Phe Ser
 205
 ataatcatta tcatttaatt atagagagat gaacctctct gttccccaac ccctctatca 1224
 gatcaagatt taaaaaactt ggcgctgccc ccgccaagtt ttttatttgc atggaatccc 1284
 gcacttcaaa tagctgcggg atttttgggc attaggcgcg cgcaggaata agacaatcct 1344
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 ttcattgtatg acatgaaaaa agaaaactca aactatgaaa aagcgggtttt tctttttcat 1464
 gatcaaaaag gaaaaatgtc atcggtgat actttgtggt atgatgcttt gtagaacttg 1524
 tattataatt aatacttggt gatcctgaag ttgttttttt gaaaggagtc ttttttagaa 1584
 tgtcacaatt aatgggtatc atcacgagac tgcagagcct gca 1627

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 <212> PRT
 <213> Bacillus licheniformis

<400> 172

Met Lys Asn Val Trp Ser Ser Leu Leu Cys Ala Leu Leu Ala Ala Ala
 1 5 10 15

Leu Val Phe Phe Cys Ala Asp Phe Ala Lys Ala Gly Glu Lys Pro Thr
 20 25 30

Arg Ala Ser Leu Phe Glu Thr Leu Gln Ser Val Ser Asp Val His Phe
 35 40 45

Gln Leu Thr Glu Lys Glu Arg Thr Lys Thr Asp Met Ile Ser Leu Leu
 50 55 60

Glu Pro Tyr Met Glu His Ala Met Ala Val Lys Tyr Val Glu Ala Asn
 65 70 75 80

Ala Phe Pro Glu Gln Ala Gly Trp Ile Phe Tyr Gly Thr Asp Ala Pro
 85 90 95

Glu Val Ala Ile Pro Phe Phe Ser Tyr Gly Gly Asp Thr Lys Val Ala
 100 105 110

Gly Lys Asp Gly Ser Tyr Thr Val Tyr Glu Phe Val Gly Asp Gln Asn
 115 120 125

10294.204.ST25.txt

Asp Gly Pro Val Ser Tyr Gln Lys Asn Tyr Gln Thr Val Thr Leu Lys
 130 135 140

Asn Thr Gly Gly Ser Phe Lys Val Thr Asp Ile Gly Gln Ser Asp Thr
 145 150 155 160

Lys Pro Ala Gly Glu Glu Ile Met Ser Lys Gln Pro Asp Glu Lys Glu
 165 170 175

Thr Ser Ser Asn Phe Ala Asp Lys Gly Glu Gly Asp Gln Ala Ala Phe
 180 185 190

Pro Leu Phe Ala Thr Asp Val Asn Trp Thr Leu Ala Gly Ile Phe Ser
 195 200 205

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 <212> DNA
 <213> Bacillus licheniformis

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 ggcctagtca tgctggttct cgaccattca aggccggctt ccggcggcga gcaccatctt 120
 tcccactacc ttgaaatgaa agcgctggag aacaataagc ggcaagtgcct ccacggtgct 180
 aaagtcggct gcagcgcgat tatgctgact gacatttacc gatctcttat cggtgcaagc 240
 ctgggtgatc aacacgctga gcaagcgatt cgctccgttt atgaaaagct ccctgacggt 300
 aagaaaatgg cagagtggat gaggcgtatc ggcgggcctg tatcattcaa agaactcgat 360
 gttgaagaag agctggtgag agaagcgctc gcatacgccc atcagctcag agaccggtat 420
 acgggactga aaatcatcaa tcaatacggc cttttgccgg ggcttttagg caaaggacca 480
 ggcgtgaaag gggttaaaat gtg aaa agg ttc ctt tca tct atc ttt atg gtc 533
 Val Lys Arg Phe Leu Ser Ser Ile Phe Met Val
 1 5 10
 acg gtc gct gta tgt ttg ctt tta tcg ggg tgc aag gcg agt cct gcc 581
 Thr Val Ala Val Cys Leu Leu Leu Ser Gly Cys Lys Ala Ser Pro Ala
 15 20 25
 tcc gat caa gcg gac ggc acc gaa ctg aca ttt tgg aca ttc aac ggc 629
 Ser Asp Gln Ala Asp Gly Thr Glu Leu Thr Phe Trp Thr Phe Asn Gly
 30 35 40
 ctt cat gaa cag ttt tat gct gag atg gtg aaa gaa tgg aac aaa aag 677
 Leu His Glu Gln Phe Tyr Ala Glu Met Val Lys Glu Trp Asn Lys Lys
 45 50 55
 tat ccc gag cga aaa atc aaa tta aat aca gtg gtg tat ccg tat gga 725
 Tyr Pro Glu Arg Lys Ile Lys Leu Asn Thr Val Val Tyr Pro Tyr Gly
 60 65 70 75

10294.204.ST25.txt

cag atg cat gac aat tta tct atc tcg ctt tta gcc ggg aaa ggg gtt Gln Met His Asp Asn Leu Ser Ile Ser Leu Leu Ala Gly Lys Gly Val 80 85 90	773
cca gat att gcc gat gtt gag ctg ggg cgc tat tcg aac ttt ttg aag Pro Asp Ile Ala Asp Val Glu Leu Gly Arg Tyr Ser Asn Phe Leu Lys 95 100 105	821
ggc tct gac att cct ctt acc gat tta acg ccg ctt gtg gag gac gaa Gly Ser Asp Ile Pro Leu Thr Asp Leu Thr Pro Leu Val Glu Asp Glu 110 115 120	869
cgc gac aag ttt gtt gaa gcg agg ctg acg ctc tac agc aag aac ggc Arg Asp Lys Phe Val Glu Ala Arg Leu Thr Leu Tyr Ser Lys Asn Gly 125 130 135	917
aag ctt tac gga ctt gac aca cat gtc gga act acc gtg atg tat tac Lys Leu Tyr Gly Leu Asp Thr His Val Gly Thr Thr Val Met Tyr Tyr 140 145 150 155	965
aac atg gaa atg atg aat aaa gca ggc gtt gat ccg gac gac atc aaa Asn Met Glu Met Met Asn Lys Ala Gly Val Asp Pro Asp Asp Ile Lys 160 165 170	1013
aca tgg gaa gat tac agg gaa gcg ggc aaa aag gtc gtc aaa gct ctc Thr Trp Glu Asp Tyr Arg Glu Ala Gly Lys Lys Val Val Lys Ala Leu 175 180 185	1061
gga aag ccg atg acg acg att gaa acg acc gac ccg aat tca ttt ctg Gly Lys Pro Met Thr Thr Ile Glu Thr Thr Asp Pro Asn Ser Phe Leu 190 195 200	1109
ccg ctg gtt tcc cag cag gga tcc ggt tac ttt gat gag cag ggg cgg Pro Leu Val Ser Gln Gln Gly Ser Gly Tyr Phe Asp Glu Gln Gly Arg 205 210 215	1157
ttg aca tta aac aat gag aca aac gtg aaa acg ctc gaa ttt tta aag Leu Thr Leu Asn Asn Glu Thr Asn Val Lys Thr Leu Glu Phe Leu Lys 220 225 230 235	1205
act tta att gag aaa gac aaa att gcc gtc aca acg ccc gga ggc aat Thr Leu Ile Glu Lys Asp Lys Ile Ala Val Thr Thr Pro Gly Gly Asn 240 245 250	1253
cat cac agt gaa gag tat tac gga ttt atg aac caa ggc ggc gcg gcg His His Ser Glu Glu Tyr Tyr Gly Phe Met Asn Gln Gly Gly Ala Ala 255 260 265	1301
tct gtc tta atg ccg atc tgg tat atg ggc cgt ttt ttg gat tat atg Ser Val Leu Met Pro Ile Trp Tyr Met Gly Arg Phe Leu Asp Tyr Met 270 275 280	1349
cct gac ttg aaa ggg aaa atc gcg atc aga ccg ctg ccg gca tgg gaa Pro Asp Leu Lys Gly Lys Ile Ala Ile Arg Pro Leu Pro Ala Trp Glu 285 290 295	1397
gaa ggg gga gac cgc tca gcg gga atg ggc gga acg gcc acc gtg att Glu Gly Gly Asp Arg Ser Ala Gly Met Gly Gly Thr Ala Thr Val Ile 300 305 310 315	1445
cca aaa cag gcg aaa cag gtc gat ctg gcc aag gat ttc ttg aaa ttt Pro Lys Gln Ala Lys Gln Val Asp Leu Ala Lys Asp Phe Leu Lys Phe 320 325 330	1493
gcc aaa gcg tca aaa gaa ggc aac atc aag ctg tgg acc gtg ctc ggg Ala Lys Ala Ser Lys Glu Gly Asn Ile Lys Leu Trp Thr Val Leu Gly 335 340 345	1541

10294.204.ST25.txt

ttc gat ccg ctc aga tgg gat gtg tgg gac tcg gac gaa ttg aaa aaa 1589
 Phe Asp Pro Leu Arg Trp Asp Val Trp Asp Ser Asp Glu Leu Lys Lys
 350 355 360

cca aat caa tat aca gaa tac ttt caa aac gga caa cac atc ttt tcc 1637
 Pro Asn Gln Tyr Thr Glu Tyr Phe Gln Asn Gly Gln His Ile Phe Ser
 365 370 375

gtg ctt ctt gac ata aag gat gag atc aat ccg ctt tac ctt act gag 1685
 Val Leu Leu Asp Ile Lys Asp Glu Ile Asn Pro Leu Tyr Leu Thr Glu
 380 385 390

gat tat gcg aag act tcc gat ctc gtc aac aga aac ata ctg tac gaa 1733
 Asp Tyr Ala Lys Thr Ser Asp Leu Val Asn Arg Asn Ile Leu Tyr Glu
 400 405 410

gcg ctc aaa acg aag agc aaa aca ccg aaa gaa gca ttg gac aaa gca 1781
 Ala Leu Lys Thr Lys Ser Lys Thr Pro Lys Glu Ala Leu Asp Lys Ala
 415 420 425

gca gct gaa gtg aaa ggg caa tagtctttca ttactgtaaa gcgaggcgat 1832
 Ala Ala Glu Val Lys Gly Gln
 430

aacttgaaga ctgttaaaac agatacagtg cattcgtttc cgccggtgag cagaaaaaga 1892
 aagatcagac gtttattata ttcagcaaaa gccgcaccct acattttttac agcacctttt 1952
 gtactctcct ttigcatatt ttttctttat ccgcttatca gcgtcgtcat catgagtttt 2012
 caaagcattc tccccgggga agtccgcttc atcgggacgg agaactataa agcattaaac 2072
 aatcctacat tttataccgc actattcaac accgtaaaat acaccttttg gacattgctg 2132
 attttaatac ctgttctctt tattctggca gtcttttttag attctaaact cgtaaagttt 2192
 aaaaacgtgt tcaaatcggc tttattcatc ccggctctga cttcaaccat tgtggcgggg 2252
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<210> 174
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 <212> PRT
 <213> Bacillus licheniformis

<400> 174

Val Lys Arg Phe Leu Ser Ser Ile Phe Met Val Thr Val Ala Val Cys
 1 5 10 15

Leu Leu Leu Ser Gly Cys Lys Ala Ser Pro Ala Ser Asp Gln Ala Asp
 20 25 30

Gly Thr Glu Leu Thr Phe Trp Thr Phe Asn Gly Leu His Glu Gln Phe
 35 40 45

Tyr Ala Glu Met Val Lys Glu Trp Asn Lys Lys Tyr Pro Glu Arg Lys
 50 55 60

Ile Lys Leu Asn Thr Val Val Tyr Pro Tyr Gly Gln Met His Asp Asn
 65 70 75 80

10294.204.ST25.txt

Leu Ser Ile Ser Leu Leu Ala Gly Lys Gly Val Pro Asp Ile Ala Asp
85 90 95

Val Glu Leu Gly Arg Tyr Ser Asn Phe Leu Lys Gly Ser Asp Ile Pro
100 105 110

Leu Thr Asp Leu Thr Pro Leu Val Glu Asp Glu Arg Asp Lys Phe Val
115 120 125

Glu Ala Arg Leu Thr Leu Tyr Ser Lys Asn Gly Lys Leu Tyr Gly Leu
130 135 140

Asp Thr His Val Gly Thr Thr Val Met Tyr Tyr Asn Met Glu Met Met
145 150 155 160

Asn Lys Ala Gly Val Asp Pro Asp Asp Ile Lys Thr Trp Glu Asp Tyr
165 170 175

Arg Glu Ala Gly Lys Lys Val Val Lys Ala Leu Gly Lys Pro Met Thr
180 185 190

Thr Ile Glu Thr Thr Asp Pro Asn Ser Phe Leu Pro Leu Val Ser Gln
195 200 205

Gln Gly Ser Gly Tyr Phe Asp Glu Gln Gly Arg Leu Thr Leu Asn Asn
210 215 220

Glu Thr Asn Val Lys Thr Leu Glu Phe Leu Lys Thr Leu Ile Glu Lys
225 230 235 240

Asp Lys Ile Ala Val Thr Thr Pro Gly Gly Asn His His Ser Glu Glu
245 250 255

Tyr Tyr Gly Phe Met Asn Gln Gly Gly Ala Ala Ser Val Leu Met Pro
260 265 270

Ile Trp Tyr Met Gly Arg Phe Leu Asp Tyr Met Pro Asp Leu Lys Gly
275 280 285

Lys Ile Ala Ile Arg Pro Leu Pro Ala Trp Glu Glu Gly Gly Asp Arg
290 295 300

Ser Ala Gly Met Gly Gly Thr Ala Thr Val Ile Pro Lys Gln Ala Lys
305 310 315 320

Gln Val Asp Leu Ala Lys Asp Phe Leu Lys Phe Ala Lys Ala Ser Lys
325 330 335

Glu Gly Asn Ile Lys Leu Trp Thr Val Leu Gly Phe Asp Pro Leu Arg
340 345 350

10294.204.ST25.txt

Trp Asp Val Trp Asp Ser Asp Glu Leu Lys Lys Pro Asn Gln Tyr Thr
 355 360 365

Glu Tyr Phe Gln Asn Gly Gln His Ile Phe Ser Val Leu Leu Asp Ile
 370 375 380

Lys Asp Glu Ile Asn Pro Leu Tyr Leu Thr Glu Asp Tyr Ala Lys Thr
 385 390 395 400

Ser Asp Leu Val Asn Arg Asn Ile Leu Tyr Glu Ala Leu Lys Thr Lys
 405 410 415

Ser Lys Thr Pro Lys Glu Ala Leu Asp Lys Ala Ala Ala Glu Val Lys
 420 425 430

Gly Gln

<210> 175
 <211> 1864
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (533)..(991)

<400> 175
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 tacgggcggc gagccgatgc tctcattaaa atctgtaaag gaatatgtcg ttcctttatt 180
 aaaatacgct catgaacgcg gcgtgcggac gcagatcaac tcaaacttga cgctcgatat 240
 cggccgctac gagctgatca tcccctacct ggatgtgctt catattttccc acaactgggg 300
 aacggtcgaa gactttgcag aaatcggctt cgctatgatg gataaaaagc cgacgtttgc 360
 acagcgggcg cgctatttcg aaaaaatgat cgaaaacagc cggacgccttg ttgatgaagg 420
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 tcaccggcaa attgtcgaag acatgaaatg ccagcgccat gaggtccatc cg atg tat 538
 Met Tyr
 1

ccg agc gac ttt gca agc gca ctt gaa tct tta agc tta aaa gac atg 586
 Pro Ser Asp Phe Ala Ser Ala Leu Glu Ser Leu Ser Leu Lys Asp Met
 5 10 15

aga aaa gcg atc cac cgc ctt ctt gac att cgc gac gaa aat acg tgg 634
 Arg Lys Ala Ile His Arg Leu Leu Asp Ile Arg Asp Glu Asn Thr Trp
 20 25 30

atg ctg ttc ggc act ctg ccg ttt tac gcg tgc agc cct gat cct gaa 682
 Met Leu Phe Gly Thr Leu Pro Phe Tyr Ala Cys Ser Pro Asp Pro Glu
 35 40 45 50

gat cac gcc ctc tta cag cgg ctg cgc gaa gcg aaa aac gtc acc gtc 730
 Page 277

10294.204.ST25.txt

Asp His Ala Leu Leu Gln Arg Leu Arg Glu Ala Lys Asn Val Thr Val
 55 60 65
 aga aac gac cct gac ggc aga tcg cgc ctg aac gtc aat att ttt gac 778
 Arg Asn Asp Pro Asp Gly Arg Ser Arg Leu Asn Val Asn Ile Phe Asp
 70 75 80
 ggc aat atc atc gtg acc gat ttc gga gat act ccg ccg ctc ggc aac 826
 Gly Asn Ile Ile Val Thr Asp Phe Gly Asp Thr Pro Pro Leu Gly Asn
 85 90 95
 att cag aca gac agc ctg cca agc gcc tac gcg aag tgg aga aaa aca 874
 Ile Gln Thr Asp Ser Leu Pro Ser Ala Tyr Ala Lys Trp Arg Lys Thr
 100 105 110
 gag ctt gcc aaa gaa ctc aac tgc cac tgc ccg cac gtc cgg tgc ctc 922
 Glu Leu Ala Lys Glu Leu Asn Cys His Cys Pro His Val Arg Cys Leu
 115 120 125 130
 gga ccg aat gtg ctc gtc aaa aac agc tat tat caa gat gtt gat ttt 970
 Gly Pro Asn Val Leu Val Lys Asn Ser Tyr Tyr Gln Asp Val Asp Phe
 135 140 145
 act tcc aga aca gca aga gta tgaaaaaagc aagccgcaaa ggcttgcttt 1021
 Thr Ser Arg Thr Ala Arg Val
 150
 tttatttcgg ctgatggctg agctgaaagc cgaatgtcag gtgatcctgt acaggaatcc 1081
 aagcgccgat tccttgcgag gtgatatttt tgacgactag ctttcttttg ttgcctttta 1141
 atacgatgta cacttcgccg taggtgactt ttcctttttc attgacggca ggtgcatagg 1201
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 ggtatgtggt ctctttggaa atattcgatga cagagcttgg aatcttgatc ggcttggtg 1741
 cgtcagcttc ctgtacagcg aaaaaactaa aggataaaaa cgagtcagc gtaaaacaca 1801
 aaagcttttt catactatca ctctttctgt ttctttttcc ttattgtttt ccggatgctc 1861
 tct 1864
 <210> 176
 <211> 153
 <212> PRT
 <213> Bacillus licheniformis
 <400> 176
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 1 5 10 15

10294.204.ST25.txt

Asp Met Arg Lys Ala Ile His Arg Leu Leu Asp Ile Arg Asp Glu Asn
 20 25 30

Thr Trp Met Leu Phe Gly Thr Leu Pro Phe Tyr Ala Cys Ser Pro Asp
 35 40 45

Pro Glu Asp His Ala Leu Leu Gln Arg Leu Arg Glu Ala Lys Asn Val
 50 55 60

Thr Val Arg Asn Asp Pro Asp Gly Arg Ser Arg Leu Asn Val Asn Ile
 65 70 75 80

Phe Asp Gly Asn Ile Ile Val Thr Asp Phe Gly Asp Thr Pro Pro Leu
 85 90 95

Gly Asn Ile Gln Thr Asp Ser Leu Pro Ser Ala Tyr Ala Lys Trp Arg
 100 105 110

Lys Thr Glu Leu Ala Lys Glu Leu Asn Cys His Cys Pro His Val Arg
 115 120 125

Cys Leu Gly Pro Asn Val Leu Val Lys Asn Ser Tyr Tyr Gln Asp Val
 130 135 140

Asp Phe Thr Ser Arg Thr Ala Arg Val
 145 150

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 <211> 1763
 <212> DNA
 <213> Bacillus licheniformis

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 <222> (503)..(1264)

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 agttcgtcac atcctgtgac aacatctgca tgacctgcat cgtgcaggcc cctgactacg 180
 cacactcaaa tgtgcgattt ataaaaatga attaacaggt acgttttgtc ttgttttagtt 240
 ttcaaagatc atttccgctt cgttcagcgg ctttaataat ataacatcaa gctcacatat 300
 ttgtcaataa cttttctcaa aattatTTTT tggagctttt tcatgtcagc tgtttatcag 360
 cgacgaataa caatataaca tgttttattta attccgggtca accctctttt taattttttt 420
 cttaagatga attattgtta tgttctattt taaacaagca taggatgaaa acaaagcagc 480
 atggacaagg aggagttttt ct gtg aac cat ttt tat gtg tgg cat atc aaa 532
 Val Asn His Phe Tyr Val Trp His Ile Lys
 1 5 10

10294.204.ST25.txt

cg	att	aag	cag	cta	atc	att	att	atg	ata	gcc	gct	ttt	gcg	aca	gca	580
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				15				20						25		
agt	ttt	ttt	tat	gtg	caa	aac	ctg	ctc	cct	ctt	cct	gtg	ttt	tct	aca	628
Ser	Phe	Phe	Tyr	Val	Gln	Asn	Leu	Leu	Pro	Leu	Pro	Val	Phe	Ser	Thr	
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gaa	ggc	gga	gca	aaa	gcg	gta	tat	aga	gga	gat	tca	gat	aca	aat	gaa	676
Glu	Gly	Gly	Ala	Lys	Ala	Val	Tyr	Arg	Gly	Asp	Ser	Asp	Thr	Asn	Glu	
		45					50					55				
gta	gcc	ctt	aca	ttt	aat	atc	agc	tgg	gga	gat	caa	aag	gca	atg	ccc	724
Val	Ala	Leu	Thr	Phe	Asn	Ile	Ser	Trp	Gly	Asp	Gln	Lys	Ala	Met	Pro	
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Ile	Leu	Asp	Thr	Leu	Lys	Ala	Asn	Gly	Ile	Lys	Asp	Ala	Thr	Phe	Phe	
	75				80					85				90		
cta	tca	gct	tca	tgg	gca	gag	cgc	cac	ccg	gat	gtc	gta	gaa	aga	atc	820
Leu	Ser	Ala	Ser	Trp	Ala	Glu	Arg	His	Pro	Asp	Val	Val	Glu	Arg	Ile	
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cgt	aaa	gat	ggg	cac	cag	atc	ggg	agt	atg	ggc	tat	gct	tat	aaa	aac	868
Arg	Lys	Asp	Gly	His	Gln	Ile	Gly	Ser	Met	Gly	Tyr	Ala	Tyr	Lys	Asn	
			110					115					120			
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Tyr	Ser	Gln	Met	Lys	Lys	Ser	Glu	Ile	Lys	Lys	Asp	Leu	Ala	Lys	Ala	
		125					130					135				
cga	cac	tcc	ttt	caa	aaa	ctc	ggg	ctt	gac	gac	ctt	acg	ctt	tta	aga	964
Arg	His	Ser	Phe	Gln	Lys	Leu	Gly	Leu	Asp	Asp	Leu	Thr	Leu	Leu	Arg	
	140					145					150					
ccg	ccg	acc	ggc	cag	ttt	aat	aaa	gac	gta	ctc	gat	ggt	gct	aaa	cag	1012
Pro	Pro	Thr	Gly	Gln	Phe	Asn	Lys	Asp	Val	Leu	Asp	Val	Ala	Lys	Gln	
	155				160					165					170	
tac	ggc	tac	acc	gtt	gtt	cat	tat	agt	att	aac	tcg	gat	gac	tgg	acg	1060
Tyr	Gly	Tyr	Thr	Val	Val	His	Tyr	Ser	Ile	Asn	Ser	Asp	Asp	Trp	Thr	
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aac	ccg	ggg	gtt	caa	aag	atc	gtc	caa	aac	gta	aat	gga	acg	gta	aac	1108
Asn	Pro	Gly	Val	Gln	Lys	Ile	Val	Gln	Asn	Val	Asn	Gly	Thr	Val	Asn	
			190					195					200			
gcc	ggg	gac	atc	gtg	ctc	ttt	cac	gct	tca	gat	tcc	gcc	aaa	caa	aca	1156
Ala	Gly	Asp	Ile	Val	Leu	Phe	His	Ala	Ser	Asp	Ser	Ala	Lys	Gln	Thr	
		205					210					215				
aaa	gaa	gcc	ctg	cca	gag	atc	gtg	cac	cat	ctc	aga	agc	aag	ggg	ctc	1204
Lys	Glu	Ala	Leu	Pro	Glu	Ile	Val	His	His	Leu	Arg	Ser	Lys	Gly	Leu	
	220					225					230					
aaa	aac	gta	aca	gtc	agc	gaa	tta	atc	gca	aat	acg	gat	gca	aaa	tct	1252
Lys	Asn	Val	Thr	Val	Ser	Glu	Leu	Ile	Ala	Asn	Thr	Asp	Ala	Lys	Ser	
	235				240					245					250	
tca	gaa	gta	aag	tagcagccgg	tctaagcgcg	tgcctgaaat	tttggcagca									1304
Ser	Glu	Val	Lys													
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10294.204.ST25.txt

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 ctaccgcaa aataaagagc ggcagccaaa tgtacggaat gatggagcct ccatcttttt 1544
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 gaatcgaatt ccacaaagaa tgagatctga aaatttccag tgcaaagcgg tgaatcgta 1664
 agaaaatcac aaatcccatt tgagcaatca cgctaaagat catgccaacc ccgataaacc 1724
 agaaaagaac agacagaatc tccaatacct cgaaggaaa 1763

<210> 178
 <211> 254
 <212> PRT
 <213> Bacillus licheniformis
 <400> 178

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Asn Leu Leu Pro Leu Pro Val Phe Ser Thr Glu Gly Gly Ala Lys Ala
 35 40 45

Val Tyr Arg Gly Asp Ser Asp Thr Asn Glu Val Ala Leu Thr Phe Asn
 50 55 60

Ile Ser Trp Gly Asp Gln Lys Ala Met Pro Ile Leu Asp Thr Leu Lys
 65 70 75 80

Ala Asn Gly Ile Lys Asp Ala Thr Phe Phe Leu Ser Ala Ser Trp Ala
 85 90 95

Glu Arg His Pro Asp Val Val Glu Arg Ile Arg Lys Asp Gly His Gln
 100 105 110

Ile Gly Ser Met Gly Tyr Ala Tyr Lys Asn Tyr Ser Gln Met Lys Lys
 115 120 125

Ser Glu Ile Lys Lys Asp Leu Ala Lys Ala Arg His Ser Phe Gln Lys
 130 135 140

Leu Gly Leu Asp Asp Leu Thr Leu Leu Arg Pro Pro Thr Gly Gln Phe
 145 150 155 160

Asn Lys Asp Val Leu Asp Val Ala Lys Gln Tyr Gly Tyr Thr Val Val
 165 170 175

His Tyr Ser Ile Asn Ser Asp Asp Trp Thr Asn Pro Gly Val Gln Lys
 180 185 190

10294.204.ST25.txt

Ile Val Gln Asn Val Asn Gly Thr Val Asn Ala Gly Asp Ile Val Leu
 195 200 205

Phe His Ala Ser Asp Ser Ala Lys Gln Thr Lys Glu Ala Leu Pro Glu
 210 215 220

Ile Val His His Leu Arg Ser Lys Gly Leu Lys Asn Val Thr Val Ser
 225 230 235 240

Glu Leu Ile Ala Asn Thr Asp Ala Lys Ser Ser Glu Val Lys
 245 250

<210> 179
 <211> 1610
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1304)

<400> 179
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 gctgcgcaga aagcttgctc aggaacaagg cgtgcctcct tttgttgat tctctgacga 120
 aacgctgcgg gaaatgagcg ggaaagtccc tctgacagac gaagagcttt tgtcagtcaa 180
 aggagtggga gaacaaaaaa gagtaaaata cggagctgta tttctacagg agcttcaagc 240
 ctataaaact gagaaagaag cataaaaacc caaaatttat atatgtaaaa ttttttttag 300
 taaatctcct atttcagttg aaaaacgatt ggaacccttg atacatctga atttcggccg 360
 attttagggc ggctgaaatt cctcctcgta aaacaactgt aatcaaaaac aaattgtttt 420
 gttattgatt tgacattttc atatgttacg attgctcctg ttagccggac aataaaaagc 480
 taacaaggga ggatttactt atg aag aag acg ttt atg tcc ttt gtt gca gtt 533
 Met Lys Lys Thr Phe Met Ser Phe Val Ala Val
 1 5 10
 gca gca tta tct tca act gca ttc gga gcg agt gcc tct gca aaa gaa 581
 Ala Ala Leu Ser Ser Thr Ala Phe Gly Ala Ser Ala Ser Ala Lys Glu
 15 20 25
 gta aca gtc caa aaa ggt gac acc ctt tgg gga atc tcg caa aaa caa 629
 Val Thr Val Gln Lys Gly Asp Thr Leu Trp Gly Ile Ser Gln Lys Gln
 30 35 40
 ggg gta aat ctg cag gac tta aaa gaa tgg aat cag ctt tcc tct gac 677
 Gly Val Asn Leu Gln Asp Leu Lys Glu Trp Asn Gln Leu Ser Ser Asp
 45 50 55
 ttg att att ccg gga caa aag ctg aac gtt tct gaa aaa cag aca gaa 725
 Leu Ile Ile Pro Gly Gln Lys Leu Asn Val Ser Glu Lys Gln Thr Glu
 60 65 70 75
 gaa aag aaa caa tat acc att aaa aag gga gac act ctc tgg aaa atc 773
 Glu Lys Lys Gln Tyr Thr Ile Lys Lys Gly Asp Thr Leu Trp Lys Ile
 80 85 90
 gcc caa aaa ttc ggc gtt tca gtg aat gac ctt aaa aat tgg aac aac 821
 Page 282

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Ala Gln Lys Phe Gly Val Ser Val Asn Asp Leu Lys Asn Trp Asn Asn
 95 100 105

ata aaa tca gat atc att tac ccg aat aca tcc ata act gtt gac gga 869
 Ile Lys Ser Asp Ile Ile Tyr Pro Asn Thr Ser Ile Thr Val Asp Gly
 110 115 120

cag gcg acg gtc cag gct gct gcg gcg caa cct gcg gaa aca aag cct 917
 Gln Ala Thr Val Gln Ala Ala Ala Ala Gln Pro Ala Glu Thr Lys Pro
 125 130 135

gcc gta caa aaa gaa gcg aaa gtc gag aag gct gcg cct gcc cct gca 965
 Ala Val Gln Lys Glu Ala Lys Val Glu Lys Ala Ala Pro Ala Pro Ala
 140 145 150 155

cct aag cag gaa aaa gaa ccg gct tcc cgt tca aac gta tct caa agc 1013
 Pro Lys Gln Glu Lys Glu Pro Ala Ser Arg Ser Asn Val Ser Gln Ser
 160 165 170

act gcc aaa gaa ctg acg gtt aca gca acg gca tac act gcc aat gac 1061
 Thr Ala Lys Glu Leu Thr Val Thr Ala Thr Ala Tyr Thr Ala Asn Asp
 175 180 185

ggc ggt atg aca ggc gtg aca gcc acg ggt atc gat ctg aag gcc aat 1109
 Gly Gly Met Thr Gly Val Thr Ala Thr Gly Ile Asp Leu Lys Ala Asn
 190 195 200

aaa aac gcc aag gtt att gcg gtg gat cca aac gta atc ccg ctt gga 1157
 Lys Asn Ala Lys Val Ile Ala Val Asp Pro Asn Val Ile Pro Leu Gly
 205 210 215

tcc aag gtg tat gtg gaa ggc tac gga gaa gcg acc gct gcc gat acc 1205
 Ser Lys Val Tyr Val Glu Gly Tyr Gly Glu Ala Thr Ala Asp Thr
 220 225 230 235

ggc ggt gcg atc aag ggg aac aaa atc gac gta ttt gtt cca agc aaa 1253
 Gly Gly Ala Ile Lys Gly Asn Lys Ile Asp Val Phe Val Pro Ser Lys
 240 245 250

tcc gca gca aaa aac tgg ggc gtt aaa acg gtt aaa gtt aaa gtt tta 1301
 Ser Ala Ala Lys Asn Trp Gly Val Lys Thr Val Lys Val Lys Val Leu
 255 260 265

aaa taatagggttt accattgatg gacactgacc atgaagatga tcagtgtctt 1354
 Lys

ttttctgttt tctgcatctt ttttctatt ttgatgtttt tttagattgg caaatgggta 1414

gttcaataga taaatacata tcagctgatc taaaaaggag ttgcagaagt attggtgtgg 1474

attatcatga catttttatt gattaatgca ggaattttta ttttttctta tttgaggaca 1534

aaagatattg atttaaaaac gtcagacggc tatttttctcg gcgggcgcag tctcactgcc 1594

ctctatatcg gaagtt 1610

<210> 180
 <211> 268
 <212> PRT
 <213> Bacillus licheniformis
 <400> 180

Met Lys Lys Thr Phe Met Ser Phe Val Ala Val Ala Ala Leu Ser Ser
 1 5 10 15

10294.204.ST25.txt

Thr Ala Phe Gly Ala Ser Ala Ser Ala Lys Glu Val Thr Val Gln Lys
 20 25 30

Gly Asp Thr Leu Trp Gly Ile Ser Gln Lys Gln Gly Val Asn Leu Gln
 35 40 45

Asp Leu Lys Glu Trp Asn Gln Leu Ser Ser Asp Leu Ile Ile Pro Gly
 50 55 60

Gln Lys Leu Asn Val Ser Glu Lys Gln Thr Glu Glu Lys Lys Gln Tyr
 65 70 75 80

Thr Ile Lys Lys Gly Asp Thr Leu Trp Lys Ile Ala Gln Lys Phe Gly
 85 90 95

Val Ser Val Asn Asp Leu Lys Asn Trp Asn Asn Ile Lys Ser Asp Ile
 100 105 110

Ile Tyr Pro Asn Thr Ser Ile Thr Val Asp Gly Gln Ala Thr Val Gln
 115 120 125

Ala Ala Ala Ala Gln Pro Ala Glu Thr Lys Pro Ala Val Gln Lys Glu
 130 135 140

Ala Lys Val Glu Lys Ala Ala Pro Ala Pro Ala Pro Lys Gln Glu Lys
 145 150 155 160

Glu Pro Ala Ser Arg Ser Asn Val Ser Gln Ser Thr Ala Lys Glu Leu
 165 170 175

Thr Val Thr Ala Thr Ala Tyr Thr Ala Asn Asp Gly Gly Met Thr Gly
 180 185 190

Val Thr Ala Thr Gly Ile Asp Leu Lys Ala Asn Lys Asn Ala Lys Val
 195 200 205

Ile Ala Val Asp Pro Asn Val Ile Pro Leu Gly Ser Lys Val Tyr Val
 210 215 220

Glu Gly Tyr Gly Glu Ala Thr Ala Ala Asp Thr Gly Gly Ala Ile Lys
 225 230 235 240

Gly Asn Lys Ile Asp Val Phe Val Pro Ser Lys Ser Ala Ala Lys Asn
 245 250 255

Trp Gly Val Lys Thr Val Lys Val Lys Val Leu Lys
 260 265

<210> 181
 <211> 1547
 <212> DNA

10294.204.ST25.txt

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1046)

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<400> 181
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tctggcgcgt tttcattcat agacaatttt tgatattcat aaattaattg atccagctcc      120
tggctccgcc tgatcgtttc atcccctgta tatccataga tttcagcggc ttcaaccatc      180
atttgccgct tcttgctgat ggaaacgagc aatgcttctt tttcaatata cctttgcacc      240
cgctcccggg aggtcccaaa aaaatTTTTT tgcaaaaaaa aatttttccc cataaggctc      300
tagtgttatg agaaaaaaat ccgggaacgg aatcaaggac cataaaaatt ttttctggcc      360
aacccaaaac cccggtgcgt ttaagtcgtc ataaataaga aaccagcgga ggaaaaattt      420
ttctcgcaac cctcttgtaa tctatctgac gttattgtaa catttgtaat ataagagata      480
tatttaagga gagaggacca ttg aaa aag tta atc gtt tgt tta tta gct gtt      533
                1      5      10
                Leu Lys Lys Leu Ile Val Cys Leu Leu Ala Val

tta ctg atc ttg cct gcc gga gcg tcc ctc gca gcg aaa aat caa aca      581
Leu Leu Ile Leu Pro Ala Gly Ala Ser Leu Ala Ala Lys Asn Gln Thr
                15      20      25

tca ggg aat tta aca aat aag caa gtc atg caa tta acc ttg cag gca      629
Ser Gly Asn Leu Thr Asn Lys Gln Val Met Gln Leu Thr Leu Gln Ala
                30      35      40

cgg gag cac ttt tgg aat acg atg agc ggc cac aat cca aaa gcg aaa      677
Arg Glu His Phe Trp Asn Thr Met Ser Gly His Asn Pro Lys Ala Lys
                45      50      55

aac tca act tgc cca tcc aaa aca ttt gaa tac cgc ggt ctt cca tat      725
Asn Ser Thr Cys Pro Ser Lys Thr Phe Glu Tyr Arg Gly Leu Pro Tyr
                60      65      70      75

acg tat atg tgc agt gaa ttc agc aca aaa gca aaa tta aca gac tac      773
Thr Tyr Met Cys Ser Glu Phe Ser Thr Lys Ala Lys Leu Thr Asp Tyr
                80      85      90

ttg acg ccg gtt ttc aca aaa gac gcc att aaa aaa ggc ttg gaa aaa      821
Leu Thr Pro Val Phe Thr Lys Asp Ala Ile Lys Lys Gly Leu Glu Lys
                95      100      105

tac aac atc att tct tat aaa gga aaa atg gcc gtg cct gtc ggc gat      869
Tyr Asn Ile Ile Ser Tyr Lys Gly Lys Met Ala Val Pro Val Gly Asp
                110      115      120

ggg gac aac ctc tta gga tgg gac aag gca aaa atc aaa ctg atc tct      917
Gly Asp Asn Leu Leu Gly Trp Asp Lys Ala Lys Ile Lys Leu Ile Ser
                125      130      135

caa aaa aac aat acc cgc act tat gaa ttt tcc gta ccg gca ttg gat      965
Gln Lys Asn Asn Thr Arg Thr Tyr Glu Phe Ser Val Pro Ala Leu Asp
                140      145      150      155

gga tcg gtg act gcg aaa aga aag atc acg ttt gtg aaa gaa aac aac      1013
Gly Ser Val Thr Ala Lys Arg Lys Ile Thr Phe Val Lys Glu Asn Asn
                160      165      170

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10294.204.ST25.txt

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aaa tgg aaa atc aat cag ctc gat gct gcc atc taaacgaaaa agctaattgtc 1066
Lys Trp Lys Ile Asn Gln Leu Asp Ala Ala Ile
175 180
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tccagaatga ctctttcata ataccgtct cccgtgacgc gcggctttcc ggcaacctgg 1186
tattcttctt tttcaaagcg gctcgtcatc tcgtcaacct cttgccgcga ccctaaggaa 1246
aacgccatat gtgcatagcc ggaagcggtt tcctctcctt ttgcaagggtc ggggcgtctc 1306
atcagctcaa gccgtgttcc cgattcaaac tggatgaaat atgattcgaa atgctttttc 1366
ggattgacat atttttcatt cgtctttccg tgaaaaaaac gggatatagaa atcttttcatt 1426
tcctctaaat tgttcgtcca tatggcgatg tgttcgattt tcataaatct ccctccatt 1486
tcatattacc atatagatcc tctgcctttt tttacacttt tttaaattga taagtattca 1546
t 1547

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<210> 182
 <211> 182
 <212> PRT
 <213> Bacillus licheniformis

<400> 182

Leu Lys Lys Leu Ile Val Cys Leu Leu Ala Val Leu Leu Ile Leu Pro
 1 5 10 15

Ala Gly Ala Ser Leu Ala Ala Lys Asn Gln Thr Ser Gly Asn Leu Thr
 20 25 30

Asn Lys Gln Val Met Gln Leu Thr Leu Gln Ala Arg Glu His Phe Trp
 35 40 45

Asn Thr Met Ser Gly His Asn Pro Lys Ala Lys Asn Ser Thr Cys Pro
 50 55 60

Ser Lys Thr Phe Glu Tyr Arg Gly Leu Pro Tyr Thr Tyr Met Cys Ser
 65 70 75 80

Glu Phe Ser Thr Lys Ala Lys Leu Thr Asp Tyr Leu Thr Pro Val Phe
 85 90 95

Thr Lys Asp Ala Ile Lys Lys Gly Leu Glu Lys Tyr Asn Ile Ile Ser
 100 105 110

Tyr Lys Gly Lys Met Ala Val Pro Val Gly Asp Gly Asp Asn Leu Leu
 115 120 125

Gly Trp Asp Lys Ala Lys Ile Lys Leu Ile Ser Gln Lys Asn Asn Thr
 130 135 140

Arg Thr Tyr Glu Phe Ser Val Pro Ala Leu Asp Gly Ser Val Thr Ala
 145 150 155 160

10294.204.ST25.txt

Lys Arg Lys Ile Thr Phe Val Lys Glu Asn Asn Lys Trp Lys Ile Asn
 165 170 175

Gln Leu Asp Ala Ala Ile
 180

<210> 183
 <211> 1317
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(818)

<400> 183
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 attgtcatgc tgtatgtttc cacatcatga aatgatgcgt ttgtatgctg tgacagctga 120
 ctccccaatc caattaacag gtatatgatc agcagcgttt gaaaaacgat aatgtttttt 180
 ccggctcttt ttcggcatct cctagttcga gataatcgga acatgactac cctcctagcg 240
 agtatgtaat ggcttttgtt tccgttcggt ttaaagaact ttatagtttag agtataaaga 300
 acaagtgtgc cgtttgaaaa ctgtcaaaaa agtcgattaa gttcgttcta aagaacattt 360
 tcgtttaatt cctcaaaaaa cctctcaaat tctcatcttt ttgaaaagtt tgtagttctt 420
 tatagtgtac acaatttctt cttaattttt gtataaacac tgttgacaag gaaaaaatag 480
 gatagaaagg atgatgaccc gtg ctg aaa aat gtc ata tta tgt tct ttt tta 533
 Val Leu Lys Asn Val Ile Leu Cys Ser Phe Leu 10
 1 5
 ctg ctt tct agc att ggg ccg ctc aat gcc cat gcg gca gct tac gaa 581
 Leu Leu Ser Ser Ile Gly Pro Leu Asn Ala His Ala Ala Ala Tyr Glu 25
 15 20 25
 aca gcc cgc atg tct aag tgg gaa gaa aaa gcg gtt gag gaa gca aaa 629
 Thr Ala Arg Met Ser Lys Trp Glu Glu Lys Ala Val Glu Glu Ala Lys 30 35 40
 30 35 40
 aag aga tat ccg gaa gca gaa gtg cgc ctc acg aaa aaa gta tgg gat 677
 Lys Arg Tyr Pro Glu Ala Glu Val Arg Leu Thr Lys Lys Val Trp Asp 45 50 55
 45 50 55
 cga aag cgg gcc gat gaa gcg gtc aaa caa tac cat gtc aca ttg agt 725
 Arg Lys Arg Ala Asp Glu Ala Val Lys Gln Tyr His Val Thr Leu Ser 60 65 70 75
 60 65 70 75
 gaa gga aat aaa aat ttc gga gtg ttt gtc aca att tca ttt gaa cct 773
 Glu Gly Asn Lys Asn Phe Gly Val Phe Val Thr Ile Ser Phe Glu Pro 80 85 90
 80 85 90
 gcg aca cac aaa att aac aaa gtc gtc gtt gtg gaa gaa tat aaa 818
 Ala Thr His Lys Ile Asn Lys Val Val Val Val Glu Glu Tyr Lys 95 100 105
 95 100 105
 taagccgcat tgcagtgcaa agcggcttgt ctttatttat gctttttaaa aaacatgata 878
 cagccaaggg gaagaatgcc gaaccattga tatatcctgg acggcggcctt taattcttta 938

10294.204.ST25.txt

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cgtttttctt tcatttcttt tctttcctgc ttaggcgtgt ccatatattt tacgagctgt    998
tccgtcatat atttaacata atcggttcgtt ttcacgcgat cacctcttgg ggagttctgt    1058
cagttgaagt gttgtcatcc gaatcttttt ttatacatcc ttcacgattt ggacacacaa    1118
tttttaatat tccttccact gcgtgatttt ttgatttctt aaatcatatt gaaattgagc    1178
gcttgtttct gtgccggaag ctgtcgttac ctgaatctgg actcgtgtga gctgctgatg    1238
agccgggctg acagaatacg atatcaagcc atgctgtttt tgaacttttt cttttgtctc    1298
ttcgtgaata tgggacaag                                     1317

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<210> 184
 <211> 106
 <212> PRT
 <213> *Bacillus licheniformis*

<400> 184

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Val Leu Lys Asn Val Ile Leu Cys Ser Phe Leu Leu Leu Ser Ser Ile
 1          5          10          15
Gly Pro Leu Asn Ala His Ala Ala Ala Tyr Glu Thr Ala Arg Met Ser
          20          25          30
Lys Trp Glu Glu Lys Ala Val Glu Glu Ala Lys Lys Arg Tyr Pro Glu
          35          40          45
Ala Glu Val Arg Leu Thr Lys Lys Val Trp Asp Arg Lys Arg Ala Asp
          50          55          60
Glu Ala Val Lys Gln Tyr His Val Thr Leu Ser Glu Gly Asn Lys Asn
          65          70          75          80
Phe Gly Val Phe Val Thr Ile Ser Phe Glu Pro Ala Thr His Lys Ile
          85          90          95
Asn Lys Val Val Val Val Glu Glu Tyr Lys
          100          105

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<210> 185
 <211> 2347
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
 <221> CDS
 <222> (518)..(1906)

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<400> 185
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aatgctcgat gcggcggatc cgggtgaact cgggggcacc tacgccggaa gtccgcttgg    120
atgcgtagcc gctttggcag tgctcgatat tatcgaatcg gaacagctca acaagcgctc    180

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10294.204.ST25.txt

tgaagaaatc ggcaaagcca tcgaagagcg ggcgcttgaa tggaagatga aatatccgca	240
gattgggggaa gtccgccgac ttggcgcaat ggctgcgatt gaaattgtcc gggacgaaaa	300
gacgcggggag ccggacaaaag cagctgcggc caagattgcc aagtacgcca atgaacacgg	360
tctgctcttg ttgacggcag ggatcaacgg caacattatc cgttttctgt ctccgctcgt	420
cattactgat gaattacttg aggaagggtt cggcatcatt gaagaagcgc tggaacagct	480
ctagtttgac atcttctaaa agaaggagcg gattttg atg ggt aaa cag caa atg	535
Met Gly Lys Gln Gln Met	
1 5	
aaa aaa acg atg tcg cag acg gat gtg cta ttt tta gcg atc gga gct	583
Lys Lys Thr Met Ser Gln Thr Asp Val Leu Phe Leu Ala Ile Gly Ala	
10 15 20	
atg ctc ggc tgg ggc tgg gtc gtc ctt tcc ggc gac tgg att tcg aca	631
Met Leu Gly Trp Gly Trp Val Val Leu Ser Gly Asp Trp Ile Ser Thr	
25 30 35	
gcc ggc ttt ttg ggc agc acg atc gcg ttt atc atc ggc ggc ata ctc	679
Ala Gly Phe Leu Gly Ser Thr Ile Ala Phe Ile Ile Gly Gly Ile Leu	
40 45 50	
gtc atc tta atc ggg tta acg tac gcg gag ctg tct tct gcc atc cct	727
Val Ile Leu Ile Gly Leu Thr Tyr Ala Glu Leu Ser Ser Ala Ile Pro	
55 60 65 70	
gaa acg ggt ggc ggc ttg att ttc gtc tac agg gcg ttc gga cga aaa	775
Glu Thr Gly Gly Gly Leu Ile Phe Val Tyr Arg Ala Phe Gly Arg Lys	
75 80 85	
acg gct ttt gtc gcc gct tgg ggt gtg ctg ttc ggc tat gtt tcg gtg	823
Thr Ala Phe Val Ala Ala Trp Gly Val Leu Phe Gly Tyr Val Ser Val	
90 95 100	
att aca ttt gag gcg gtc gca ttg cct acc gtc atc gat tac gtc ctg	871
Ile Thr Phe Glu Ala Val Ala Leu Pro Thr Val Ile Asp Tyr Val Leu	
105 110 115	
cct gtc gaa cat cag ggg ttt ctc tgg tcg cta agc ggc tgg gac gtg	919
Pro Val Glu His Gln Gly Phe Leu Trp Ser Leu Ser Gly Trp Asp Val	
120 125 130	
tat gtc act tgg gtg ttg atc ggt tcg gga ggt gcg gtc gtc ctg aca	967
Tyr Val Thr Trp Val Leu Ile Gly Ser Gly Ala Val Val Leu Thr	
135 140 145 150	
gcg ctc aat tac ttc ggc gtc aag ccg gcc gcg att ttt cag tcg gtc	1015
Ala Leu Asn Tyr Phe Gly Val Lys Pro Ala Ala Ile Phe Gln Ser Val	
155 160 165	
ttt acg att gcg att atc gcc acg ggc ttt ctc ctt ttg ggc ggc gcc	1063
Phe Thr Ile Ala Ile Ile Ala Thr Gly Phe Leu Leu Leu Gly Gly Ala	
170 175 180	
ttg gta aac ggt gat ttc gaa cat gta cag ccc ctt ttt aaa gac ggg	1111
Leu Val Asn Gly Asp Phe Glu His Val Gln Pro Leu Phe Lys Asp Gly	
185 190 195	
ttt tcc ggt atg atg tcc gtc ctt gtc atg att ccg ttt cta ttt gtc	1159
Phe Ser Gly Met Met Ser Val Leu Val Met Ile Pro Phe Leu Phe Val	
200 205 210	
gga ttt gac gtc atc cct cag gtt gcg gct gaa att aat gcc ccg aaa	1207
Gly Phe Asp Val Ile Pro Gln Val Ala Ala Glu Ile Asn Ala Pro Lys	

10294.204.ST25.txt

215	220	225	230	
aaa atc atc ggc Lys Ile Ile Gly	aaa att ttg att att Lys Ile Leu Ile Ile	tcg att atc agt ggc gtc gtg Ser Ile Ile Ser Ala Val Val		1255
	235	240	245	
ttt tat ttg ctg att gta ttc ggc gta acg atg ggt ctg tca gaa agc Phe Tyr Leu Leu Ile Val Phe Gly Val Thr Met Gly Leu Ser Glu Ser		255	260	1303
	250			
gag ctt gcg acg act tct ttg gca acc gcg gat gca atg gtc aat ctg Glu Leu Ala Thr Thr Ser Leu Ala Thr Ala Asp Ala Met Val Asn Leu		270	275	1351
	265			
ctc ggg aac cag ctg ttc ggc acg gtg ctt gtc ctc ggc ggc gtc gcc Leu Gly Asn Gln Leu Phe Gly Thr Val Leu Val Leu Gly Gly Val Ala		285	290	1399
	280			
gga atc att acg agc tgg aac gca ttt atc atc ggc gcg agc cgg att Gly Ile Ile Thr Ser Trp Asn Ala Phe Ile Ile Gly Ala Ser Arg Ile		300	305	1447
	295			
ctg ttt gca atg tcg gaa aag ggc atg gtg ccg aaa tgg ttc ggc ttc Leu Phe Ala Met Ser Glu Lys Gly Met Val Pro Lys Trp Phe Gly Phe		315	320	1495
	310			
atc cat ccg aag tat aaa acg ccg act aat gca att tta ttt ctg ggt Ile His Pro Lys Tyr Lys Thr Pro Thr Asn Ala Ile Leu Phe Leu Gly		330	335	1543
	325			
gcg ctg gcg ttt ttt gcc ccg ctg ctc gga cgc cct gcc ctt gtt tgg Ala Leu Ala Phe Phe Ala Pro Leu Leu Gly Arg Pro Ala Leu Val Trp		350	355	1591
	345			
atc gtc aat gca ggg gga aca ggt att ata gtc gga tat ttg atc gtc Ile Val Asn Ala Gly Gly Thr Gly Ile Ile Val Gly Tyr Leu Ile Val		365	370	1639
	360			
tcg att gca ttc atg aag ctg aga aaa aca gag ccg gat tta cac agg Ser Ile Ala Phe Met Lys Leu Arg Lys Thr Glu Pro Asp Leu His Arg		380	385	1687
	375			
ccg tat aaa atc aat aag tgg aaa aca acg ggt ata tct gct atc ctc Pro Tyr Lys Ile Asn Lys Trp Lys Thr Thr Gly Ile Ser Ala Ile Leu		395	400	1735
	390			
tta agt gtt atc ttc ctt gcc ttt tat ttg cca ggc atg ccg gcc gcg Leu Ser Val Ile Phe Leu Ala Phe Tyr Leu Pro Gly Met Pro Ala Ala		410	415	1783
	405			
ctc aca tgg ccg tat gag tgg ctg atc ttg gcg gga tgg aca ttg atc Leu Thr Trp Pro Tyr Glu Trp Leu Ile Leu Ala Gly Trp Thr Leu Ile		430	435	1831
	425			
ggt ttt ctt tta tac aac agc agt tca aaa cgt aaa ggg gag gag att Gly Phe Leu Leu Tyr Asn Ser Ser Ser Lys Arg Lys Gly Glu Glu Ile		445	450	1879
	440			
caa cat gac cag cat gct aga agt ata taatcctgcg actggagaaa Gln His Asp Gln His Ala Arg Ser Ile		460		1926
	455			
aaatcaaatc gggtccccag caatccgcaa aggaagtcga agaagctgtc gtacgctcgc				1986
atgaggcatt tcaaaaatgg tcgaaaacat cggctgcaga acgagcgggc ttgctgaaaa				2046
aatggtttga ttttaattgtg gagcagaagg acgagctggc aaaattgatt acgcttgaaa				2106

10294.204.ST25.txt

acggcaagcc gtacgctgaa ggcgagggcg aagtccttata tagcgagggc tatatcgaat 2166
 ggtatgcgga ggaagcgaag cgcattctacg gaagaacggt tcccgctctt gtgacgaaca 2226
 agcgcatcat cgtcacacgc cagggagtcg gacctgttgc ggcgattacc ccgtggaatt 2286
 ttccggcggc gatgatcacg agaaaagcgg ggccggcttt ggcggcgggc tgtaccttta 2346
 t 2347

<210> 186
 <211> 463
 <212> PRT
 <213> Bacillus licheniformis

<400> 186

Met Gly Lys Gln Gln Met Lys Lys Thr Met Ser Gln Thr Asp Val Leu
 1 5 10 15

Phe Leu Ala Ile Gly Ala Met Leu Gly Trp Gly Trp Val Val Leu Ser
 20 25 30

Gly Asp Trp Ile Ser Thr Ala Gly Phe Leu Gly Ser Thr Ile Ala Phe
 35 40 45

Ile Ile Gly Gly Ile Leu Val Ile Leu Ile Gly Leu Thr Tyr Ala Glu
 50 55 60

Leu Ser Ser Ala Ile Pro Glu Thr Gly Gly Gly Leu Ile Phe Val Tyr
 65 70 75 80

Arg Ala Phe Gly Arg Lys Thr Ala Phe Val Ala Ala Trp Gly Val Leu
 85 90 95

Phe Gly Tyr Val Ser Val Ile Thr Phe Glu Ala Val Ala Leu Pro Thr
 100 105 110

Val Ile Asp Tyr Val Leu Pro Val Glu His Gln Gly Phe Leu Trp Ser
 115 120 125

Leu Ser Gly Trp Asp Val Tyr Val Thr Trp Val Leu Ile Gly Ser Gly
 130 135 140

Gly Ala Val Val Leu Thr Ala Leu Asn Tyr Phe Gly Val Lys Pro Ala
 145 150 155 160

Ala Ile Phe Gln Ser Val Phe Thr Ile Ala Ile Ile Ala Thr Gly Phe
 165 170 175

Leu Leu Leu Gly Gly Ala Leu Val Asn Gly Asp Phe Glu His Val Gln
 180 185 190

Pro Leu Phe Lys Asp Gly Phe Ser Gly Met Met Ser Val Leu Val Met
 195 200 205

10294.204.ST25.txt

Ile Pro Phe Leu Phe Val Gly Phe Asp Val Ile Pro Gln Val Ala Ala
 210 215 220
 Glu Ile Asn Ala Pro Lys Lys Ile Ile Gly Lys Ile Leu Ile Ile Ser
 225 230 235 240
 Ile Ile Ser Ala Val Val Phe Tyr Leu Leu Ile Val Phe Gly Val Thr
 245 250 255
 Met Gly Leu Ser Glu Ser Glu Leu Ala Thr Thr Ser Leu Ala Thr Ala
 260 265 270
 Asp Ala Met Val Asn Leu Leu Gly Asn Gln Leu Phe Gly Thr Val Leu
 275 280 285
 Val Leu Gly Gly Val Ala Gly Ile Ile Thr Ser Trp Asn Ala Phe Ile
 290 295 300
 Ile Gly Ala Ser Arg Ile Leu Phe Ala Met Ser Glu Lys Gly Met Val
 305 310 315 320
 Pro Lys Trp Phe Gly Phe Ile His Pro Lys Tyr Lys Thr Pro Thr Asn
 325 330 335
 Ala Ile Leu Phe Leu Gly Ala Leu Ala Phe Phe Ala Pro Leu Leu Gly
 340 345 350
 Arg Pro Ala Leu Val Trp Ile Val Asn Ala Gly Gly Thr Gly Ile Ile
 355 360 365
 Val Gly Tyr Leu Ile Val Ser Ile Ala Phe Met Lys Leu Arg Lys Thr
 370 375 380
 Glu Pro Asp Leu His Arg Pro Tyr Lys Ile Asn Lys Trp Lys Thr Thr
 385 390 395 400
 Gly Ile Ser Ala Ile Leu Leu Ser Val Ile Phe Leu Ala Phe Tyr Leu
 405 410 415
 Pro Gly Met Pro Ala Ala Leu Thr Trp Pro Tyr Glu Trp Leu Ile Leu
 420 425 430
 Ala Gly Trp Thr Leu Ile Gly Phe Leu Leu Tyr Asn Ser Ser Ser Lys
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 Arg Lys Gly Glu Glu Ile Gln His Asp Gln His Ala Arg Ser Ile
 450 455 460

<210> 187
 <211> 2506

10294.204.ST25.txt

<212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1985)

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<400> 187
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actttgttaa agaaaaatca aatggctatg ttctatcaaa cggaanaactt tcttaaaaaa      180
cagcagattat ttccgtgacg acgactcaat taagatcgat gctgggcggc atgaatatga      240
agagcacgta tgcttctgta tccagcaata cgaacgcttt tactctcagc ggtaaaggat      300
tcggacacgg catcggcatg agtcagtacg gatcaaatgc cagagctgct gccgggcacg      360
attacaagaa gattttaagt ttctactatc caaatacgac tctatcaagc tattaataga      420
gtttgaacag gaagcagcag tgcctcctct gttcatgttc aggggaaaaac ataacattta      480
catttttgga ggattatttt ttg aag gtc ttt ctt aaa gct gta cct atg ttg      533
                  Leu Lys Val Phe Leu Lys Ala Val Pro Met Leu
                  1                      5                      10

tggt tta cgg ttc ttt ttg ttt gtg cct aat gta ttt gcg gcc aac tct      581
Trp Leu Arg Phe Phe Leu Phe Val Pro Asn Val Phe Ala Ala Asn Ser
                  15                      20                      25

gtc aca aga ttg gac ggt gca aac cga tat gag gtt gcg gtg aac gtt      629
Val Thr Arg Leu Asp Gly Ala Asn Arg Tyr Glu Val Ala Val Asn Val
                  30                      35                      40

tcc aag cag ggg tgg aca agt gca agc act gtg att gtt gca aat gga      677
Ser Lys Gln Gly Trp Thr Ser Ala Ser Thr Val Ile Val Ala Asn Gly
                  45                      50                      55

aag gca tat gca gac gtc ctt tca gcg act cca ttt gcc tat cga aac      725
Lys Ala Tyr Ala Asp Val Leu Ser Ala Thr Pro Phe Ala Tyr Arg Asn
                  60                      65                      70                      75

aac gcg cct gtt cta tta acg gaa gcg tct aaa ctg cca acg gcc act      773
Asn Ala Pro Val Leu Leu Thr Glu Ala Ser Lys Leu Pro Thr Ala Thr
                  80                      85                      90

aaa aac cga atc agt caa tta aaa cct agc aaa gtg atc gta atc ggc      821
Lys Asn Arg Ile Ser Gln Leu Lys Pro Ser Lys Val Ile Val Ile Gly
                  95                      100                      105

gga acc gtc agc gtt caa aac ggt gtc gta agc gag atc aaa aag ctt      869
Gly Thr Val Ser Val Gln Asn Gly Val Val Ser Glu Ile Lys Lys Leu
                  110                      115                      120

ggt gtg tca tct gtc gaa cgc atc ggc gga gcg aat cgc tac gag gtt      917
Gly Val Ser Ser Val Glu Arg Ile Gly Gly Ala Asn Arg Tyr Glu Val
                  125                      130                      135

gcg gcg aat att gcg aat aag ctg ccg agc aat tcg aaa gct gtc atc      965
Ala Ala Asn Ile Ala Asn Lys Leu Pro Ser Asn Ser Lys Ala Val Ile
                  140                      145                      150                      155

gca aac ggg acg gcc tat gct gac agc ctt gcg atc ggc gca tat gcc      1013
Ala Asn Gly Thr Ala Tyr Ala Asp Ser Leu Ala Ile Gly Ala Tyr Ala
                  160                      165                      170

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10294.204.ST25.txt

gcg aga aac ggc atc ccg att ctt tta aca tcg tcg aat tcc ata ccg Ala Arg Asn Gly Ile Pro Ile Leu Thr Ser Ser Asn Ser Ile Pro 175 180 185	1061
aca gcg aca aaa aat gcg atg aag agc aaa gga aca aca tcg acc att Thr Ala Thr Lys Asn Ala Met Lys Ser Lys Gly Thr Thr Ser Thr Ile 190 195 200	1109
gtc gta ggc ggt gaa gtc agc atc tcc agc agc gtt tac aaa cag ctt Val Val Gly Gly Glu Val Ser Ile Ser Ser Ser Val Tyr Lys Gln Leu 205 210 215	1157
gct tct ccg acg cgg atc ggc ggc agc aac cgc tat gaa gtc gcg gcc Ala Ser Pro Thr Arg Ile Gly Gly Ser Asn Arg Tyr Glu Val Ala Ala 220 225 230 235	1205
aat gtc gtc aag aaa tat tat tct tct gcc aag aat gca atc atc agc Asn Val Val Lys Lys Tyr Tyr Ser Ser Ala Lys Asn Ala Ile Ile Ser 240 245 250	1253
aac ggc tat gcg tat gcc gac gga tta aca gga tct gtt ctg gcg gct Asn Gly Tyr Ala Tyr Ala Asp Gly Leu Thr Gly Ser Val Leu Ala Ala 255 260 265	1301
aag caa aac cgt ccg atg atg ttc acg aat gca tca tct ttg ccg aca Lys Gln Asn Arg Pro Met Met Phe Thr Asn Ala Ser Ser Leu Pro Thr 270 275 280	1349
ccg aca aga gaa gtg atc ggt tcc aaa aac atg acg acg ttt act gtg Pro Thr Arg Glu Val Ile Gly Ser Lys Asn Met Thr Thr Phe Thr Val 285 290 295	1397
ctt ggc gga acg gtt tct ctt caa tcc aat gtc gtg tca cag ctg aag Leu Gly Gly Thr Val Ser Leu Gln Ser Asn Val Val Ser Gln Leu Lys 300 305 310 315	1445
aat ccg atc gtc ggc aaa aaa atc ttc att gat gca ggg cac gga ggt Asn Pro Ile Val Gly Lys Lys Ile Phe Ile Asp Ala Gly His Gly Gly 320 325 330	1493
aca gac agc ggt gcc ctc ggc aac ggt tta tat gag aaa agc gtg aac Thr Asp Ser Gly Ala Leu Gly Asn Gly Leu Tyr Glu Lys Ser Val Asn 335 340 345	1541
ctt gat gtt gca aaa tta att aat acg aaa cta tca aac ggc ggt gct Leu Asp Val Ala Lys Leu Ile Asn Thr Lys Leu Ser Asn Gly Gly Ala 350 355 360	1589
ctg cca att atg gcg aga acg aac gac act tac ctg acg ctc gca cag Leu Pro Ile Met Ala Arg Thr Asn Asp Thr Tyr Leu Thr Leu Ala Gln 365 370 375	1637
cgc gtg tca aaa gcg cag tca aat cat gcg gat ttg ttt gtc agc atc Arg Val Ser Lys Ala Gln Ser Asn His Ala Asp Leu Phe Val Ser Ile 380 385 390 395	1685
cat gca aac tcg gca acg cca gct gct tcc gga aca gaa acc tac tat His Ala Asn Ser Ala Thr Pro Ala Ala Ser Gly Thr Glu Thr Tyr Tyr 400 405 410	1733
tat aca aca tat gaa tct gcc aac agc aaa cgg ctg gca acc gag att Tyr Thr Thr Tyr Glu Ser Ala Asn Ser Lys Arg Leu Ala Thr Glu Ile 415 420 425	1781
caa aac cgt ctc tat gtt gca ttg aat aca aaa aac cgc ggt gta aag Gln Asn Arg Leu Tyr Val Ala Leu Asn Thr Lys Asn Arg Gly Val Lys 430 435 440	1829

10294.204.ST25.txt

atc ggc aac ttc cat gtc atc agg gaa tca aaa atg cca agc tgc ctt 1877
 ile Gly Asn Phe His Val Ile Arg Glu Ser Lys Met Pro Ser Cys Leu
 445 450 455
 gtt gaa ctt gcg ttt atc agc aat gta agc gat gcg aca aaa ctc aaa 1925
 Val Glu Leu Ala Phe Ile Ser Asn Val Ser Asp Ala Thr Lys Leu Lys
 460 465 470 475
 agc tcg act tac aaa gaa aaa ggc gct aaa gcg att tac gac gga atc 1973
 Ser Ser Thr Tyr Lys Glu Lys Gly Ala Lys Ala Ile Tyr Asp Gly Ile
 480 485 490
 gtt gct tac tat taaaatataa acagaaaact cgtttttcga aaaattgcct 2025
 Val Ala Tyr Tyr
 495
 atgctgcctt tgttttgtct ttattatata gtatgatatt tttggtgaaa ttaaagataa 2085
 aacggaggcg gtgcattttt aacaaaaaat caacgaattt actaatttta ataactcctt 2145
 tacattgtgt ttacgttcgt atgctacact gacgaataga tcaaacagta acatactaat 2205
 cgagggtgtat gctagtgagt atcgacaaaa gtttaagaat gtacaatgaa tattcaagcc 2265
 agcaaactta ttcctgtgct ctatctaaaa aagcagtagc ttatttatat atgaaacgga 2325
 taatggatat cgtcctttcc ttgattgggc tcgctcttac actgccgttt attctgctgt 2385
 tttgtatatatt aatctgtatc gaaacaccgg gttctccgtt ataccggcag gaacgcgtcg 2445
 gaaaagacgg gaagcatttc aaggatgatca agctgcgttc tatgagaatt gacgcagaaa 2505
 a 2506

<210> 188
 <211> 495
 <212> PRT
 <213> Bacillus licheniformis

<400> 188

Leu Lys Val Phe Leu Lys Ala Val Pro Met Leu Trp Leu Arg Phe Phe
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Leu Phe Val Pro Asn Val Phe Ala Ala Asn Ser Val Thr Arg Leu Asp
 20 25 30

Gly Ala Asn Arg Tyr Glu Val Ala Val Asn Val Ser Lys Gln Gly Trp
 35 40 45

Thr Ser Ala Ser Thr Val Ile Val Ala Asn Gly Lys Ala Tyr Ala Asp
 50 55 60

Val Leu Ser Ala Thr Pro Phe Ala Tyr Arg Asn Asn Ala Pro Val Leu
 65 70 75 80

Leu Thr Glu Ala Ser Lys Leu Pro Thr Ala Thr Lys Asn Arg Ile Ser
 85 90 95

Gln Leu Lys Pro Ser Lys Val Ile Val Ile Gly Gly Thr Val Ser Val
 Page 295

10294.204.ST25.txt

100

105

110

Gln Asn Gly Val Val Ser Glu Ile Lys Lys Leu Gly Val Ser Ser Val
 115 120 125

Glu Arg Ile Gly Gly Ala Asn Arg Tyr Glu Val Ala Ala Asn Ile Ala
 130 135 140

Asn Lys Leu Pro Ser Asn Ser Lys Ala Val Ile Ala Asn Gly Thr Ala
 145 150 155 160

Tyr Ala Asp Ser Leu Ala Ile Gly Ala Tyr Ala Ala Arg Asn Gly Ile
 165 170 175

Pro Ile Leu Leu Thr Ser Ser Asn Ser Ile Pro Thr Ala Thr Lys Asn
 180 185 190

Ala Met Lys Ser Lys Gly Thr Thr Ser Thr Ile Val Val Gly Gly Glu
 195 200 205

Val Ser Ile Ser Ser Ser Val Tyr Lys Gln Leu Ala Ser Pro Thr Arg
 210 215 220

Ile Gly Gly Ser Asn Arg Tyr Glu Val Ala Ala Asn Val Val Lys Lys
 225 230 235 240

Tyr Tyr Ser Ser Ala Lys Asn Ala Ile Ile Ser Asn Gly Tyr Ala Tyr
 245 250 255

Ala Asp Gly Leu Thr Gly Ser Val Leu Ala Ala Lys Gln Asn Arg Pro
 260 265 270

Met Met Phe Thr Asn Ala Ser Ser Leu Pro Thr Pro Thr Arg Glu Val
 275 280 285

Ile Gly Ser Lys Asn Met Thr Thr Phe Thr Val Leu Gly Gly Thr Val
 290 295 300

Ser Leu Gln Ser Asn Val Val Ser Gln Leu Lys Asn Pro Ile Val Gly
 305 310 315 320

Lys Lys Ile Phe Ile Asp Ala Gly His Gly Gly Thr Asp Ser Gly Ala
 325 330 335

Leu Gly Asn Gly Leu Tyr Glu Lys Ser Val Asn Leu Asp Val Ala Lys
 340 345 350

Leu Ile Asn Thr Lys Leu Ser Asn Gly Gly Ala Leu Pro Ile Met Ala
 355 360 365

Arg Thr Asn Asp Thr Tyr Leu Thr Leu Ala Gln Arg Val Ser Lys Ala
 Page 296

375

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10294.204.ST25.txt

30

35

40

gta Val	aaa Lys 45	gag Glu	gag Glu	aag Lys	gag Glu	caa Gln 50	gac Asp	aaa Lys	aca Thr	gac Asp	aaa Lys 55	acc Thr	aaa Lys	gat Asp	aaa Lys	677
aca Thr 60	gaa Glu	gac Asp	aaa Lys	ggc Gly	agc Ser 65	aaa Lys	acg Thr	aca Thr	agc Ser	gac Asp 70	gat Asp	aaa Lys	gcc Ala	gct Ala	caa Gln 75	725
acg Thr	ggc Gly	gat Asp	acg Thr	gtc Val 80	atg Met	aga Arg	gag Glu	ctt Leu	tat Tyr 85	ctc Leu	att Ile	gat Asp	aag Lys	aac Asn 90	ggc Gly	773
tat Tyr	gtg Val	aca Thr	gcg Ala 95	cag Gln	acg Thr	ctg Leu	ccg Pro	ctg Leu 100	cca Pro	aag Lys	cag Gln	gaa Glu	ggg Gly 105	acg Thr	gct Ala	821
aaa Lys	caa Gln	gcg Ala 110	ctt Leu	gaa Glu	tac Tyr	ctc Leu	gtt Val 115	gaa Glu	ggc Gly	ggc Gly	cct Pro	gtt Val 120	tca Ser	aac Asn	atc Ile	869
ctg Leu	cca Pro 125	aac Asn	gga Gly	ttc Phe	aga Arg	gcc Ala 130	gtg Val	ctg Leu	ccg Pro	gcg Ala	gat Asp 135	aca Thr	acg Thr	gtc Val	aat Asn	917
gtt Val 140	gat Asp	att Ile	aaa Lys	gaa Glu	gac Asp 145	gga Gly	aca Thr	gcg Ala	atc Ile	gct Ala 150	gat Asp	ttc Phe	tca Ser	aat Asn	gaa Glu 155	965
ttt Phe	aaa Lys	aac Asn	tat Tyr	aaa Lys 160	gct Ala	gaa Glu	gat Asp	gag Glu	caa Gln 165	aaa Lys	atc Ile	gta Val	cag Gln	gcg Ala 170	att Ile	1013
aca Thr	tgg Trp	acg Thr	tta Leu 175	acg Thr	cag Gln	ttt Phe	aac Asn	tcg Ser 180	att Ile	gat Asp	aaa Lys	gtg Val	aag Lys 185	ctc Leu	cgc Arg	1061
atg Met	aac Asn	ggc Gly 190	cat His	gat Asp	ttg Leu	aaa Lys	gaa Glu 195	atg Met	cct Pro	gtt Val	aac Asn	ggc Gly 200	acg Thr	ccg Pro	att Ile	1109
tca Ser	gaa Glu 205	gaa Glu	ctc Leu	agc Ser	cgc Arg	gag Glu 210	gac Asp	ggc Gly	att Ile	aac Asn	ctc Leu 215	gac Asp	acg Thr	gcg Ala	ggt Gly	1157
gtg Val 220	aca Thr	gat Asp	ata Ile	acg Thr	gcg Ala 225	aca Thr	cag Gln	ccg Pro	gtc Val	acc Thr 230	gtc Val	tat Tyr	tat Tyr	ttg Leu	gct Ala 235	1205
gaa Glu	tca Ser	gat Asp	aaa Lys	ggc Gly 240	aca Thr	tat Tyr	tac Tyr	gtt Val	ccg Pro 245	gtg Val	aca Thr	aag Lys	cgg Arg	acg Thr 250	tct Ser	1253
gca Ala	aaa Lys	gaa Glu	aaa Lys 255	gat Asp	cag Gln	gtg Val	acg Thr	gcg Ala 260	gcg Ala	att Ile	aaa Lys	gag Glu	ctg Leu 265	act Thr	gaa Glu	1301
gga Gly	ccg Pro	gac Asp 270	aat Asn	aaa Lys	agc Ser	ggc Gly	ctg Leu 275	ctc Leu	tcc Ser	gat Asp	ttc Phe	cag Gln 280	ggc Gly	gac Asp	gtc Val	1349
aag Lys	ctt Leu 285	gaa Glu	aac Asn	aag Lys	ccg Pro	aag Lys 290	att Ile	gaa Glu	gac Asp	ggc Gly	cat His 295	gta Val	acc Thr	ctc Leu	gac Asp	1397
ttt Phe	aac Asn	gaa Glu	gcg Ala	atc Ile	tac Tyr	gga Gly	agt Ser	gcc Ala	gac Asp	ggc Gly	cag Gln	aaa Lys	aaa Lys	gtg Val	ata Ile	1445

10294.204.ST25.txt

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300          305          310          315
tcg gat gaa gtg tta aac agt atc gtg ttg aca tta acc gaa ctg cct      1493
Ser Asp Glu Val Leu Asn Ser Ile Val Leu Thr Leu Thr Glu Leu Pro
          320          325          330

gat gtg aaa agt gtg tcg gtt acc gtg aac gga aaa tcc gag ctc gtg      1541
Asp Val Lys Ser Val Ser Val Thr Val Asn Gly Lys Ser Glu Leu Val
          335          340          345

aat gaa aaa gga gaa aag ctt tcc aag ccg gtt tca aga ccg agc aag      1589
Asn Glu Lys Gly Glu Lys Leu Ser Lys Pro Val Ser Arg Pro Ser Lys
          350          355          360

gtg aac aca ggt agt ttt taagccgaaa tttttgatata actatagaaa      1637
Val Asn Thr Gly Ser Phe
          365

aagaggtgag cgatcaaagc tgcctctttc tttattcagc tttttggaag agcggaatga      1697

ttgtgaaagg tttatgtaca tacaatcgga ggtaaaaaat gagatacgat ggaagaaaaa      1757

acaatgaact gcgccctgtc acaatggacc tcgactttat tacgcatccg gaaggatcgg      1817

tcctgattac agtcggcggg acaaaggtga tatgcaacgc gtctgtggaa gaccgcgtac      1877

cgcccttttt gagaggagaa gggaagggct ggatcaccgc ggaatacagc atgctgccgc      1937

gggccacgaa ccaaaggacg atcaggggaat cgtcaaaaagg gaaaatctcc gggcggacga      1997

tggaatcca acggctgacg ggacgagctc ttcgggcggg tggtgatttg gaaaagctcg      2057

gtgagcggac gatctggacg gactgcgacg tcattcaggc ggacggaggt acg      2110

<210> 190
<211> 369
<212> PRT
<213> Bacillus licheniformis

<400> 190
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Ala Leu Leu Leu Ser Gly Cys Gly Ile Phe Gln Ser Asp Gln Ala Ser
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Glu Glu Ile Asp Pro Pro Gln Asp Ile Thr Tyr Val Lys Glu Glu Lys
35          40          45

Glu Gln Asp Lys Thr Asp Lys Thr Lys Asp Lys Thr Glu Asp Lys Gly
50          55          60

Ser Lys Thr Thr Ser Asp Asp Lys Ala Ala Gln Thr Gly Asp Thr Val
65          70          75          80

Met Arg Glu Leu Tyr Leu Ile Asp Lys Asn Gly Tyr Val Thr Ala Gln
85          90          95

Thr Leu Pro Leu Pro Lys Gln Glu Gly Thr Ala Lys Gln Ala Leu Glu
100          105          110

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10294.204.ST25.txt

Tyr Leu Val Glu Gly Gly Pro Val Ser Asn Ile Leu Pro Asn Gly Phe
 115 120 125
 Arg Ala Val Leu Pro Ala Asp Thr Thr Val Asn Val Asp Ile Lys Glu
 130 135 140
 Asp Gly Thr Ala Ile Ala Asp Phe Ser Asn Glu Phe Lys Asn Tyr Lys
 145 150 155 160
 Ala Glu Asp Glu Gln Lys Ile Val Gln Ala Ile Thr Trp Thr Leu Thr
 165 170 175
 Gln Phe Asn Ser Ile Asp Lys Val Lys Leu Arg Met Asn Gly His Asp
 180 185 190
 Leu Lys Glu Met Pro Val Asn Gly Thr Pro Ile Ser Glu Glu Leu Ser
 195 200 205
 Arg Glu Asp Gly Ile Asn Leu Asp Thr Ala Gly Val Thr Asp Ile Thr
 210 215 220
 Ala Thr Gln Pro Val Thr Val Tyr Tyr Leu Ala Glu Ser Asp Lys Gly
 225 230 235 240
 Thr Tyr Tyr Val Pro Val Thr Lys Arg Thr Ser Ala Lys Glu Lys Asp
 245 250 255
 Gln Val Thr Ala Ala Ile Lys Glu Leu Thr Glu Gly Pro Asp Asn Lys
 260 265 270
 Ser Gly Leu Leu Ser Asp Phe Gln Gly Asp Val Lys Leu Glu Asn Lys
 275 280 285
 Pro Lys Ile Glu Asp Gly His Val Thr Leu Asp Phe Asn Glu Ala Ile
 290 295 300
 Tyr Gly Ser Ala Asp Gly Gln Lys Lys Val Ile Ser Asp Glu Val Leu
 305 310 315 320
 Asn Ser Ile Val Leu Thr Leu Thr Glu Leu Pro Asp Val Lys Ser Val
 325 330 335
 Ser Val Thr Val Asn Gly Lys Ser Glu Leu Val Asn Glu Lys Gly Glu
 340 345 350
 Lys Leu Ser Lys Pro Val Ser Arg Pro Ser Lys Val Asn Thr Gly Ser
 355 360 365

Phe

<210> 191
<211> 2169
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501) .. (1667)

[illegible]

10294.204.ST25.txt

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 Val Ser Lys Tyr Leu Pro Asn Phe Pro Asn Gly Ser Lys Ile Thr Leu
 160 165 170

tat cat ttc ttg acg cac aca tcc gga att agg ggt cac aaa gaa ggc 1061
 Tyr His Phe Leu Thr His Thr Ser Gly Ile Arg Gly His Lys Glu Gly
 175 180 185

cgc gga tat att tcg ccg gaa gat tta att aaa gat atc gaa aaa cgg 1109
 Arg Gly Tyr Ile Ser Pro Glu Asp Leu Ile Lys Asp Ile Glu Lys Arg
 190 195 200

ggt gta aaa tac cca aca ggg aaa tgg gat tat aga gac tcc aat tac 1157
 Gly Val Lys Tyr Pro Thr Gly Lys Trp Asp Tyr Arg Asp Ser Asn Tyr
 205 210 215

tcg gtt ctg gca tac att gtt tcc atg gta agc ggt gaa cca gtc gac 1205
 Ser Val Leu Ala Tyr Ile Val Ser Met Val Ser Gly Glu Pro Val Asp
 220 225 230 235

caa tac atc aaa aag cat att ttt aaa cct gcc ggt atg aaa cat gca 1253
 Gln Tyr Ile Lys Lys His Ile Phe Lys Pro Ala Gly Met Lys His Ala
 240 245 250

ggc ttt tat aaa aca ttt gct aaa gag tca aat cca tcg aca gga tat 1301
 Gly Phe Tyr Lys Thr Phe Ala Lys Glu Ser Asn Pro Ser Thr Gly Tyr
 255 260 265

aaa tta aac ctg caa aaa aag ctt tat acg cct gac atg ccg gat tta 1349
 Lys Leu Asn Leu Gln Lys Lys Leu Tyr Thr Pro Asp Met Pro Asp Leu
 270 275 280

tca cag ctt tac ggg gcc ggt gat att tat atg acc gct tat gac atg 1397
 Ser Gln Leu Tyr Gly Ala Gly Asp Ile Tyr Met Thr Ala Tyr Asp Met
 285 290 295

tat ttg ttt gat aaa gca ctt tac gaa aga aaa atc att tcc aat gaa 1445
 Tyr Leu Phe Asp Lys Ala Leu Tyr Glu Arg Lys Ile Ile Ser Asn Glu
 300 305 310 315

agt ttt atg aaa atg ttt acg ccg aat aaa gca aca tac ggc atg ggc 1493
 Ser Phe Met Lys Met Phe Thr Pro Asn Lys Ala Thr Tyr Gly Met Gly
 320 325 330

ttt tat gtg tct cca gga agc tat tca agc cac ggt gtc atg ccc ggc 1541
 Phe Tyr Val Ser Pro Gly Ser Tyr Ser Ser His Gly Val Met Pro Gly
 335 340 345

tac aac ata tta aac agt ttc agt ctg aca ggg agc aga tac gtc att 1589
 Tyr Asn Ile Leu Asn Ser Phe Ser Leu Thr Gly Ser Arg Tyr Val Ile
 350 355 360

cta ttt tca aac atc caa aac aac att aag tct ttt ggc agt gtg aat 1637
 Leu Phe Ser Asn Ile Gln Asn Asn Ile Lys Ser Phe Gly Ser Val Asn
 365 370 375

aat cgg atc ttc tct att tta aat gga ttt tgaacagcag agaaagtttt 1687
 Asn Arg Ile Phe Ser Ile Leu Asn Gly Phe
 380 385

tacagctaaa agggatttta attataaatg tagaagatag atgataaatg aattttcaat 1747

ataaaggaag gtcgtcatgt cattattaac gcttagcaaa atcgtgacca ttttataggc 1807

gttgctgcat tatttatatg gacttttaaa gactcaaaac agcatgaacc tgatacgtta 1867

aagtacgcaa gttatatgtt gtctcttctt gtctttgaag tcacactgaa cgttttatgg 1927

10294.204.ST25.txt

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ggataaaaaat aaaagcaggc atttagcctg cttttatata ttcaataagt ctaaaagcaa 1987
aatatcgcaa aaacaaaaaa agctttcccc acaacaggag aaaccttgct atatcaacgt 2047
attcacttaa gcttccaagc gggctcgaac cgctgacctc ttccttacca tggaagtgct 2107
ctacctgctg agctatggaa gcattggctc cgcaggcagg attcgaacct gcgaccgatc 2167
gg 2169

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<210> 192
 <211> 389
 <212> PRT
 <213> Bacillus licheniformis

<400> 192

Met Ala Arg Thr Tyr Arg Thr Arg Ile Lys Lys Arg Lys Lys Gln Lys
1 5 10 15

Thr Lys Arg Arg Leu Ile Ile Phe Ser Phe Leu Val Val Cys Gly Leu
20 25 30

Ile Tyr Leu Ala Leu Pro Ser Gly Met Arg Asp His Gln Glu Asn Gln
35 40 45

Leu Gln Ala Thr Glu Lys Lys Ala Gln Pro Glu Ala Lys Lys Lys Pro
50 55 60

Thr Gln Asn Glu Thr Lys Lys Ser Lys Ile Val Thr Lys Asn Asp Asn
65 70 75 80

Ala Gln Leu Asp Gln Tyr Leu Lys Ser Ile Gly Phe Ser Gly Thr Ala
85 90 95

Leu Ile Val Glu Asp Gly Lys Val Val Thr Ser Lys Gly Tyr Leu Tyr
100 105 110

Ala Asn Arg Glu Glu Met Val Pro Asn Thr Pro Asp Thr Val Phe Tyr
115 120 125

Val Gly Ser Ser Gln Lys Ala Ile Ile Ala Thr Ala Ile Leu Gln Leu
130 135 140

Glu Glu Lys Gly Leu Leu Ser Val Asn Asp Pro Val Ser Lys Tyr Leu
145 150 155 160

Pro Asn Phe Pro Asn Gly Ser Lys Ile Thr Leu Tyr His Phe Leu Thr
165 170 175

His Thr Ser Gly Ile Arg Gly His Lys Glu Gly Arg Gly Tyr Ile Ser
180 185 190

Pro Glu Asp Leu Ile Lys Asp Ile Glu Lys Arg Gly Val Lys Tyr Pro
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195

200

205

Thr Gly Lys Trp Asp Tyr Arg Asp Ser Asn Tyr Ser Val Leu Ala Tyr
 210 215 220
 Ile Val Ser Met Val Ser Gly Glu Pro Val Asp Gln Tyr Ile Lys Lys
 225 230 235 240
 His Ile Phe Lys Pro Ala Gly Met Lys His Ala Gly Phe Tyr Lys Thr
 245 250 255
 Phe Ala Lys Glu Ser Asn Pro Ser Thr Gly Tyr Lys Leu Asn Leu Gln
 260 265 270
 Lys Lys Leu Tyr Thr Pro Asp Met Pro Asp Leu Ser Gln Leu Tyr Gly
 275 280 285
 Ala Gly Asp Ile Tyr Met Thr Ala Tyr Asp Met Tyr Leu Phe Asp Lys
 290 295 300
 Ala Leu Tyr Glu Arg Lys Ile Ile Ser Asn Glu Ser Phe Met Lys Met
 305 310 315 320
 Phe Thr Pro Asn Lys Ala Thr Tyr Gly Met Gly Phe Tyr Val Ser Pro
 325 330 335
 Gly Ser Tyr Ser Ser His Gly Val Met Pro Gly Tyr Asn Ile Leu Asn
 340 345 350
 Ser Phe Ser Leu Thr Gly Ser Arg Tyr Val Ile Leu Phe Ser Asn Ile
 355 360 365
 Gln Asn Asn Ile Lys Ser Phe Gly Ser Val Asn Asn Arg Ile Phe Ser
 370 375 380
 Ile Leu Asn Gly Phe
 385

<210> 193
 <211> 1492
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(989)

<400> 193
 gaacaccagc cattcgaggc agccggcaat aatcggagcg ctgccgatgg cgacgaccgt 60
 tccgacggcg attcctgaca ggctgacggc tgaaaaaag aaaggctggt aaaatgccat 120
 gctcaatgct gcgatgatca gcgttttaac gggccagccg cttcgtttca attgaccgcg 180

[illegible]

10294.204.ST25.txt

ccggtttcag tgcttgtttt ccaccccggc accggttcac actgctgaaa ttc

1492

<210> 194
 <211> 163
 <212> PRT
 <213> Bacillus licheniformis

<400> 194

Met Lys Lys Arg Thr Val Leu Phe Phe Leu Leu Ile Trp Leu Ala Gly
 1 5 10 15

Cys Ala Ser Ala Gln Glu Ala Glu Glu Gln Thr Lys Trp Val Asn Ser
 20 25 30

Glu Gln Lys Ala Ile Glu Asn Gly Ile Arg Tyr Glu Ser Ile Thr Lys
 35 40 45

Asp Asp Ile Ile Asp Lys Ile Asp Leu Asn Gly Glu Gln Val Val Val
 50 55 60

Phe Arg Phe Gly Asp Ser Glu Gly Glu Gly Ile Gly Leu Ala His Ile
 65 70 75 80

Lys Arg Glu Asn Gly Asn Tyr Gln Trp Tyr Arg Asp Leu Asn Tyr Ala
 85 90 95

Ile Val Lys Ser Asp His Pro Lys Thr Glu Asn Ala Glu Ala Ser Ala
 100 105 110

Pro Phe Thr Thr Pro Lys Gly Arg Lys Tyr Thr Leu Tyr Thr Gly Asp
 115 120 125

Ala Asp Arg Leu Asn Gly Thr Phe Glu Thr Asp Asp Gly Leu His Leu
 130 135 140

Glu Pro Val Val Asp Gln Lys Thr Gly Met Tyr Tyr Gln Ile Val Gln
 145 150 155 160

Asp Ser Asp

<210> 195
 <211> 1988
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1490)

<400> 195
 ttactgccac ctcccggaaa atttgattca aatgacctgt tgggttccgt tcattaaagg 60

accttattaa tggtacaaca tgggtataaat gagttgaatg ggaaaaatgt accgtgaaca 120

10294.204.ST25.txt

aagaatctag ttgagcgggtg gagcagggga ttccttatta tgactgcgat tttgcacatt	180
tctccattttt cctgcaagggt caaaagacat agttcttaag ttttggattt ttggtgtggt	240
tatttttttgt ttcacaaact ttaaggtaat ttttaagaaag aggcgatctt gccaacccta	300
aacaggggttt ttcgaacaga atgtcaaata gattagatat ttcataagaa caagggggaa	360
ttgtctgttt gtgatgaata aaggaggacg ggcggaattt ctgtcaggat gctcagctgg	420
gttcttagaa aaaaatgcgg ctaaatatat atttatagat tgtaaacgct gtcttgtcct	480
cgaccaacag ggggatgaag atg aag aag ctg tta gtt gtt tat gcc gtg atg	533
Met Lys Lys Leu Leu Val Val Tyr Ala Val Met	
1 5 10	
ctc tgt ttg ttt ttt ctg tat gtc tac gac tac tcc cgg ggc gat aaa	581
Leu Cys Leu Phe Phe Leu Tyr Val Tyr Asp Tyr Ser Arg Gly Asp Lys	
15 20 25	
gcc ggt tct gca gaa gaa agc agg agg cct gcg gcc gca ggc agt ctg	629
Ala Gly Ser Ala Glu Glu Ser Arg Arg Pro Ala Ala Ala Gly Ser Leu	
30 35 40	
tcc gaa aaa tac gtg atg gtc acg ttt caa tcg gga atc gaa tat tgg	677
Ser Glu Lys Tyr Val Met Val Thr Phe Gln Ser Gly Ile Glu Tyr Trp	
45 50 55	
aag agc ggt ctg aaa ggc ttt gag gat gcc gcg cag ctt ttc aac gtc	725
Lys Ser Gly Leu Lys Gly Phe Glu Asp Ala Ala Gln Leu Phe Asn Val	
60 65 70 75	
tct gtc gag tat cgg ggg gcg gcc cat tat gat gtc cat gag caa acg	773
Ser Val Glu Tyr Arg Gly Ala Ala His Tyr Asp Val His Glu Gln Thr	
80 85 90	
acc gtc ctc gag cag gtg att gca aaa aaa ccg gcg gga atc gct gtt	821
Thr Val Leu Glu Gln Val Ile Ala Lys Lys Pro Ala Gly Ile Ala Val	
95 100 105	
tcg gca ata aac cca aaa gct tta aac cct gtc atc gac aag gcg cac	869
Ser Ala Ile Asn Pro Lys Ala Leu Asn Pro Val Ile Asp Lys Ala His	
110 115 120	
gag cag ggt att ccg atc gtt tta ttt gat tca gac gcc ccg ctc agc	917
Glu Gln Gly Ile Pro Ile Val Leu Phe Asp Ser Asp Ala Pro Leu Ser	
125 130 135	
aaa gct tct aca tat atc ggc aca aat aat atg gaa gcg ggt gct gtg	965
Lys Ala Ser Thr Tyr Ile Gly Thr Asn Asn Met Glu Ala Gly Ala Val	
140 145 150 155	
gcc gca agg cga atg gcc gaa ttt ttg aat gga aag gga gaa acc gcg	1013
Ala Ala Arg Arg Met Ala Glu Phe Leu Asn Gly Lys Gly Glu Thr Ala	
160 165 170	
gtc att acc cag ccg cag cag tac aat cat cag gaa agg acg aag ggc	1061
Val Ile Thr Gln Pro Gln Gln Tyr Asn His Gln Glu Arg Thr Lys Gly	
175 180 185	
ttt gaa caa acg atc aag caa aaa tac ccg aac atg aag gtt gcc gcg	1109
Phe Glu Gln Thr Ile Lys Gln Lys Tyr Pro Asn Met Lys Val Ala Ala	
190 195 200	
gtt ttg gac gga aaa ggg gat gag ctg acg tcg aaa aaa gaa gcg gcg	1157
Val Leu Asp Gly Lys Gly Asp Glu Leu Thr Ser Lys Lys Glu Ala Ala	
205 210 215	

10294.204.ST25.txt

aag att ttg gag gaa aat ccg tcc atc aaa gga att ttc acg act gaa 1205
Lys Ile Leu Glu Glu Asn Pro Ser Ile Lys Gly Ile Phe Thr Thr Glu
220 225 230 235
gcc aat gga gcg agc ggc gtg gcc cgt gct gtg aag gag gcg gga ctt 1253
Ala Asn Gly Ala Ser Gly Val Ala Arg Ala Val Lys Glu Ala Gly Leu
240 245 250
gaa ggg gaa gta tgt atc atc ggc ttt gat aaa gac aag aaa acg ctg 1301
Glu Gly Glu Val Cys Ile Ile Gly Phe Asp Lys Asp Lys Lys Thr Leu
255 260 265
gac ggc atc aaa aac gga tcg att tcc gcg aca atg agc cag gac aca 1349
Asp Gly Ile Lys Asn Gly Ser Ile Ser Ala Thr Met Ser Gln Asp Thr
270 275 280
tgg caa atg ggc tat tgg tcg ctg cac atg ctg ttt ttc tca aat cac 1397
Trp Gln Met Gly Tyr Trp Ser Leu His Met Leu Phe Phe Ser Asn His
285 290 295
cat ctg aag cat gaa cgc ccg ctt ccg gcc gca atc gac aca ggc att 1445
His Leu Lys His Glu Arg Pro Leu Pro Ala Ala Ile Asp Thr Gly Ile
300 305 310 315
acc atc ata acg aaa gaa aat gtg gca gcc tat tat gcg aat gat 1490
Thr Ile Ile Thr Lys Glu Asn Val Ala Ala Tyr Tyr Ala Asn Asp
320 325 330
taaacgtttg atcaataatg cgccgatccg tcataagctg atcagccttc tcttggttaat 1550
cagcatgctg ccgacgatcg gcctgggcat tttatcggga tgggccgttg aaaatattat 1610
tgaaaaacag gtgatcgacc aaacactgca gctgatcggc gaagtgaaca agacggctga 1670
agtgtatgtc agccacatgc agaactgac atatttaata tcaatgaatg aagaaatgga 1730
agcgtttttt agtcataaaa aggaggatgg agaggcggat tataagcgaa ggacgttttt 1790
gcagggcctg acttctttat attccgaagc agcgggtatt ctcgttgtca atgataaggg 1850
tgagatgatc agcaatgaga tgtatgaacg cacgccgaca gatttgacaa aagaaccatg 1910
gtatcaggcg gctctcgaca atgaaggat tttcaagatg atcgggaagc ctgtcaaccg 1970
gaatatcaga agccatgt 1988

<210> 196
<211> 330
<212> PRT
<213> Bacillus licheniformis

<400> 196

Met Lys Lys Leu Leu Val Val Tyr Ala Val Met Leu Cys Leu Phe Phe
1 5 10 15

Leu Tyr Val Tyr Asp Tyr Ser Arg Gly Asp Lys Ala Gly Ser Ala Glu
20 25 30

Glu Ser Arg Arg Pro Ala Ala Ala Gly Ser Leu Ser Glu Lys Tyr Val
35 40 45

Met Val Thr Phe Gln Ser Gly Ile Glu Tyr Trp Lys Ser Gly Leu Lys
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50

55

60

Gly Phe Glu Asp Ala Ala Gln Leu Phe Asn Val Ser Val Glu Tyr Arg
 65 70 75 80
 Gly Ala Ala His Tyr Asp Val His Glu Gln Thr Thr Val Leu Glu Gln
 85 90 95
 Val Ile Ala Lys Lys Pro Ala Gly Ile Ala Val Ser Ala Ile Asn Pro
 100 105 110
 Lys Ala Leu Asn Pro Val Ile Asp Lys Ala His Glu Gln Gly Ile Pro
 115 120 125
 Ile Val Leu Phe Asp Ser Asp Ala Pro Leu Ser Lys Ala Ser Thr Tyr
 130 135 140
 Ile Gly Thr Asn Asn Met Glu Ala Gly Ala Val Ala Ala Arg Arg Met
 145 150 155 160
 Ala Glu Phe Leu Asn Gly Lys Gly Glu Thr Ala Val Ile Thr Gln Pro
 165 170 175
 Gln Gln Tyr Asn His Gln Glu Arg Thr Lys Gly Phe Glu Gln Thr Ile
 180 185 190
 Lys Gln Lys Tyr Pro Asn Met Lys Val Ala Ala Val Leu Asp Gly Lys
 195 200 205
 Gly Asp Glu Leu Thr Ser Lys Lys Glu Ala Ala Lys Ile Leu Glu Glu
 210 215 220
 Asn Pro Ser Ile Lys Gly Ile Phe Thr Thr Glu Ala Asn Gly Ala Ser
 225 230 235 240
 Gly Val Ala Arg Ala Val Lys Glu Ala Gly Leu Glu Gly Glu Val Cys
 245 250 255
 Ile Ile Gly Phe Asp Lys Asp Lys Lys Thr Leu Asp Gly Ile Lys Asn
 260 265 270
 Gly Ser Ile Ser Ala Thr Met Ser Gln Asp Thr Trp Gln Met Gly Tyr
 275 280 285
 Trp Ser Leu His Met Leu Phe Phe Ser Asn His His Leu Lys His Glu
 290 295 300
 Arg Pro Leu Pro Ala Ala Ile Asp Thr Gly Ile Thr Ile Ile Thr Lys
 305 310 315 320
 Glu Asn Val Ala Ala Tyr Tyr Ala Asn Asp

325

330

<210>	197
<211>	1677
<212>	DNA
<213>	Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1190)

[illegible]

10294.204.ST25.txt

140 145 150 155

gaa aaa aac aac ctc tac ctg aga ccg cct cgg ggc att ttc agc gag 1013
 Glu Lys Asn Asn Leu Tyr Leu Arg Pro Pro Arg Gly Ile Phe Ser Glu
 160 165 170

cgg gtg ctc gaa gaa acg aaa aag ctc ggc tat caa acg gta ttc tgg 1061
 Arg Val Leu Glu Thr Lys Lys Leu Gly Tyr Gln Thr Val Phe Trp
 175 180 185

tct gtt gct ttt gtc gat tgg aaa atc aat gcc caa aaa ggg tgg cgc 1109
 Ser Val Ala Phe Val Asp Trp Lys Ile Asn Ala Gln Lys Gly Trp Arg
 190 195 200

tat gcg tac gac aat atg atg aaa cag gct cac ccc ggc gcc atc tat 1157
 Tyr Ala Tyr Asp Asn Met Met Lys Gln Ala His Pro Gly Ala Ile Tyr
 205 210 215

ctg ctt cac acc gtc ttc agg cga tca ccg act tgaaaaaaga aggttataca 1210
 Leu Leu His Thr Val Phe Arg Arg Ser Pro Thr
 220 225 230

tttaaaagcc tcgatgacct gatgtttgaa aaatctatga tgcttgagac ccttgaaaga 1270

acaatgcccc ggtgcccagg tcgcaatgcg taaaacattt gtttttcccc cccccgaaga 1330

ccccgtctca aataatataa aatagatata aaaaaaaga atcataataa aaaaagaata 1390

tctatcccca ccaaagggag ggtgggtttg ataaccagtc gcagtcgggg gaaagtgctc 1450

aaccatggaa aaggggtgtg ttttatcatt aggcaggtgt gtgacaaagg cggtaaaata 1510

cagcgaagca tccaatgttt tattaaaagc tattagcagg atggcaaagt gcatctcgct 1570

gttcaagact ttggaggggg catcgattca aaaagatatg ccgcgcgtgt tgacaaaggc 1630

tttacatcaa caacggagca tcatgatcag gccgccacgg gaatggg 1677

<210> 198
 <211> 230
 <212> PRT
 <213> Bacillus licheniformis

<400> 198

Met Lys Arg Ile Cys Ala Ile Cys Trp Gly Ser Leu Leu Thr Leu Ala
 1 5 10 15

Phe Ser Gly Asn Ala Glu Ala Ile Ser Asn Lys Ala Ile His Trp Gly
 20 25 30

Phe Ser Lys Ser Lys Asn His Gln Pro Ala Asp Ala Gly Gln Glu Leu
 35 40 45

Thr Asn Leu Leu Gln Gln Tyr Asp Ala Phe Tyr Leu Gly Asn Thr Lys
 50 55 60

Glu Lys Thr Ile Tyr Leu Thr Phe Asp Asn Gly Tyr Glu Asn Gly Tyr
 65 70 75 80

Thr Pro Gln Val Leu Asp Val Leu Lys Lys Gln Asn Val Lys Ala Ala
 85 90 95

10294.204.ST25.txt

Phe Phe Val Thr Gly His Phe Val Lys Asp Gln Pro Glu Leu Ile Lys
 100 105 110

Arg Met Ala Glu Glu Gly His Ile Ile Gly Asn His Ser Tyr His His
 115 120 125

Pro Asp Leu Thr Thr Lys Thr Ser Arg Val Ile Gln Glu Glu Leu Glu
 130 135 140

Ser Val Asp Glu Glu Val Tyr Lys Ile Thr Gly Glu Lys Asn Asn Leu
 145 150 155 160

Tyr Leu Arg Pro Pro Arg Gly Ile Phe Ser Glu Arg Val Leu Glu Glu
 165 170 175

Thr Lys Lys Leu Gly Tyr Gln Thr Val Phe Trp Ser Val Ala Phe Val
 180 185 190

Asp Trp Lys Ile Asn Ala Gln Lys Gly Trp Arg Tyr Ala Tyr Asp Asn
 195 200 205

Met Met Lys Gln Ala His Pro Gly Ala Ile Tyr Leu Leu His Thr Val
 210 215 220

Phe Arg Arg Ser Pro Thr
 225 230

<210> 199
 <211> 4041
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(3641)

<400> 199
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 cttttcataa agtattttca gtccacacca tttatttttg gacggatttc aaacaggcat 120
 taaaagaaat ttaccgtgtt ttacagggttg acggcacgct gtttctcgct gtgcatctgg 180
 aaggggcaa at gaaaaaatcg aaaaaaaca aaggcttttc cttatactca gaagagcaaa 240
 tcaagcaact gcttgaggaa agccatttca gagacatcac ggtacatatg aacaaaaaatt 300
 actgctgcat ttctgcggtg aaatcatgaa ctttgtatga tcatcccttt caatacggaa 360
 gggatttttt atgtttgata gagttgaaac tggatcttaa atatcatatt tttgattttt 420
 aaagaaaagt attccattaa catagcaaac atggtttaat atcaaagtga acgttttttac 480
 tatattttcc ggaggtattt atg aac aaa agg atc gtg aaa agt tca att gtt 533
 Met Asn Lys Arg Ile Val Lys Ser Ser Ile Val
 1 5 10

10294.204.ST25.txt

ttc ttt ctc ctt gcc gca tta att ttt ggc cag ctg cct tta ccg aag Phe Phe Leu Leu Ala Ala Leu Ile Phe Gly Gln Leu Pro Leu Pro Lys 15 20 25	581
aca atg gca gcg gaa gac agc gtt ccg aat aac gaa acc aca ttg acc Thr Met Ala Ala Glu Asp Ser Val Pro Asn Asn Glu Thr Leu Thr 30 35 40	629
agc gcg tcc cct gtt gaa gct tcg ttt caa agc gat gac gag gtg cat Ser Ala Ser Pro Val Glu Ala Ser Phe Gln Ser Asp Asp Glu Val His 45 50 55	677
tgg tat aaa gtc aat cct tca aat cag gaa atc gca aac tat acg cac Trp Tyr Lys Val Asn Pro Ser Asn Gln Glu Ile Ala Asn Tyr Thr His 60 65 70 75	725
ttc cgc gtc aaa ttg aaa tca gat gca gag ctg aac att tcc gtc tac Phe Arg Val Lys Leu Lys Ser Asp Ala Glu Leu Asn Ile Ser Val Tyr 80 85 90	773
tcc agc ctg gaa aat gca act ggt cat caa acg ttt gac cga tac aac Ser Ser Leu Glu Asn Ala Thr Gly His Gln Thr Phe Asp Arg Tyr Asn 95 100 105	821
ggc tac tcc tat gaa aat aat cct gct tta atc gat ttt ccg att gcc Gly Tyr Ser Tyr Glu Asn Asn Pro Ala Leu Ile Asp Phe Pro Ile Ala 110 115 120	869
tgg aaa ggt cct tac tac ata aaa gta gaa aat cac cat gat gag gaa Trp Lys Gly Pro Tyr Tyr Ile Lys Val Glu Asn His His Asp Glu Glu 125 130 135	917
aac gaa acc act tca att aca gat att tct tac acc atc agc tat gaa Asn Glu Thr Thr Ser Ile Thr Asp Ile Ser Tyr Thr Ile Ser Tyr Glu 140 145 150 155	965
ggc gtc acc ctg cct ccg tca atc caa gag gca gaa gaa gag tgt ccg Gly Val Thr Leu Pro Pro Ser Ile Gln Glu Ala Glu Glu Glu Cys Pro 160 165 170	1013
gca gaa tta agc gtt tcc gaa agg gaa aca ggc aag ggc ata tta aaa Ala Glu Leu Ser Val Ser Glu Arg Glu Thr Gly Lys Gly Ile Leu Lys 175 180 185	1061
cag tta aga acg atc agg gat gaa gtt ctt tca aaa act gaa aaa gga Gln Leu Arg Thr Ile Arg Asp Glu Val Leu Ser Lys Thr Glu Lys Gly 190 195 200	1109
aaa gag ctg tct tcc ctt tac tat aaa gca gct cca ttc atc agc gca Lys Glu Leu Ser Ser Leu Tyr Tyr Lys Ala Ala Pro Phe Ile Ser Ala 205 210 215	1157
aaa atg ctc ttt aac aaa tcg atg aga gac agt gtc tac aaa gac ctg Lys Met Leu Phe Asn Lys Ser Met Arg Asp Ser Val Tyr Lys Asp Leu 220 225 230 235	1205
gtg cag ctg aag ccg ctg ttt gca gat gtc gct aaa aac gga caa gtg Val Gln Leu Lys Pro Leu Phe Ala Asp Val Ala Lys Asn Gly Gln Val 240 245 250	1253
agc gca tac tcg att acg aat gat gat caa aaa gcg atc agt cgc ctg Ser Ala Tyr Ser Ile Thr Asn Asp Asp Gln Lys Ala Ile Ser Arg Leu 255 260 265	1301
tac gaa aca gct cgc gcg tcc gtt ccc gag ccg ttg aaa aaa cag ctg Tyr Glu Thr Ala Arg Ala Ser Val Pro Glu Pro Leu Lys Lys Gln Leu 270 275 280	1349

10294.204.ST25.txt

gat caa gtc gcg aaa gac atc ggc atc gaa caa tta aca ggc agc aaa Asp Gln Val Ala Lys Asp Ile Gly Ile Glu Gln Leu Thr Gly Ser Lys 285 290 295	1397
gta tcg gct gtg ctt gaa aaa gcg ggg atg gcg aca gct tca tca agc Val Ser Ala Val Leu Glu Lys Ala Gly Met Ala Thr Ala Ser Ser Ser 300 305 310 315	1445
gcg ccc gaa aac cgt tac atc gta aaa ttg aaa gaa ggc aaa aaa ccg Ala Pro Glu Asn Arg Tyr Ile Val Lys Leu Lys Glu Gly Lys Lys Pro 320 325 330	1493
gga tct ttc aaa tct aaa gcc caa tca tcc ggc gtc cag gca tta gag Gly Ser Phe Lys Ser Lys Ala Gln Ser Ser Gly Val Gln Ala Leu Glu 335 340 345	1541
ccc ctc ggt aaa agc aaa acg gca ttt aaa gat atg tac gtt gtg gaa Pro Leu Gly Lys Ser Lys Thr Ala Phe Lys Asp Met Tyr Val Val Glu 350 355 360	1589
atg aag gaa agc cgt tct tcc gga ttc aaa gcg gcg gca aag caa tat Met Lys Glu Ser Arg Ser Ser Gly Phe Lys Ala Ala Ala Lys Gln Tyr 365 370 375	1637
cag gcg gca gcc tcc aag atc gcc aag atg cct gaa gtg gaa ttc gtc Gln Ala Ala Ala Ser Lys Ile Ala Lys Met Pro Glu Val Glu Phe Val 380 385 390 395	1685
gaa cag gtt cag caa tat gaa gca ctg tca aga gac acc caa tat cca Glu Gln Val Gln Gln Tyr Glu Ala Leu Ser Arg Asp Thr Gln Tyr Pro 400 405 410	1733
tat caa tgg tcg ctc aaa aat aac ggc aaa aac cgt gct gcg aat gct Tyr Gln Trp Ser Leu Lys Asn Asn Gly Lys Asn Arg Ala Ala Asn Ala 415 420 425	1781
gac ata caa ttt gaa cag ctt cag aag ctg atg aaa ggc aaa aag ctg Asp Ile Gln Phe Glu Gln Leu Gln Lys Leu Met Lys Gly Lys Lys Leu 430 435 440	1829
aaa gat aca gta atc gcc gtc gtt gac aca ggc gtt gat cat acc ctt Lys Asp Thr Val Ile Ala Val Val Asp Thr Gly Val Asp His Thr Leu 445 450 455	1877
gcg gat tta agc ggc agc gtc aaa aaa gac gaa ggc tat aac tat gtc Ala Asp Leu Ser Gly Ser Val Lys Lys Asp Glu Gly Tyr Asn Tyr Val 460 465 470 475	1925
ggc cgc acg gcg gat gcg atg gat gac aat ggc cac ggc aca cac gtg Gly Arg Thr Ala Asp Ala Met Asp Asp Asn Gly His Gly Thr His Val 480 485 490	1973
tca ggc atc att gca gcc gcg caa gac aac cat ttt tcg atg gcg gga Ser Gly Ile Ile Ala Ala Ala Gln Asp Asn His Phe Ser Met Ala Gly 495 500 505	2021
atc aat gct tat gcc aaa att ctg cct gtc aaa gtg ctg gat tct tca Ile Asn Ala Tyr Ala Lys Ile Leu Pro Val Lys Val Leu Asp Ser Ser 510 515 520	2069
ggc agt gga gat acg gaa cag att gca aac ggc atc atc tat gcc gcc Gly Ser Gly Asp Thr Glu Gln Ile Ala Asn Gly Ile Ile Tyr Ala Ala 525 530 535	2117
gac cac ggt gca aaa gtc atc aat tta agt ctt ggc ggg cca tac agc Asp His Gly Ala Lys Val Ile Asn Leu Ser Leu Gly Gly Pro Tyr Ser 540 545 550 555	2165

10294.204.ST25.txt

cgg gtg atg gaa tat gcg ctt aaa tat gcg gct tct aaa aat gtg acg Arg Val Met Glu Tyr 560 Ala Leu Lys Tyr 565 Ala Ser Lys Asn Val 570 Thr	2213
atc gtt gcc gcc acc gga aat gac gga gta tcg gag att tcc tac cct Ile Val Ala Ala 575 Thr Gly Asn Asp Gly 580 Val Ser Glu Ile 585 Ser Tyr Pro	2261
gca tct tcg aaa tat acg ctt tca gtc ggg gcg acc aat aat ctc gat Ala Ser Ser 590 Lys Tyr Thr Leu Ser 595 Val Gly Ala Thr 600 Asn Asn Leu Asp	2309
ctt gtc tcg gac tac tcc aat tat gga aaa ggt ctc gat atg gtg gcg Leu Val Ser Asp Tyr Ser Asn Tyr Gly Lys Gly 615 Leu Asp Met Val Ala	2357
ccg gga acc gat att cca agc ctc gtt ccg gac ggg aat gtc act tat Pro Gly Thr Asp Ile Pro Ser Leu Val Pro Asp 630 Gly Asn Val Thr Tyr 635	2405
atg agc gga aca tcg atg gcg gcg ccg cac gtg gca gct gca gca gga Met Ser Gly Thr 640 Ser Met Ala Ala Pro His Val Ala Ala Ala Gly 650	2453
ctt ctt ttg tca cag aat ccg tcc ttg aaa cca aag caa atc gca agc Leu Leu Leu Ser 655 Gln Asn Pro Ser Leu 660 Lys Pro Lys Gln Ile Ala Ser 665	2501
cta ttg acc gag acg aca gca gat gtg gca ttt gaa gag cag gat aat Leu Leu Thr 670 Glu Thr Thr Ala Asp 675 Val Ala Phe Glu Glu Gln Asp Asn 680	2549
cca aac ccg gat tat gac ctg gat ata gaa ccg gct gca caa att ccc Pro Asn Pro Asp Tyr Asp Leu 690 Ile Glu Pro Ala Ala Gln Ile Pro 695	2597
gga tat gac ttc gtc tcc ggg tgg gga agg ctg aat gtt ttt cat gca Gly Tyr Asp Phe Val Ser 705 Gly Trp Gly Arg Leu 710 Asn Val Phe His Ala 715	2645
gcc agc gtt ttt gag ctg aac atg aag gtt cat ccc gtt tta aac cgc Ala Ser Val Phe Glu Leu Asn Met Lys Val 725 His Pro Val Leu Asn Arg 730	2693
cat acg gca gtg aca ggc aca gcc aaa agc ggt gtg acg gtc aaa atc His Thr Ala Val 735 Thr Gly Thr Ala Lys 740 Ser Gly Val Thr 745 Lys Ile	2741
ttg cga ggg aag caa gta ttg ggg acg ggc acg gcc gga aaa tca ggc Leu Arg Gly Lys Gln Val Leu Gly 755 Thr Gly Thr Ala Gly 760 Lys Ser Gly	2789
gcg ttt tca gtg aaa att ccg gcc cag aag gcg ggg caa gtt ctt cat Ala Phe Ser Val Lys Ile Pro Ala Gln Lys Ala Gly 775 Gln Val Leu His 765	2837
gtc gcg gca tcg ggc cat cag gcg gaa acc tcg ctc aga acc gtc gtg Val Ala Ala Ser Gly His 785 Gln Ala Glu Thr Ser 790 Leu Arg Thr Val Val 795	2885
gaa aaa gcg ccg aaa aac ccg tcc gtc aaa cgc atc acg aac aaa gat Glu Lys Ala Pro Lys Asn Pro Ser Val Lys 805 Arg Ile Thr Asn Lys Asp 810	2933
act gcc gta acg ggt aga acg gca gcc ggc tac acg atc aaa gtg aaa Thr Ala Val Thr 815 Gly Arg Thr Ala Ala Gly Tyr Thr Ile Lys Val Lys 825	2981

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 Ser Val Lys Val Lys Ile Asn Lys Gln Lys Glu Tyr 855
 845 850

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 Val Ser Ala Ser Ala Asp Asp His Arg Glu Ser Gly Asp Val Lys Met
 860 865 870 875

acg gtg gct gac gtc atc ccg cca ggc gcc ccg aaa gtt tat cag gtt 3173
 Thr Val Ala Asp Val Ile Pro Pro Gly Ala Pro Lys Val Tyr Gln Val
 880 885 890

tcc gat aaa agt acg gtg att cag gga aaa aca gaa gca aac gcg caa 3221
 Ser Asp Lys Ser Thr Val Ile Gln Gly Lys Thr Glu Ala Asn Ala Gln
 895 900 905

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 Val Ser Ala Lys Ala Lys Gly Lys Thr Ile Ala Ser Gly Lys Ala Asn
 910 915 920

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 Gly Lys Gly Glu Tyr Lys Leu Lys Ile Ser Arg Gln Lys Ala Gly Thr
 925 930 935

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 Val Ile Gly Val Thr Ala Lys Asp Lys Ala Gly Asn Val Ser Lys Ala
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 960 965 970

aat ccg gtg aca aac aag agc acg gcc gtt aag ggg aaa gca gaa gcg 3461
 Asn Pro Val Thr Asn Lys Ser Thr Ala Val Lys Gly Lys Ala Glu Ala
 975 980 985

aac gcc gcc atc atc gtc aaa tca gga aag aaa acg atc gga acc gcc 3509
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 990 995 1000

aag gcc gat aaa aaa ggc gcg ttt ttt gtc aaa ata aaa aaa caa 3554
 Lys Ala Asp Lys Lys Gly Ala Phe Phe Val Lys Ile Lys Lys Lys Gln
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aag gca aac acc gtt tta gcg gtc act gca aaa gat aaa gcc gcc 3599
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 1020 1025 1030

aat acg agc aaa gtg agc aaa ata aaa gtc aaa aag gca aaa 3641
 Asn Thr Ser Lys Val Ser Lys Ile Lys Val Lys Lys Ala Lys
 1035 1040 1045

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4041

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Glu Ala Ser Phe Gln Ser Asp Asp Glu Val His Trp Tyr Lys Val Asn
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Lys Ser Asp Ala Glu Leu Asn Ile Ser Val Tyr Ser Ser Leu Glu Asn
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Ala Thr Gly His Gln Thr Phe Asp Arg Tyr Asn Gly Tyr Ser Tyr Glu
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Asn Asn Pro Ala Leu Ile Asp Phe Pro Ile Ala Trp Lys Gly Pro Tyr
 115 120 125

Tyr Ile Lys Val Glu Asn His His Asp Glu Glu Asn Glu Thr Thr Ser
 130 135 140

Ile Thr Asp Ile Ser Tyr Thr Ile Ser Tyr Glu Gly Val Thr Leu Pro
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Pro Ser Ile Gln Glu Ala Glu Glu Glu Cys Pro Ala Glu Leu Ser Val
 165 170 175

Ser Glu Arg Glu Thr Gly Lys Gly Ile Leu Lys Gln Leu Arg Thr Ile
 180 185 190

Arg Asp Glu Val Leu Ser Lys Thr Glu Lys Gly Lys Glu Leu Ser Ser
 195 200 205

Leu Tyr Tyr Lys Ala Ala Pro Phe Ile Ser Ala Lys Met Leu Phe Asn
 210 215 220

Lys Ser Met Arg Asp Ser Val Tyr Lys Asp Leu Val Gln Leu Lys Pro
 Page 317

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225 230 235 240
 Leu Phe Ala Asp Val₂₄₅ Ala Lys Asn Gly Gln₂₅₀ Val Ser Ala Tyr Ser₂₅₅ Ile
 Thr Asn Asp Asp₂₆₀ Gln Lys Ala Ile Ser₂₆₅ Arg Leu Tyr Glu₂₇₀ Thr Ala Arg
 Ala Ser Val₂₇₅ Pro Glu Pro Leu Lys₂₈₀ Lys Gln Leu Asp Gln₂₈₅ Val Ala Lys
 Asp Ile₂₉₀ Gly Ile Glu Gln₂₉₅ Leu Thr Gly Ser Lys Val₃₀₀ Ser Ala Val Leu
 Glu₃₀₅ Lys Ala Gly Met Ala₃₁₀ Thr Ala Ser Ser₃₁₅ Ser Ala Pro Glu Asn Arg₃₂₀
 Tyr Ile Val Lys₃₂₅ Leu Lys Glu Gly Lys Lys₃₃₀ Pro Gly Ser Phe Lys₃₃₅ Ser
 Lys Ala Gln Ser₃₄₀ Ser Gly Val Gln Ala₃₄₅ Leu Glu Pro Leu Gly₃₅₀ Lys Ser
 Lys Thr Ala₃₅₅ Phe Lys Asp Met Tyr Val Val Glu Met Lys₃₆₅ Glu Ser Arg
 Ser Ser₃₇₀ Gly Phe Lys Ala Ala₃₇₅ Ala Lys Gln Tyr Gln₃₈₀ Ala Ala Ala Ser
 Lys₃₈₅ Ile Ala Lys Met₃₉₀ Pro Glu Val Glu Phe Val₃₉₅ Glu Gln Val Gln₄₀₀
 Tyr Glu Ala Leu Ser₄₀₅ Arg Asp Thr Gln Tyr₄₁₀ Pro Tyr Gln Trp Ser₄₁₅ Leu
 Lys Asn Asn Gly₄₂₀ Lys Asn Arg Ala Ala₄₂₅ Asn Ala Asp Ile Gln₄₃₀ Phe Glu
 Gln Leu Gln₄₃₅ Lys Leu Met Lys Gly₄₄₀ Lys Lys Leu Lys Asp₄₄₅ Thr Val Ile
 Ala Val₄₅₀ Val Asp Thr Gly Val₄₅₅ Asp His Thr Leu Ala₄₆₀ Asp Leu Ser Gly
 Ser Val₄₆₅ Lys Lys Asp Glu₄₇₀ Gly Tyr Asn Tyr Val₄₇₅ Gly Arg Thr Ala Asp₄₈₀
 Ala Met Asp Asp Asn Gly His Gly Thr His₄₉₀ Val Ser Gly Ile Ile₄₉₅ Ala
 Ala Ala Gln Asp Asn His Phe Ser Met Ala Gly Ile Asn Ala Tyr Ala
 Page 318

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500

505

510

Lys Ile Leu Pro Val Lys Val Leu Asp Ser Ser Gly Ser Gly Asp Thr
 515 520 525

Glu Gln Ile Ala Asn Gly Ile Ile Tyr Ala Ala Asp His Gly Ala Lys
 530 535 540

Val Ile Asn Leu Ser Leu Gly Gly Pro Tyr Ser Arg Val Met Glu Tyr
 545 550 555 560

Ala Leu Lys Tyr Ala Ala Ser Lys Asn Val Thr Ile Val Ala Ala Thr
 565 570 575

Gly Asn Asp Gly Val Ser Glu Ile Ser Tyr Pro Ala Ser Ser Lys Tyr
 580 585 590

Thr Leu Ser Val Gly Ala Thr Asn Asn Leu Asp Leu Val Ser Asp Tyr
 595 600 605

Ser Asn Tyr Gly Lys Gly Leu Asp Met Val Ala Pro Gly Thr Asp Ile
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Pro Ser Leu Val Pro Asp Gly Asn Val Thr Tyr Met Ser Gly Thr Ser
 625 630 635 640

Met Ala Ala Pro His Val Ala Ala Ala Ala Gly Leu Leu Leu Ser Gln
 645 650 655

Asn Pro Ser Leu Lys Pro Lys Gln Ile Ala Ser Leu Leu Thr Glu Thr
 660 665 670

Thr Ala Asp Val Ala Phe Glu Glu Gln Asp Asn Pro Asn Pro Asp Tyr
 675 680 685

Asp Leu Asp Ile Glu Pro Ala Ala Gln Ile Pro Gly Tyr Asp Phe Val
 690 695 700

Ser Gly Trp Gly Arg Leu Asn Val Phe His Ala Ala Ser Val Phe Glu
 705 710 715 720

Leu Asn Met Lys Val His Pro Val Leu Asn Arg His Thr Ala Val Thr
 725 730 735

Gly Thr Ala Lys Ser Gly Val Thr Val Lys Ile Leu Arg Gly Lys Gln
 740 745 750

Val Leu Gly Thr Gly Thr Ala Gly Lys Ser Gly Ala Phe Ser Val Lys
 755 760 765

Ile Pro Ala Gln Lys Ala Gly Gln Val Leu His Val Ala Ala Ser Gly
 Page 319

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770 .

775

780

His Gln Ala Glu Thr Ser Leu Arg Thr Val Val Glu Lys Ala Pro Lys
 785 790 795 800

Asn Pro Ser Val Lys Arg Ile Thr Asn Lys Asp Thr Ala Val Thr Gly
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Arg Thr Ala Ala Gly Tyr Thr Ile Lys Val Lys Asn Ala Cys Lys Lys
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Val Ile Ala Gln Gly Arg Ala Asp Ala Ser Val Ser Val Lys Val Lys
 835 840 845

Ile Asn Lys Gln Lys Glu Tyr Ala Val Leu Tyr Val Ser Ala Ser Ala
 850 855 860

Asp Asp His Arg Glu Ser Gly Asp Val Lys Met Thr Val Ala Asp Val
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Ile Pro Pro Gly Ala Pro Lys Val Tyr Gln Val Ser Asp Lys Ser Thr
 885 890 895

Val Ile Gln Gly Lys Thr Glu Ala Asn Ala Gln Val Ser Ala Lys Ala
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Lys Gly Lys Thr Ile Ala Ser Gly Lys Ala Asn Gly Lys Gly Glu Tyr
 915 920 925

Lys Leu Lys Ile Ser Arg Gln Lys Ala Gly Thr Val Ile Gly Val Thr
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Ala Lys Asp Lys Ala Gly Asn Val Ser Lys Ala Thr Ala Val Thr Val
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Leu Asp Lys Thr Pro Pro Ser Ala Pro Lys Val Asn Pro Val Thr Asn
 965 970 975

Lys Ser Thr Ala Val Lys Gly Lys Ala Glu Ala Asn Ala Ala Ile Ile
 980 985 990

Val Lys Ser Gly Lys Lys Thr Ile Gly Thr Gly Lys Ala Asp Lys Lys
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 1025 1030 1035

Ser Lys Ile Lys Val Lys Lys Ala Lys

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1040

1045

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<400> 205

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Ala Leu Leu Val Tyr Val Val Tyr Arg Ala Val Gln Phe Leu Gly Ser
                        15           20           25

ccg gac aga agg ctg aaa tca gca cag gca aaa aag cac ttt tat gtt      629
Pro Asp Arg Arg Leu Lys Ser Ala Gln Ala Lys Lys His Phe Tyr Val
                        30           35           40

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Leu Asp Glu Gln Lys Asn Thr Arg Lys Asn Leu Lys Leu Thr Phe Lys
                        45           50           55

ggc gtg ctt ttc gaa gga gaa aaa cac att cct tca aaa gac cat ccg      725
Gly Val Leu Phe Glu Gly Glu Lys His Ile Pro Ser Lys Asp His Pro
                        60           65           70           75

ctg ttc atc cat acg att ttt gta tgg acg gaa gcg cct gaa gaa aag      773
Leu Phe Ile His Thr Ile Phe Val Trp Thr Glu Ala Pro Glu Glu Lys
                        80           85           90

ctc agc tct ttt acg gaa gaa gac ttc gcg gaa ctt gaa gaa aat att      821
Leu Ser Ser Phe Thr Glu Glu Asp Phe Ala Glu Leu Glu Glu Asn Ile
                        95           100           105

aaa gag cac tat ccc gat tgc aaa atc gac tgg gat tcg aac atc caa      869
Lys Glu His Tyr Pro Asp Cys Lys Ile Asp Trp Asp Ser Asn Ile Gln
                        110           115           120

aag tgg aaa aac aaa aaa gca gaa gag caa taaagcctcg tctgcttttt      919
Lys Trp Lys Asn Lys Lys Ala Glu Glu Gln
                        125           130

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gcggagccaa aagcagccgc aacgagccag atgcggcgct cagacaccct ccatttgcct      1099
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atgtatatcc atatgagagt caattgttca tttccccttg tttttcggtt tgggcgcctg      1219
ctgcggccgg cctccccgaa tcgttttaca tcctgctcga agaacaaaag aaaaaggccg      1279

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Lys Ser Ala Gln Ala Lys Lys His Phe Tyr Val Leu Asp Glu Gln Lys
 35 40 45

Asn Thr Arg Lys Asn Leu Lys Leu Thr Phe Lys Gly Val Leu Phe Glu
 50 55 60

Gly Glu Lys His Ile Pro Ser Lys Asp His Pro Leu Phe Ile His Thr
 65 70 75 80

Ile Phe Val Trp Thr Glu Ala Pro Glu Glu Lys Leu Ser Ser Phe Thr
 85 90 95

Glu Glu Asp Phe Ala Glu Leu Glu Glu Asn Ile Lys Glu His Tyr Pro
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 aagaaaagca gtacattggt acaggggcag acaaaaaagg cgacaaaatg tatgtttggg 240
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cgaaacaggg	ggaaatcgag	ttg aat cta gct aaa aga gta tca gcg tta aca	Leu Asn Leu Ala Lys Arg Val Ser Ala Leu Thr	1	5	10	533
cca tct gca aca ttg gca atc act gca aaa gca aaa gaa tta aaa gcg	Pro Ser Ala Thr Leu Ala Ile Thr Ala Lys Ala Lys Glu Leu Lys Ala	15	20	25	581		
gca ggg cac gac gtc atc ggt ctt ggg gca ggt gag ccg gat ttt aat	Ala Gly His Asp Val Ile Gly Leu Gly Ala Gly Glu Pro Asp Phe Asn	30	35	40	629		
acg cct gag cac atc att gaa gcg gct gtc cgt tcg atg aac gaa gga	Thr Pro Glu His Ile Ile Glu Ala Ala Val Arg Ser Met Asn Glu Gly	45	50	55	677		
cat acc aaa tac acg cct tcc ggc ggt ctt gcg gcg ctg aaa gac agc	His Thr Lys Tyr Thr Pro Ser Gly Gly Leu Ala Ala Leu Lys Asp Ser	60	65	70	725		
atc cgc gat aaa ttc aag cgc gat cag gga att gaa tac agc caa tcg	Ile Arg Asp Lys Phe Lys Arg Asp Gln Gly Ile Glu Tyr Ser Gln Ser	80	85	90	773		
gaa gtt att gtg tgc aca ggt gca aag cat gct ctt tac acc cta ttt	Glu Val Ile Val Cys Thr Gly Ala Lys His Ala Leu Tyr Thr Leu Phe	95	100	105	821		
caa gtg ctc ctc gac gaa ggg gac gaa gtg att att ccg act ccg tac	Gln Val Leu Leu Asp Glu Gly Asp Glu Val Ile Ile Pro Thr Pro Tyr	110	115	120	869		
tggtgtc agc tat cct gaa caa gtc aag ctt gca ggc ggc aaa cct gtg	Trp Val Ser Tyr Pro Glu Gln Val Lys Leu Ala Gly Gly Lys Pro Val	125	130	135	917		
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10294.204.ST25.txt

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10294.204.ST25.txt

Ala Ile Thr Ala Lys Ala Lys Glu Leu Lys Ala Ala Gly His Asp Val
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 35 40 45
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 Pro Ser Gly Gly Leu Ala Ala Leu Lys Asp Ser Ile Arg Asp Lys Phe
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 Lys Arg Asp Gln Gly Ile Glu Tyr Ser Gln Ser Glu Val Ile Val Cys
 85 90 95
 Thr Gly Ala Lys His Ala Leu Tyr Thr Leu Phe Gln Val Leu Leu Asp
 100 105 110
 Glu Gly Asp Glu Val Ile Ile Pro Thr Pro Tyr Trp Val Ser Tyr Pro
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 Glu Gln Val Lys Leu Ala Gly Gly Lys Pro Val Phe Val Glu Gly Leu
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 Thr Glu Lys Thr Lys Ala Val Ile Ile Asn Ser Pro Ser Asn Pro Thr
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 Gly Met Met Tyr Thr Glu Glu Glu Leu Lys Ala Leu Gly Glu Val Cys
 180 185 190
 Leu Arg Arg Asn Val Leu Ile Val Ser Asp Glu Ile Tyr Glu Lys Leu
 195 200 205
 Ile Tyr Gly Gly Lys Lys His Val Ser Ile Ala Gln Leu Ser Pro Glu
 210 215 220
 Leu Lys Asn Gln Thr Val Ile Ile Asn Gly Val Ser Lys Ser His Ser
 225 230 235 240
 Met Thr Gly Trp Arg Ile Gly Tyr Ala Ala Gly Ser Glu Pro Ile Ile
 245 250 255
 Lys Ala Met Thr Asn Leu Ala Ser His Ser Thr Ser Asn Pro Thr Ser
 260 265 270
 Val Ala Gln Tyr Gly Ala Ile Ala Ala Tyr Asn Gly Pro Asn Glu Pro
 275 280 285

Val Glu Glu Met Arg Lys Ala Phe Glu Glu Arg Leu Asn Lys Val Tyr
290 295 300

Glu 305 Leu Leu Val Asp Ile 310 Pro Gly Leu Thr Cys 315 Leu Lys Pro Glu Gly 320

Ala Phe Tyr Leu **Phe** Pro Asn Ala Lys **Lys** Ala Ala Glu Ser **Cys** Gly
325 330 335

Phe Ser Ser Val Asp Glu Phe Ala Glu Ala Leu Leu Glu Glu Glu Lys
340 345 350

Val Ala Ile Val Pro Gly Ser Gly Phe Gly Ala Pro Asp Asn Ile Arg
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[illegible]

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<213> Bacillus licheniformis

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Thr Tyr Ser Leu Asp Lys Asn Ile Arg Ser Glu Glu Asp Phe Asp Leu
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Ile Gly Lys Tyr Val His Ala Glu Asp Asp Gln Ile Thr Leu Glu Ile
 65 70 75 80

Lys Asp Lys Glu Leu Ile Val Pro Lys Ser Ser Arg Phe His Ser Glu
 85 90 95

Glu Asp His Asp Asp Leu Ile Gly Lys Leu Val Lys Val Glu Val Asp
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Gly Lys Thr Gln Glu Ala Glu Glu Ala Glu Leu Met Pro Gln Ser Lys
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Ala Asp Gln Asn Gly Val Tyr Glu Glu Glu Lys Asp Gly Ser Arg Lys
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Ile Ile Ala Thr Phe Val Ser Glu Ser Glu Gln Asn Ile Thr Ile Lys
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Thr Lys Ala Gly Glu Lys Thr Tyr Gln Lys Thr Ala Asp Phe Glu Arg
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Asp	Ser	Glu	Met	Leu	Leu	Lys	Glu	Ile	Lys	Glu	Met	Ser	Asp	Thr	Lys	
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Glu	Glu	Ile	Lys	Lys	Phe	Ala	Glu	Glu	Trp	His	Gln	Tyr	Ser	Thr	Gly	
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10294.204.ST25.txt

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 35 40 45
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 50 55 60
 Ala Val Ser Leu Ala Asp Glu Tyr Pro Ser Val Arg Ser Gln Val Ile
 65 70 75 80
 Asn Glu Lys Asn Pro Ile His Leu Ile Lys Ala Val Tyr Arg Met Phe
 85 90 95
 Arg Cys Lys Phe Val Leu Thr Asp Asn Tyr Phe Leu Leu Thr Ser Val
 100 105 110
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 115 120 125
 Gly Ala Leu Lys Lys Phe Gly Leu Glu Asp Ile Gly Asn Arg Tyr Arg
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 Ser Ala Gly Asp Ile Lys Arg Phe Lys Lys Val Tyr Arg Ser Phe Asp
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 His Ile Val Val Gly Ser Glu Lys Met Ala Asp Ile Phe Lys Arg Ser
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 Phe Gly Leu Gly Asp Asp Arg Phe Leu Arg Thr Gly Val Pro Leu Thr
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 Asp Glu Tyr Phe His Ala Gly Arg Gln Thr Ala Glu Arg Pro Asp Gln
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 Lys Val Ile Leu Tyr Ala Pro Thr Tyr Arg Asp Tyr Cys Leu Thr Ser
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 Val Arg Leu Pro Phe Ser Lys Glu Gln Leu Ser Gly Glu Leu Gln Gly
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 Glu Phe Leu Leu Leu Val Lys Leu His Pro Ala Val Arg Glu Gln Ile

10294.204.ST25.txt
250

245

255

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Ser ^{Val} Ala Phe Glu Tyr ^{Ala} Leu Leu Asn Lys ^{Pro} Ile Leu Phe Phe
290 295 300

Thr Tyr Asp Met Ala ^{Glu} Tyr Asn Glu Lys ^{Arg} Gly Leu Ile Asp ^{Asp}
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Phe Glu Ala Val ^{Ile} Pro Gly Lys Ala ^{Cys} Met Asp Ser Glu ^{Met} Leu
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Phe Ala ^{Glu} Glu Trp His Gln Tyr Ser Thr Gly Asp ^{Ala} Ser Met Arg
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ccaatatgca accagatcgt tcttttacac gtcttgtcat aaacgtggta aaatttaa 360
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Val Thr Glu Ser Gln His Asp Pro Ala Glu Ile

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Ala Val Phe Thr Leu Phe Ala Ala Leu Ile Val Lys Leu Gly Leu Val	30 35	40	
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Gln Ile Val Asn Gly Glu Ala Tyr Glu Gln Glu Ala Ser Lys Thr Glu	45 50	55	
gcg aaa att gcg tca tac ccg gca ccg cgg ggt aaa atg tat gac aga			725
Ala Lys Ile Ala Ser Tyr Pro Ala Pro Arg Gly Lys Met Tyr Asp Arg	60 65 70	75	
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Tyr Gly Arg Val Val Val Asp Asn Gln Ser Val Pro Ala Ile Thr Tyr	80 85	90	
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Thr Met Met Thr Ser Thr Lys Thr Glu Glu Lys Ile Ser Thr Ala Lys	95 100	105	
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Lys Leu Ala Glu Leu Ile Asp Ile Asp Thr Ser Phe Leu Lys Glu Arg	110 115	120	
gat ctg aaa gat tac tgg ctt gcc aga cac ccg aaa aaa gct gct gca			917
Asp Leu Lys Asp Tyr Trp Leu Ala Arg His Pro Lys Lys Ala Ala Ala	125 130	135	
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Leu Leu Lys Asp Ser Glu Lys Thr Leu Lys Ser Asp Gln Thr Tyr Lys	140 145	150 155	
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Met Pro Ala Asn Asp Leu Thr Tyr Glu Glu Val Ser Arg Val Ser Glu	220 225	230 235	
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Lys Tyr Pro Tyr Glu Lys Thr Leu Tyr Ser Ile Phe Gly Gly Val Thr	255 260	265	
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Ser Lys Asp				
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10294.204.ST25.txt

Ser Arg Leu Trp Arg Ile Asn Leu Tyr Phe Phe Ala Val Phe Thr Leu
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 Phe Ala Ala Leu Ile Val Lys Leu Gly Leu Val Gln Ile Val Asn Gly
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 Glu Ala Tyr Glu Gln Glu Ala Ser Lys Thr Glu Ala Lys Ile Ala Ser
 50 55 60
 Tyr Pro Ala Pro Arg Gly Lys Met Tyr Asp Arg Tyr Gly Arg Val Val
 65 70 75 80
 Val Asp Asn Gln Ser Val Pro Ala Ile Thr Tyr Thr Met Met Thr Ser
 85 90 95
 Thr Lys Thr Glu Glu Lys Ile Ser Thr Ala Lys Lys Leu Ala Glu Leu
 100 105 110
 Ile Asp Ile Asp Thr Ser Phe Leu Lys Glu Arg Asp Leu Lys Asp Tyr
 115 120 125
 Trp Leu Ala Arg His Pro Lys Lys Ala Ala Ala Leu Leu Lys Asp Ser
 130 135 140
 Glu Lys Thr Leu Lys Ser Asp Gln Thr Tyr Lys Leu Gln Val Asp Arg
 145 150 155 160
 Val Pro Ala Glu Glu Ile Lys Ala Leu Glu Lys Asp Lys Asp Glu Leu
 165 170 175
 Lys Val Ala Ala Ile Phe Arg Arg Phe Ser Gly Gly Tyr Ala Tyr Glu
 180 185 190
 Pro Gln Ile Val Lys Ala Met Ser Pro Lys Thr Ala Gly Lys Asn Asp
 195 200 205
 Ala Gln Leu Leu Asp Glu Lys Ala Ser Lys Gln Met Pro Ala Asn Asp
 210 215 220
 Leu Thr Tyr Glu Glu Val Ser Arg Val Ser Glu His Leu Glu Glu Leu
 225 230 235 240
 Pro Gly Val Asp Val Ile Met Asp Trp Thr Arg Lys Tyr Pro Tyr Glu
 245 250 255
 Lys Thr Leu Tyr Ser Ile Phe Gly Gly Val Thr Thr Pro Glu Gln Gly
 260 265 270
 Leu Ile Lys Asp Arg Glu Asp Phe Tyr Leu Thr Arg Gly Tyr Ala Arg
 275 280 285

10294.204.ST25.txt

Asn Asp Arg Val Gly Lys Ser Tyr Leu Glu Tyr Gln Tyr Glu Glu Tyr
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 Leu Asn Pro Lys Lys Ala Lys Val Gln Tyr Thr Glu Asn Arg Ser Gly
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 Lys Val Ile Ser Gln Glu Thr Val Asp Glu Gly Arg Arg Gly Tyr Asp
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 Ile Glu Glu Glu Leu Asn Lys Phe Arg Gly Ser Asn Tyr Met Leu Asp
 355 360 365
 Arg Ala Phe Val Val Met Met Asp Pro Asn Asn Gly Asp Ile Leu Ser
 370 375 380
 Met Ala Gly Lys Arg Ile Val Asp Gly Lys Ile Thr Asp Tyr Ala Ile
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 Gly Ala Phe Thr Thr Gln Tyr Glu Met Gly Ser Ala Val Lys Gly Ala
 405 410 415
 Thr Val Leu Ala Gly Tyr Gln Asp Gly Met Pro His Gly Gln Ser Tyr
 420 425 430
 Leu Asp Gln Glu Leu Ser Phe Ala Gly Gly Val Lys Lys Gly Ser Tyr
 435 440 445
 Arg Gly Asn Thr Ile Gly Trp Ala Asn Glu Val Arg Ala Leu Glu Lys
 450 455 460
 Ser Ser Asn Val Tyr Met Phe Tyr Val Ala Met Arg Met Ala Gly Ile
 465 470 475 480
 Thr Tyr Val Pro Asn Gly Pro Leu Pro Ala Asn Leu Glu Asp Leu Lys
 485 490 495
 Lys Met Arg Tyr Tyr Phe Asn Gln Phe Gly Leu Gly Val Lys Thr Gly
 500 505 510
 Ile Asp Leu Pro Gln Glu Ser Ala Gly Met Gln Thr Asn Pro Lys Ile
 515 520 525
 Val Gly Gly Leu Leu Leu Asp Glu Ala Ile Gly Gln Phe Asp Thr Tyr
 530 535 540
 Thr Pro Leu Gln Leu Ala Gln Tyr Val Ser Thr Ile Ala Asn Gly Gly
 545 550 555 560

10294.204.ST25.txt

Tyr Arg Leu Gln Pro Arg Val Val Lys Ser Ile His Gln Pro Glu Ser
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Glu Lys Leu Gly Pro Val Ile Glu Glu Arg Ser Ala Asn Val Leu Asn
580 585 590

Arg Ile Asn Asn Ser Gln Ser Asp Ile Ala Ile Val Lys Gln Gly Phe
595 600 605

Lys Arg Val Thr Gln Thr Gly Thr Ala Ala Gly Ala Phe Gly Ser Leu
610 615 620

Asp Val Ser Gly Lys Thr Gly Thr Ala Gln Thr Gln Tyr Tyr Gly Thr
625 630 635 640

Asn Arg Asn Trp Trp Gly Thr Arg Thr Tyr Asn Ile Thr Phe Ala Gly
645 650 655

Tyr Tyr Pro Ser Glu Asn Pro Gln Val Ala Phe Ser Val Val Val Pro
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ccgaatccac gccagtcaat gccgatacag cggatatccct ttcgcgaaag atcgtcaaat 240
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cccatgccgt cgccccgat catgtcttta ccataagata ctccaagat gtaaataagg 420
gaatgtctcc gagggctgaa catgaagaat ttgaaaaggc gtgactgggt aaactatttc 480
aagaaacgga ggggtgttca atg atg gca ctt ctg aga agt ctg gcg ata tcg 533
Met Met Ala Leu Leu Arg Ser Leu Ala Ile Ser
1 5 10

10294.204.ST25.txt

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 Phe Val Leu Ile Leu Pro Ala Ala Ala Tyr Ala Gln Val Pro Tyr
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 Pro Cys Ser Val Val Leu Asp Pro Val Arg Asp Ile Pro Asn Ala Arg
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 gga acg gct tta att gcg aaa gtg aag aaa ccg tat acc gaa gcc ccc 677
 Gly Thr Ala Leu Ile Ala Lys Val Lys Lys Pro Tyr Thr Glu Ala Pro
 45 50 55
 ggg agt cct gtc agg gaa agg cag agt gtc ggc atc tac gct gat tgg 725
 Gly Ser Pro Val Arg Glu Arg Gln Ser Val Gly Ile Tyr Ala Asp Trp
 60 65 70 75
 ctt ccg gac cct gct tca ttt gga gat tat gat caa ttt gaa gga att 773
 Leu Pro Asp Pro Ala Ser Phe Gly Asp Tyr Asp Gln Phe Glu Gly Ile
 80 85 90
 gcc cgg ata cct gac cag atc agc tgg cgt ttc acc atg cat caa gtc 821
 Ala Arg Ile Pro Asp Gln Ile Ser Trp Arg Phe Thr Met His Gln Val
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 Gln Glu Asp Ala Pro Ser Trp Phe Gly Gly Ser Pro Trp Ala Gly Lys
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 Phe Asp Glu Ile Ser Ser Glu Leu Thr Val Asn Thr Gln Val Glu Val
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 cgc cct ttc aat tcg aag acg aaa aag gcc ggc gaa gct gtt ttg cgt 965
 Arg Pro Phe Asn Ser Lys Thr Lys Lys Ala Gly Glu Ala Val Leu Arg
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 ggg aat ttg caa gga tgc agg agc taacccaaaaa ggccgtaaaa gctccatggg 1019
 Gly Asn Leu Gln Gly Cys Arg Ser
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10294.204.ST25.txt

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Leu Asp Pro Val Arg Asp Ile Pro Asn Ala Arg Gly Thr Ala Leu Ile
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Ala Lys Val Lys Lys Pro Tyr Thr Glu Ala Pro Gly Ser Pro Val Arg
50 55 60

Glu Arg Gln Ser Val Gly Ile Tyr Ala Asp Trp Leu Pro Asp Pro Ala
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Ser Phe Gly Asp Tyr Asp Gln Phe Glu Gly Ile Ala Arg Ile Pro Asp
85 90 95

Gln Ile Ser Trp Arg Phe Thr Met His Gln Val Gln Glu Asp Ala Pro
100 105 110

Ser Trp Phe Gly Gly Ser Pro Trp Ala Gly Lys Phe Asp Glu Ile Ser
115 120 125

Ser Glu Leu Thr Val Asn Thr Gln Val Glu Val Arg Pro Phe Asn Ser
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Cys Arg Ser

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gtatccggca tcgtcgctt aatgagggaa gccaatccgg acctcacagt cgatgaaatc 180
gagcgcaccc tgctgaaaac ggcgacgcct ctgactgaca aaacgtttta aaaatccccg 240
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catcaaagtc agacaaggcg tccacaagga ggggggggaca ggaaaattca gctaatttca 480

10294.204.ST25.txt

10294.204.ST25.txt																533
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Thr	Ile	Leu	Ser	Gly	Leu	Leu	Ile	Gly	Ser	Leu	Phe	Met	Pro	Ala	Val	
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Ser	Asp	Ala	Ala	Ala	Lys	Pro	Ala	Leu	Thr	Ser	Met	Lys	Glu	Gln	Ala	
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Ala	Ala	Gly	Lys	Gly	Lys	Ile	Ser	Lys	Thr	Leu	Val	Lys	Gln	Phe	Lys	
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Lys	Glu	Asp	Gln	Val	Thr	Phe	Leu	Ile	Lys	Leu	Lys	Asp	Gln	Val	Asp	
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Ala	Leu	Arg	Val	Lys	Ala	Asp	Glu	Ser	Gln	Ser	Asp	Leu	Lys	Arg	Tyr	
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Leu	Lys	Lys	Gln	Glu	Lys	Gln	Gly	Asp	Val	Lys	Lys	Ile	Arg	Ser	Tyr	
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Tyr	Ile	Val	Asn	Gly	Met	Ala	Val	His	Ala	Thr	Lys	Glu	Val	Met	Glu	
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Gln	Val	Ala	Ala	Phe	Pro	Glu	Val	Glu	Lys	Val	Leu	Pro	Asn	Glu	Lys	
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Ile	Asp	Thr	Gly	Val	Gln	Trp	Asp	His	Pro	Ala	Leu	Lys	Glu	Lys	Tyr	
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Arg	Gly	Tyr	Asp	Pro	Gln	His	Pro	Asp	Gln	Pro	Asn	His	Glu	Phe	Ser	
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Trp	Tyr	Asp	Ala	Val	Ser	Gly	Ala	Ser	Glu	Pro	Phe	Asp	Asp	Leu	Glu	
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10294.204.ST25.txt

cac His	ggc Gly	acg Thr	cat His	gta Val	acc Thr	ggg Gly	acg Thr	atg Met	gtc Val	ggc Gly	tca Ser	gag Glu	cct Pro	gac Asp	ggc Gly	1349
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10294.204.ST25.txt

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gct gcc gag tac agc ggc aag aca tca gaa tgg aaa gac gga cag atc Ala Ala Glu Tyr Ser Gly Lys Thr Ser Glu Trp Lys Asp Gly Gln Ile 735 740 745	2741
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Val	Ser	Val	Leu	Glu	Thr	Gly	Lys	Ser	Thr	Tyr	Ser	Asn	Gln	Ala	Thr	
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Glu	Ala	Tyr	Gly	Tyr	Glu	Ser	Thr	Ala	Gln	Thr	Val	Lys	Ile	Glu	Ser	
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His	Ala	Lys	Leu	Tyr	Ile	Val	Glu	Asp	Ala	Ala	Val	Lys	Pro	Val	Gln	
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															3509	
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Trp	Ala	Phe	Tyr	Glu	Ser	Gly	Asn	Gly	Leu	Ala	Val	Lys	Met	Thr		
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Ala	Val	Glu	Val	Tyr	Asp	Ala	Ser	Gly	Glu	Lys	Gly	Ser	Pro	Gly		
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10294.204.ST25.txt															
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aaa Lys	gac Asp 1095	ttt Phe	tac Tyr	ctc Leu	gta Val	tac Tyr 1100	gtc Val	cag Gln	aaa Lys	gag Glu	gat Asp 1105	ctg Leu	gcc Ala	aac Asn	3824
tca Ser	cct Pro 1110	gga Gly	ctt Leu	gct Ala	aca Thr	gac Asp 1115	gaa Glu	gac Asp	gga Gly	gaa Glu	tat Tyr 1120	tcc Ser	ggc Gly	cgc Arg	3869
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gtg Val	cct Pro 1155	gtg Val	att Ile	acg Thr	tct Ser	cct Pro 1160	aaa Lys	gac Asp	gga Gly	ttc Phe	atc Ile 1165	acc Thr	aac Asn	caa Gln	4004
aag Lys	aac Asn 1170	gct Ala	gtc Val	att Ile	gaa Glu	ggg Gly 1175	aca Thr	tcc Ser	tcg Ser	ccg Pro	aat Asn 1180	acg Thr	acc Thr	gtt Val	4049
cat His	ctc Leu 1185	ttt Phe	aac Asn	ggg Gly	gat Asp	gaa Glu 1190	gaa Glu	gcc Ala	gga Gly	aca Thr	gcg Ala 1195	gaa Glu	acg Thr	gcg Ala	4094
gca Ala	gac Asp 1200	ggc Gly	act Thr	ttc Phe	tca Ser	aaa Lys 1205	gaa Glu	ata Ile	ccg Pro	ttg Leu	aat Asn 1210	aaa Lys	ggg Gly	gaa Glu	4139
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gct Ala	tca Ser 1230	gaa Glu	ccg Pro	gtc Val	cgg Arg	atc Ile 1235	gtc Val	ctt Leu	gac Asp	cag Gln	aaa Lys 1240	aag Lys	ccg Pro	aag Lys	4229
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acc Thr	gtc Val 1260	acc Thr	gtg Val	aaa Lys	gga Gly	aca Thr 1265	gta Val	tca Ser	gac Asp	gat Asp	cac His 1270	tta Leu	gaa Glu	tct Ser	4319
gtt Val	cat His 1275	gta Val	aac Asn	ggc Gly	aaa Lys	aaa Lys 1280	gca Ala	gct Ala	gtt Val	gac Asp	aat Asn 1285	ggc Gly	gaa Glu	tat Tyr	4364
tct Ser	gca Ala 1290	agg Arg	att Ile	atg Met	ctt Leu	gac Asp 1295	aac Asn	ggc Gly	aaa Lys	aat Asn	gaa Glu 1300	atc Ile	aaa Lys	gta Val	4409
acg Thr	gca Ala 1305	tcg Ser	gat Asp	gcg Ala	gca Ala	ggc Gly 1310	aac Asn	aaa Lys	acg Thr	acc Thr	aaa Lys 1315	aag Lys	gtc Val	acg Thr	4454
gta Val	gat Asp 1320	gtc Val	aac Asn	ttt Phe	gaa Glu	ggc Ala 1325	ccg Pro	caa Gln	atc Ile	acc Thr	ggc Gly 1330	ttg Leu	aaa Lys	ccg Pro	4499

10294.204.ST25.txt

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Ala Glu Asp Leu Glu Leu Lys Thr Gly Glu Thr Val Lys Ile Glu
1335 1340 1345

ttt gaa agc gcc gct gat ttg gat gct gtc ttt gtg atc aga atg 4589
Phe Glu Ser Ala Ala Asp Leu Asp Ala Val Phe Val Ile Arg Met
1350 1355 1360

ccg ctg acc aat ttc aaa acc gct gcc caa aac gta acg gag ctg 4634
Pro Leu Thr Asn Phe Lys Thr Ala Ala Gln Asn Val Thr Glu Leu
1365 1370 1375

ccg atc aga gaa gtc tca aaa gga aaa tat gaa gga tat tgg acc 4679
Pro Ile Arg Glu Val Ser Lys Gly Lys Tyr Glu Gly Tyr Trp Thr
1380 1385 1390

gct act tca act gca aaa gca aaa gga gcg gaa atc gag gtc atc 4724
Ala Thr Ser Thr Ala Lys Ala Lys Gly Ala Glu Ile Glu Val Ile
1395 1400 1405

gtc aga gat gat tac ggc aat gaa acg aga caa acg gca aaa ggc 4769
Val Arg Asp Asp Tyr Gly Asn Glu Thr Arg Gln Thr Ala Lys Gly
1410 1415 1420

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Lys Leu Tyr Ile Asn Glu Lys Leu Lys
1425 1430

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aatgtacgat ttacgcaaca ttaattgaca gactttacct ttgggcttga tttatactta 4936

ggaaaacaaa cactaaggctc accgagccgc agaaagggga aggatgtgga aatctattta 4996

gatgcatat ggctgttaaa cttttgtttt gacttgctgc ttttaatgat gaccgcattt 5056

attttaaagc gaagggttaa aaagcggagg ctgacccatg gggcattttgt cgcgtcaagc 5116

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<213> Bacillus licheniformis

<400> 218

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20 25 30

Lys Pro Ala Leu Thr Ser Met Lys Glu Gln Ala Ala Ala Gly Lys Gly
35 40 45

Lys Ile Ser Lys Thr Leu Val Lys Gln Phe Lys Lys Glu Asp Gln Val
50 55 60

10294.204.ST25.txt

Thr Phe Leu Ile Lys Leu Lys Asp Gln Val Asp Thr Pro Lys Val Ala
 65 70 75 80
 Lys Gln Ala Glu Lys Asn Ala Lys Lys Lys Ser Leu Ser Ala Ala Lys
 85 90 95
 Thr Glu Tyr Gln Lys Arg Ser Ala Val Val Ser Ala Leu Arg Val Lys
 100 105 110
 Ala Asp Glu Ser Gln Ser Asp Leu Lys Arg Tyr Leu Lys Lys Gln Glu
 115 120 125
 Lys Gln Gly Asp Val Lys Lys Ile Arg Ser Tyr Tyr Ile Val Asn Gly
 130 135 140
 Met Ala Val His Ala Thr Lys Glu Val Met Glu Gln Val Ala Ala Phe
 145 150 155 160
 Pro Glu Val Glu Lys Val Leu Pro Asn Glu Lys Arg Gln Leu Ile Lys
 165 170 175
 Pro Thr Lys Gln Ser Val Lys Lys Ser Ala Ala Lys Asp Glu Lys Glu
 180 185 190
 Ile Glu Trp Asn Ile Asn Arg Val Asp Ala Pro Lys Ala Trp Lys Leu
 195 200 205
 Gly Tyr Asp Gly Ser Gly Thr Val Val Ala Ser Ile Asp Thr Gly Val
 210 215 220
 Gln Trp Asp His Pro Ala Leu Lys Glu Lys Tyr Arg Gly Tyr Asp Pro
 225 230 235 240
 Gln His Pro Asp Gln Pro Asn His Glu Phe Ser Trp Tyr Asp Ala Val
 245 250 255
 Ser Gly Ala Ser Glu Pro Phe Asp Asp Leu Glu His Gly Thr His Val
 260 265 270
 Thr Gly Thr Met Val Gly Ser Glu Pro Asp Gly Gln Asn Gln Ile Gly
 275 280 285
 Val Ala Pro Gly Ala Lys Trp Ile Ala Val Lys Ala Phe Ser Asp Asp
 290 295 300
 Gly Gly Thr Asp Glu Asp Leu Ile Ala Ala Gly Glu Trp Ile Leu Ala
 305 310 315 320
 Pro Lys Asp Lys Asp Gly Asn Pro His Pro Glu Met Ala Pro Asp Val
 325 330 335

10294.204.ST25.txt

Val Asn Asn Ser Trp Ser Gly Gly Ala Gly Ile Asp Glu Phe Tyr Arg
 340 345 350
 Asp Ile Val Lys Ala Trp Arg Ala Ala Gly Ile Phe Pro Glu Phe Ser
 355 360 365
 Ala Gly Asn Val Asp Phe Ala Asn Pro Gly Gly Pro Ala Ser Ile Ala
 370 375 380
 Asn Pro Ala Asn Tyr Pro Glu Ala Phe Ala Thr Gly Ala Thr Asp Ile
 385 390 395 400
 Asp Asn Arg Leu Ala Asp Phe Ser Leu Gln Gly Pro Ser Pro Tyr Asp
 405 410 415
 Glu Thr Lys Pro Glu Ile Ser Ala Pro Gly Val Asn Ile Arg Ser Ser
 420 425 430
 Val Pro Gly Ser Gly Tyr Gln Asp Gly Trp Asp Gly Thr Ser Met Ala
 435 440 445
 Gly Pro His Val Ala Ala Ala Ala Ala Leu Ile Lys Gln Ala Asp Ser
 450 455 460
 Ser Ile Thr Val Asp Glu Thr Glu Lys Ile Leu Met Glu Thr Ala Thr
 465 470 475 480
 Pro Leu Thr Asp Ser Lys Phe Thr Glu Ser Pro Asn Asn Gly Tyr Gly
 485 490 495
 His Gly Leu Val Asn Val Phe Asp Ala Val Ser Ala Val Thr Asp Gly
 500 505 510
 Leu Gly Arg Ala Glu Gly Gln Val Gly Lys Glu Gly Glu Asp Lys Ser
 515 520 525
 Pro Pro Ala Leu Asn His Gln Glu Ile Thr Glu Ile Tyr Ser Gly Ser
 530 535 540
 Glu Thr Pro Leu Lys Ala Asp Val Glu Asp Asp Val Ser Ile Ile Ser
 545 550 555 560
 Val Lys Leu Ser Tyr Lys Thr Asp Asp Ala Asp Trp Glu Thr Ile Ala
 565 570 575
 Ala Lys Gln Thr Ser Gly Asp Tyr Lys Lys Gly Thr Tyr Glu Ala Ala
 580 585 590
 Val Thr Val Ser Glu Gly Lys Thr Leu Ser Tyr Lys Trp Ile Val Thr
 595 600 605

10294.204.ST25.txt

Asp Phe Gly Gly Asn Lys Thr Glu Ser Lys Val Tyr Glu Val Pro Ile
610 615 620

Ser Pro Ala Val Thr Thr Gly Tyr Lys Gln Asp Phe Glu Asn Ser Ala
625 630 635 640

Ser Gly Trp Leu Thr Ser Gly Val Lys Asn Ser Trp Glu Arg Gly Ile
645 650 655

Pro Gln Ser Gly Pro Asn Ala Ala Ala Ser Gly Lys Asn Val Phe Ala
660 665 670

Thr Asn Leu Thr Gly Pro Tyr Glu Ser Ser Ala Asn Met Asn Leu Leu
675 680 685

Met Pro Pro Val Ser Val Pro Lys Asn Gln Lys Leu Tyr Leu Thr Tyr
690 695 700

Lys Tyr Trp Arg Asp Ile Glu Glu Asp Phe Asp Tyr Gly Phe Val Tyr
705 710 715 720

Val Gln Pro Glu Gly Lys Gly Glu Trp Ile Pro Ala Ala Glu Tyr Ser
725 730 735

Gly Lys Thr Ser Glu Trp Lys Asp Gly Gln Ile Asp Leu Ser Glu Tyr
740 745 750

Gly Gly Gln Thr Ile Lys Val Met Phe Asn Leu Gln Ser Asp Asp Ser
755 760 765

Ile Glu Gly Asp Gly Leu Tyr Ile Asp Asp Val Ala Leu Val Lys Glu
770 775 780

Val Lys Ser Ala Gly Thr Lys Lys Arg Leu Gly Val Glu Lys Gln Pro
785 790 795 800

Ala Lys Met Lys Asp Lys Lys Thr Lys Lys Arg Met Ile Asp Pro Lys
805 810 815

Lys Ala Lys Pro Ala Glu Ala Leu Gln Glu Lys Thr Glu Thr Lys Lys
820 825 830

Ala Ala Pro Ala Val Leu Pro Val Arg Ala Gln Val Ser Val Leu Glu
835 840 845

Thr Gly Lys Ser Thr Tyr Ser Asn Gln Ala Thr Gly Ala Tyr Ser Leu
850 855 860

Ala His Ala Pro Gly Thr Tyr Thr Leu Lys Ala Glu Ala Tyr Gly Tyr
865 870 875 880

10294.204.ST25.txt

Glu Ser Thr Ala Gln Thr Val Lys Ile Glu Ser Asp Lys Thr Thr Thr
 885 890 895
 Ala Asp Phe Val Leu Lys Glu Leu Lys Lys Gly Thr Leu Thr Gly Thr
 900 905 910
 Ile Lys Asn Lys Lys Thr Gly Glu Pro Val Arg His Ala Lys Leu Tyr
 915 920 925
 Ile Val Glu Asp Ala Ala Val Lys Pro Val Gln Thr Asp Asp Asp Gly
 930 935 940
 Ser Tyr Ser Leu Thr Ala Tyr Glu Gly Ser Tyr Thr Val Lys Val Ser
 945 950 955 960
 Ala Asn Gly Tyr Tyr Ser Ser Glu Phe Ser Val Asp Leu Lys Gly Asp
 965 970 975
 Val Ser Lys Asp Ile Asp Leu Asp Pro Phe Ile Gly Tyr Pro Gly Glu
 980 985 990
 Ile Gly Tyr Asp Asp Gly Thr Gly Glu Asn Ala Trp Ala Phe Tyr Glu
 995 1000 1005
 Ser Gly Asn Gly Leu Ala Val Lys Met Thr Leu Glu Asn Gly Gln
 1010 1015 1020
 Glu Lys Ala Met Leu Lys Gly Gly Leu Phe Lys Phe Trp Asp Thr
 1025 1030 1035
 Glu Phe Pro Asp Pro Gly Gly Thr Asp Phe Ala Val Glu Val Tyr
 1040 1045 1050
 Asp Ala Ser Gly Glu Lys Gly Ser Pro Gly Lys Lys Ile Ala Gly
 1055 1060 1065
 Pro Phe Lys Ala Glu Ala Leu Arg Thr Gly Glu Trp Thr Thr Val
 1070 1075 1080
 Asp Leu Gly Asp Glu Gly Ile Ile Val Gly Lys Asp Phe Tyr Leu
 1085 1090 1095
 Val Tyr Val Gln Lys Glu Asp Leu Ala Asn Ser Pro Gly Leu Ala
 1100 1105 1110
 Thr Asp Glu Asp Gly Glu Tyr Ser Gly Arg Asn Trp Gln Tyr Thr
 1115 1120 1125
 Asp Gly Ser Trp Ser Lys Ala Pro Ser Asp Gln Gly Asn Phe Met
 1130 1135 1140

10294.204.ST25.txt

Ile Arg Ala Leu Val Asp Tyr Glu Leu Ser Val Pro Val Ile Thr
 1145 1150 1155

Ser Pro Lys Asp Gly Phe Ile Thr Asn Gln Lys Asn Ala Val Ile
 1160 1165 1170

Glu Gly Thr Ser Ser Pro Asn Thr Thr Val His Leu Phe Asn Gly
 1175 1180 1185

Asp Glu Glu Ala Gly Thr Ala Glu Thr Ala Ala Asp Gly Thr Phe
 1190 1195 1200

Ser Lys Glu Ile Pro Leu Asn Lys Gly Glu Asn Val Ile Thr Ala
 1205 1210 1215

Lys Ser Ser Ser Ala Ser Gly Thr Thr Asp Ala Ser Glu Pro Val
 1220 1225 1230

Arg Ile Val Leu Asp Gln Lys Lys Pro Lys Leu Thr Ile Asp Thr
 1235 1240 1245

Pro Glu Ser Gly Ser Lys Leu Asn Lys Glu Thr Val Thr Val Lys
 1250 1255 1260

Gly Thr Val Ser Asp Asp His Leu Glu Ser Val His Val Asn Gly
 1265 1270 1275

Lys Lys Ala Ala Val Asp Asn Gly Glu Tyr Ser Ala Arg Ile Met
 1280 1285 1290

Leu Asp Asn Gly Lys Asn Glu Ile Lys Val Thr Ala Ser Asp Ala
 1295 1300 1305

Ala Gly Asn Lys Thr Thr Lys Lys Val Thr Val Asp Val Asn Phe
 1310 1315 1320

Glu Ala Pro Gln Ile Thr Gly Leu Lys Pro Ala Glu Asp Leu Glu
 1325 1330 1335

Leu Lys Thr Gly Glu Thr Val Lys Ile Glu Phe Glu Ser Ala Ala
 1340 1345 1350

Asp Leu Asp Ala Val Phe Val Ile Arg Met Pro Leu Thr Asn Phe
 1355 1360 1365

Lys Thr Ala Ala Gln Asn Val Thr Glu Leu Pro Ile Arg Glu Val
 1370 1375 1380

Ser Lys Gly Lys Tyr Glu Gly Tyr Trp Thr Ala Thr Ser Thr Ala
 1385 1390 1395

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10294.204.ST25.txt

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Trp	Gly	Asn	Ser	Glu	Tyr	Lys	Gln	Thr	Ala	Arg	Asn	Ile	Gly	Ala	Ala	
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Leu	Arg	Lys	Tyr	Asn	Met	Asn	Asn	Gly	Ile	Leu	Thr	Asp	Phe	Tyr	Asp	
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tcc	gcc	tct	caa	tcc	gcg	gca	aaa	gat	atc	acg	ctt	tcc	tat	atc	atg	1061
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Pro	Asp	Ala	Leu	Ser	Ile	Leu	Lys	Lys	Asn	Gly	Val	Ile	Asn	Lys	Glu	
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Gly	Phe	Leu	Pro	Lys	Ala	Tyr	Ser	Thr	Glu	Thr	Lys	Ala	Tyr	Thr	Tyr	
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Asp	His	Glu	Val	Asn	Leu	Ile	Asp	Gln	Leu	Tyr	Ala	Ala	Trp	His	Leu	
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cct	ccg	aag	gat	caa	aaa	gcc	gct	gta	tta	gcg	gat	tgg	ctc	aaa	cag	1301
Pro	Pro	Lys	Asp	Gln	Lys	Ala	Ala	Val	Leu	Ala	Asp	Trp	Leu	Lys	Gln	
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Thr	Phe	Gln	Thr	Gly	Gly	Lys	Leu	Tyr	Gly	Arg	Tyr	Ser	Leu	Asp	Thr	
		270					275					280				
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Lys	Lys	Pro	Ala	Val	Gln	Tyr	Glu	Ser	Pro	Ser	Val	Tyr	Ala	Leu	Ala	
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Tyr	Tyr	Gly	Gly	Tyr	Met	Ser	Gly	Asn	Asp	Thr	His	Ser	Phe	Asp	Asn	
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ctg	ctg	ccc	cta	tta	gcc	gaa	agg	aag	ctt	tta	aat	gaa	aat	ctc	att	1589
Leu	Leu	Pro	Leu	Leu	Ala	Glu	Arg	Lys	Leu	Leu	Asn	Glu	Asn	Leu	Ile	
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Gln																
cggtgttc	cat	ccattatatc	tcagtccagc	ggttcgaacc	cgttctcatc	atttgc	catca									1702

10294.204.ST25.txt

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35      40      45
Tyr Arg His Leu Met Ser Asp Gln Gly Leu Ile Lys Thr Gly Phe Ser
50      55      60
Asp Gln Pro Val Tyr Leu Ser Glu Ser Leu Gly Leu Trp Met Glu Phe
65      70      75      80
Leu Ile Ser Lys Lys Asp Gly Glu His Phe His Glu Gln Tyr Gln His
85      90      95
Leu Asn Glu Ser Phe Leu Met Asn Asn Asn Leu Val Ser Trp Gln Ile
100     105     110
Gln Asn Gly Gln Ala Ser Gly Val Asn Ala Leu Ile Asp Asp Leu Arg
115     120     125
Ile Met Val Ser Leu Asp Gln Ala Ala Ala Leu Trp Gly Asn Ser Glu
130     135     140
Tyr Lys Gln Thr Ala Arg Asn Ile Gly Ala Ala Leu Arg Lys Tyr Asn
145     150     155     160
Met Asn Asn Gly Ile Leu Thr Asp Phe Tyr Asp Ser Ala Ser Gln Ser
165     170     175
Ala Ala Lys Asp Ile Thr Leu Ser Tyr Ile Met Pro Asp Ala Leu Ser

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10294.204.ST25.txt

180

185

190

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 195 200 205

Ala Ser Ile Leu Tyr Leu Ala Pro Leu Lys Asn Gly Phe Leu Pro Lys
 210 215 220

Ala Tyr Ser Thr Glu Thr Lys Ala Tyr Thr Tyr Asp His Glu Val Asn
 225 230 235 240

Leu Ile Asp Gln Leu Tyr Ala Ala Trp His Leu Pro Pro Lys Asp Gln
 245 250 255

Lys Ala Ala Val Leu Ala Asp Trp Leu Lys Gln Thr Phe Gln Thr Gly
 260 265 270

Gly Lys Leu Tyr Gly Arg Tyr Ser Leu Asp Thr Lys Lys Pro Ala Val
 275 280 285

Gln Tyr Glu Ser Pro Ser Val Tyr Ala Leu Ala Ile Leu Phe Phe Ile
 290 295 300

Asn Gln Asn Glu Asp Lys Thr Val Ile Lys Ala Leu Tyr Asp Arg Met
 305 310 315 320

Asn Asp Phe Glu Ile Leu Asp Ser Ser Glu Thr Tyr Tyr Gly Gly Tyr
 325 330 335

Met Ser Gly Asn Asp Thr His Ser Phe Asp Asn Leu Leu Pro Leu Leu
 340 345 350

Ala Glu Arg Lys Leu Leu Asn Glu Asn Leu Ile Gln
 355 360

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 gcatacattt acgcgcacgc agtcattcct gaatgagttt gccgaaagcc tcaagaaagc 120
 cgattatgta tatctttgcg atatattcgg atctgcccgg gaaaacgcag gaaagctgac 180
 gatcgggtgat ttgcaggaga aaattccgca ggcgaagctg atcgatgaaa atgacacatc 240
 aatttttaaag gagcatgaaa atgcggtggt aattttcatg ggcgcagggtg acattcaaaa 300

gtattttaaga gcatatgaaa atgtatttagc ataacaagaa aaaggcagtg tgagtcaatc	360
cgctgctttt ttgtacatat gaagcgggag tttctgttaa aggaattcac ccgtgcgtat	420
agaaaaagta aatatagagg tttagcattt aaacaattgg gtatacatca attgtaagcc	480
cttagctgaa ggaggataag atg att att att ctg tat tta agc gct gca ctc Met Ile Ile Ile Leu Tyr Leu Ser Ala Ala Leu 1 5 10	533
atc gct gtt agc ttt ctt att ttg gtt atc tat tta tca aaa aca tta Ile Ala Val Ser Phe Leu Ile Leu Val Ile Tyr Leu Ser Lys Thr Leu 15 20 25	581
aaa tcg ctt caa gtc aca ctt aat cat gtt gca tca acg ctg gaa ggt Lys Ser Leu Gln Val Thr Leu Asn His Val Ala Ser Thr Leu Glu Gly 30 35 40	629
gtg gaa gga caa atg aaa ggc atc acc gct gaa aca acg gag ctc ctg Val Glu Gly Gln Met Lys Gly Ile Thr Ala Glu Thr Thr Glu Leu Leu 45 50 55	677
aat aag acg aat cgg ctc gct gat gat att cag gaa aaa tct ttg aag Asn Lys Thr Asn Arg Leu Ala Asp Asp Ile Gln Glu Lys Ser Leu Lys 60 65 70 75	725
ctg aat acg gtc gtg gat gcc gtt cag gaa gtc ggc aca tcg gtc agg Leu Asn Thr Val Val Asp Ala Val Gln Glu Val Gly Thr Ser Val Arg 80 85 90	773
cag ttt aac aac tcc att cag cag gtt tca cag tcc gtc aca tca gcc Gln Phe Asn Asn Ser Ile Gln Gln Val Ser Gln Ser Val Thr Ser Ala 95 100 105	821
gca gag caa aac cgt gaa aaa att tct caa gtt gtc agc tgg agc aat Ala Glu Gln Asn Arg Glu Lys Ile Ser Gln Val Val Ser Trp Ser Asn 110 115 120	869
gca gct ttg gaa att tgg aat aga tgg aaa caa aag aag atg agg gag Ala Ala Leu Glu Ile Trp Asn Arg Trp Lys Gln Lys Lys Met Arg Glu 125 130 135	917
gaa taataaatga gtaaagacgg aatgaatact aaggattttt taatcggcac Glu 140	970
gtttgtaggc ggaatcatcg gggcggctgc agctttatct tttagcgccg aagtcgggga	1030
aagagcttcg cgatgacctt ggaaatcagg ccgtcgtttt aaaggataag accggaaagc	1090
tcacaagcga agcgagggag agaggctctg agtacgtcag catcgccaaa gagaagacat	1150
cttcgatttc acagcttggt gccgaccagt cttcacagat tatggataaa gtcaaagact	1210
tgcgaaagcaa gggtgccgaa aaagctggtg aactaaagga agaagcatcg tctgcaatcg	1270
aagaacaggc tgaagaagcc aaaaatgaaa tagaagatga agcaaggaaa acagcagata	1330
ccgctcagaa ataactgtgg aaagggagat caccgtgtcg aaacagctca ttcaaacaga	1390
ggatgaattt aaaaggcttg cagaaaacaa	1420

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10294.204.ST25.txt

<400> 222

Met Ile Ile Ile Leu Tyr Leu Ser Ala Ala Leu Ile Ala Val Ser Phe
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Leu Ile Leu Val Ile Tyr Leu Ser Lys Thr Leu Lys Ser Leu Gln Val
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Thr Leu Asn His Val Ala Ser Thr Leu Glu Gly Val Glu Gly Gln Met
 35 40 45

Lys Gly Ile Thr Ala Glu Thr Thr Glu Leu Leu Asn Lys Thr Asn Arg
 50 55 60

Leu Ala Asp Asp Ile Gln Glu Lys Ser Leu Lys Leu Asn Thr Val Val
 65 70 75 80

Asp Ala Val Gln Glu Val Gly Thr Ser Val Arg Gln Phe Asn Asn Ser
 85 90 95

Ile Gln Gln Val Ser Gln Ser Val Thr Ser Ala Ala Glu Gln Asn Arg
 100 105 110

Glu Lys Ile Ser Gln Val Val Ser Trp Ser Asn Ala Ala Leu Glu Ile
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 accgccggct tatttcacaa tggattggac aaaagcagca gattcgggtc ggaagctggc 180
 aggattaaaa ccggctgcat tattgacggg acacgggtgta ccgatgaaag gaagcgattt 240
 ttccgaagcg ctccttgatc tatcagaccg cttgcccgcc tctgattcgt aaattgtcat 300
 atgctgcgct taaaacattc agccaggctg aatgtttttt tatagggaaa aactaaccat 360
 ttacatgtg atgatggccg tccattgttc taaattccgg atgttgatgt ataccaaagg 420
 aatcattttc tgaaatttta gacaaaatat gttgatattt catttataat gcaggatatgc 480
 ctgaaaggag ctgagaaaag atg aaa att caa aaa agg gtc caa gct ttg ctg 533
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10294.204.ST25.txt

gca act tcg gca atg ttt gca gga ctg atg ctg tcc gat gcg gtg tac Ala Thr Ser Ala Met Phe Ala Gly Leu Met Leu Ser Asp Ala Val Tyr 15 20 25	581
gct gcg gaa acc cct tac tat gga aag aac tat act cag cca gag caa Ala Ala Glu Thr Pro Tyr Tyr Gly Lys Asn Tyr Thr Gln Pro Glu Gln 30 35 40	629
gtg tca tca tta tat ccg gag cct gaa gaa aca ttc tca acc cct gct Val Ser Ser Leu Tyr Pro Glu Pro Glu Glu Thr Phe Ser Thr Pro Ala 45 50 55	677
ttt gta aaa gaa ggg gaa gcc ttt acg aca caa gaa gaa atg atg aag Phe Val Lys Glu Gly Glu Ala Phe Thr Thr Gln Glu Glu Met Met Lys 60 65 70 75	725
ttt ata acc agt ctg aca aag aaa agc ccg aat gtc aaa atc ggg aat Phe Ile Thr Ser Leu Thr Lys Lys Ser Pro Asn Val Lys Ile Gly Asn 80 85 90	773
atc ggt ttt tca att gaa aaa aga aat att cct gtg ctt tac ttc aca Ile Gly Phe Ser Ile Glu Lys Arg Asn Ile Pro Val Leu Tyr Phe Thr 95 100 105	821
aag gac aag caa ata cgt tcc ata tca aaa aaa cca acc gtc tgg ctg Lys Asp Lys Gln Ile Arg Ser Ile Ser Lys Lys Pro Thr Val Trp Leu 110 115 120	869
caa gga cag ata cat gga aat gag ccg gca gcg gga gaa tct gct ctg Gln Gly Gln Ile His Gly Asn Glu Pro Ala Ala Gly Glu Ser Ala Leu 125 130 135	917
gcg ata gct gaa aaa ctg gcc gga ccg tat ggc gac aaa gtg ttg gac Ala Ile Ala Glu Lys Leu Ala Gly Pro Tyr Gly Asp Lys Val Leu Asp 140 145 150 155	965
aag atc aat gtc atc gtt gtt ccg cgg gtc aat cct gac gga tca tat Lys Ile Asn Val Ile Val Val Pro Arg Val Asn Pro Asp Gly Ser Tyr 160 165 170	1013
cag ttc aac aga cgg ctg gcg aac gga atc gac gga aac agg gat cat Gln Phe Asn Arg Arg Leu Ala Asn Gly Ile Asp Gly Asn Arg Asp His 175 180 185	1061
gtc aag ctc gag tct cca gaa gtg cgc gcc att cac caa gaa ttc aat Val Lys Leu Glu Ser Pro Glu Val Arg Ala Ile His Gln Glu Phe Asn 190 195 200	1109
aag tat tcg cct gaa gtc gtt atc gat gcc cat gaa tac ggt gtc ggc Lys Tyr Ser Pro Glu Val Val Ile Asp Ala His Glu Tyr Gly Val Gly 205 210 215	1157
caa aac gaa ttt cag agc ata ggc gaa aaa ggg tca tta aaa tac cat Gln Asn Glu Phe Gln Ser Ile Gly Glu Lys Gly Ser Leu Lys Tyr His 220 225 230 235	1205
gat att tta att tta tca gga aaa aat tta aac att ccc aag tcg atc Asp Ile Leu Ile Leu Ser Gly Lys Asn Leu Asn Ile Pro Lys Ser Ile 240 245 250	1253
agg cat gcg tcc gac agc ctt tat gtg aac ggc gtc aga gct aaa ctt Arg His Ala Ser Asp Ser Leu Tyr Val Asn Gly Val Arg Ala Lys Leu 255 260 265	1301
gat gaa aaa gga ttt tct aat gat gct tat tat acg aca gga aaa agc Asp Glu Lys Gly Phe Ser Asn Asp Ala Tyr Tyr Thr Thr Gly Lys Ser 270 275 280	1349

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 Lys Asp Gly Lys Ile Glu Ile Tyr Glu Gly Gly Thr 295 Glu Ala Arg Ile
 285 290

ggg cgt aat gca ttc gcc ctc cag cct gcc ctt tcc ttc ctg gtg gaa 1445
 Gly Arg Asn Ala Phe Ala Leu Gln Pro Ala Leu 310 Ser Phe Leu Val Glu 315
 300 305

agc agg gga ata gac atc gga cgc gaa aat ttt gca aga aga gtc gcg 1493
 Ser Arg Gly Ile Asp Ile Gly Arg Glu Asn Phe Ala Arg Arg Val 330 Ala 330
 320 325

gct cag gtt gct aca cat gag acg atc atc gac acg aca gtg aag cat 1541
 Ala Gln Val Ala Thr His Glu Thr Ile Ile Asp Thr Thr Val Lys His 345
 335 340

gca gcc gag atc aag cgc ctt gtc tcc aaa gaa aaa tta aag ctg ata 1589
 Ala Ala Glu Ile Lys Arg Leu Val Ser Lys Glu Lys Leu Lys Leu Ile 360
 350 355

caa aac ggc gct aaa gtg agc gat aaa gac caa gtg gtc atc aac agt 1637
 Gln Asn Gly Ala Lys Val Ser Asp Lys Asp Gln Val Val Ile Asn Ser 375
 365 370

gag ttt gca ggc ccg ttt aaa gac acg ctt aaa gtc gct gat att gcc 1685
 Glu Phe Ala Gly Pro Phe Lys Asp Thr Leu Lys Val Ala Asp Ile Ala 395
 380 385

tca gga caa gca gtt gac gtt cct gtc caa tat tac agc gcc tca gag 1733
 Ser Gly Gln Ala Val Asp Val Pro Val Gln Tyr Tyr Ser Ala Ser Glu 410
 400 405

gcc gtt cct gtg ctg tca aga act cgg ccg acc gct tac ctt gtc ctt 1781
 Ala Val Pro Val Leu Ser Arg Thr Arg Pro Thr Ala Tyr Leu Val Leu 425
 415 420

ccg ggc cat caa gat atc gaa cag aag ctg aag gat cag gga tta aag 1829
 Pro Gly His Gln Asp Ile Glu Gln Lys Leu Lys Asp Gln Gly Leu Lys 440
 430 435

agc gtg aca ctg gct ttc aaa caa aaa ctc acc gct gaa gcg tat gag 1877
 Ser Val Thr Leu Ala Phe Lys Gln Lys Leu Thr Thr Ala Glu Ala Tyr Glu 455
 445 450

gtt tta tcg aaa gaa aca gcg gga gaa tct gag ggc ccg cca gtg atc 1925
 Val Leu Ser Lys Glu Thr Ala Glu Gly Glu Ser Glu Gly Arg Pro Val Ile 475
 460 465

aag gta gaa acg aag ctc aaa aaa cag aaa aaa gag ttt cct aaa gga 1973
 Lys Val Glu Thr Lys Leu Lys Lys Gln Lys Lys Glu Phe Pro Lys Gly 490
 480 485

aca aaa atc tat ttt aca gct cag cag caa agc aat ctg ctg tca atc 2021
 Thr Lys Ile Tyr Phe Thr Ala Gln Gln Gln Ser Asn Leu Leu Ser Ile 505
 495 500

gca ctt gag ccg gag tcg gtt gac agt tat gta agc aca ggt tac att 2069
 Ala Leu Glu Pro Glu Ser Val Asp Ser Tyr Val Ser Thr Gly Tyr Ile 520
 510 515

cct tct caa aaa ggc aaa gag ctg ccg gtt tac cgc ttc atg ctg aac 2117
 Pro Ser Gln Lys Gly Lys Glu Leu Pro Val Tyr Arg Phe Met Leu Asn 535
 525 530

acc aaa acg ctt aat ttt aag gaa taatcaccag gcatccgtct ttgacggatg 2171
 Thr Lys Thr Leu Asn Phe Lys Glu 545
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10294.204.ST25.txt

ctttttagcg gttttttggt tttcataca taattgtttt aaactgagat cgaaacctat 2231
 acaataaata tcagtctgaa atctggaagg agagaatccg gttggaatca catgaagaat 2291
 tatggaggga agccaaggcc ttcacgagc tctgctacgg ggaactgtcg aagtccgaag 2351
 aagaaacaag gatgcgctta cataaaatag ataaagaaat cagagaaacc ggaagctata 2411
 cacatacatt agaagaaatc gaacatggag ccagaatggc gtggagaaac agcagccgct 2471
 gcatcggcag gctgttttgg cactctctta ctgtcatcga tcaaagaggc gttcaaaccg 2531
 aggcagaggt gcgggatgcg cttttccacc atattcagct tgcaacaaac ggagggaaaaa 2591
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 <212> PRT
 <213> Bacillus licheniformis

<400> 224

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Phe Ala Gly Leu Met Leu Ser Asp Ala Val Tyr Ala Ala Glu Thr Pro
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Tyr Tyr Gly Lys Asn Tyr Thr Gln Pro Glu Gln Val Ser Ser Leu Tyr
 35 40 45

Pro Glu Pro Glu Glu Thr Phe Ser Thr Pro Ala Phe Val Lys Glu Gly
 50 55 60

Glu Ala Phe Thr Thr Gln Glu Glu Met Met Lys Phe Ile Thr Ser Leu
 65 70 75 80

Thr Lys Lys Ser Pro Asn Val Lys Ile Gly Asn Ile Gly Phe Ser Ile
 85 90 95

Glu Lys Arg Asn Ile Pro Val Leu Tyr Phe Thr Lys Asp Lys Gln Ile
 100 105 110

Arg Ser Ile Ser Lys Lys Pro Thr Val Trp Leu Gln Gly Gln Ile His
 115 120 125

Gly Asn Glu Pro Ala Ala Gly Glu Ser Ala Leu Ala Ile Ala Glu Lys
 130 135 140

Leu Ala Gly Pro Tyr Gly Asp Lys Val Leu Asp Lys Ile Asn Val Ile
 145 150 155 160

Val Val Pro Arg Val Asn Pro Asp Gly Ser Tyr Gln Phe Asn Arg Arg
 165 170 175

10294.204.ST25.txt

Leu Ala Asn Gly Ile Asp Gly Asn Arg Asp His Val Lys Leu Glu Ser
 180 185 190

Pro Glu Val Arg Ala Ile His Gln Glu Phe Asn Lys Tyr Ser Pro Glu
 195 200 205

Val Val Ile Asp Ala His Glu Tyr Gly Val Gly Gln Asn Glu Phe Gln
 210 215 220

Ser Ile Gly Glu Lys Gly Ser Leu Lys Tyr His Asp Ile Leu Ile Leu
 225 230 235 240

Ser Gly Lys Asn Leu Asn Ile Pro Lys Ser Ile Arg His Ala Ser Asp
 245 250 255

Ser Leu Tyr Val Asn Gly Val Arg Ala Lys Leu Asp Glu Lys Gly Phe
 260 265 270

Ser Asn Asp Ala Tyr Tyr Thr Thr Gly Lys Ser Lys Asp Gly Lys Ile
 275 280 285

Glu Ile Tyr Glu Gly Gly Thr Glu Ala Arg Ile Gly Arg Asn Ala Phe
 290 295 300

Ala Leu Gln Pro Ala Leu Ser Phe Leu Val Glu Ser Arg Gly Ile Asp
 305 310 315 320

Ile Gly Arg Glu Asn Phe Ala Arg Arg Val Ala Ala Gln Val Ala Thr
 325 330 335

His Glu Thr Ile Ile Asp Thr Thr Val Lys His Ala Ala Glu Ile Lys
 340 345 350

Arg Leu Val Ser Lys Glu Lys Leu Lys Leu Ile Gln Asn Gly Ala Lys
 355 360 365

Val Ser Asp Lys Asp Gln Val Val Ile Asn Ser Glu Phe Ala Gly Pro
 370 375 380

Phe Lys Asp Thr Leu Lys Val Ala Asp Ile Ala Ser Gly Gln Ala Val
 385 390 395 400

Asp Val Pro Val Gln Tyr Tyr Ser Ala Ser Glu Ala Val Pro Val Leu
 405 410 415

Ser Arg Thr Arg Pro Thr Ala Tyr Leu Val Leu Pro Gly His Gln Asp
 420 425 430

Ile Glu Gln Lys Leu Lys Asp Gln Gly Leu Lys Ser Val Thr Leu Ala
 435 440 445

10294.204.ST25.txt

Phe Lys Gln Lys Leu Thr Ala Glu Ala Tyr Glu Val Leu Ser Lys Glu
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Thr Ala Gly Glu Ser Glu Gly Arg Pro Val Ile Lys Val Glu Thr Lys
 465 470 475 480

Leu Lys Lys Gln Lys Lys Glu Phe Pro Lys Gly Thr Lys Ile Tyr Phe
 485 490 495

Thr Ala Gln Gln Gln Ser Asn Leu Leu Ser Ile Ala Leu Glu Pro Glu
 500 505 510

Ser Val Asp Ser Tyr Val Ser Thr Gly Tyr Ile Pro Ser Gln Lys Gly
 515 520 525

Lys Glu Leu Pro Val Tyr Arg Phe Met Leu Asn Thr Lys Thr Leu Asn
 530 535 540

Phe Lys Glu
 545

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 acgattgggg aatgcttcat gattagaaaa tggtaaattt tgatcatgac gggatactct 240
 ttaccctctt ctataaaagt gggacagaca gttgaaaagc cggtaaattc atagccttgt 300
 atttcaacag taacttcttc tatatgcggg tttcattttt tcatctttgc ttaatacatt 360
 aaatcacctc ctttatacag tatttgtcca ttaaagaaga acaggatctt cttgtcaaat 420
 atctttatta gatcatattg tcatgtataa tgaagggtat agcatgtgac attcatactg 480
 tataagaaag gatatgacca gtg aaa atg ttg aaa aag gct gtg ttg ata gcc 533
 Val Lys Met Leu Lys Lys Ala Val Leu Ile Ala
 1 5 10
 gct gtt ttc ttg ctg gcc gca ttt gcc ggg agt aca gaa gcc ttt gct 581
 Ala Val Phe Leu Leu Ala Ala Phe Ala Gly Ser Thr Glu Ala Phe Ala
 15 20 25
 atg cct tcc aaa ggc gcg gtg aaa ttc agg acg gat gcc aat aca tat 629
 Met Pro Ser Lys Gly Ala Val Lys Phe Arg Thr Asp Ala Asn Thr Tyr
 30 35 40

10294.204.ST25.txt

acg aaa tca gcc act tcg atc gtt gtc act gga aaa agc cct gtt acg 677
 Thr Lys Ser Ala Thr Ser Ile Val Val Thr Gly Lys Ser Pro Val Thr
 45 50 55
 gga acg atg att gcc gtc agg ctg atc aat aaa aaa ggg act gtc ctg 725
 Gly Thr Met Ile Ala Val Arg Leu Ile Asn Lys Lys Gly Thr Val Leu
 60 65 70 75
 atc tat cga gat gtt cat tta acg cgc gga aag cct cat ttt cgg gtc 773
 Ile Tyr Arg Asp Val His Leu Thr Arg Gly Lys Pro His Phe Arg Val
 80 85 90
 agc ttt ccg acg aaa aag ctg aaa ccg ggc aag tat gac gtc tgg gtc 821
 Ser Phe Pro Thr Lys Lys Leu Lys Pro Gly Lys Tyr Asp Val Trp Val
 95 100 105
 gat gcc gtc aaa gga aag aag tgg cac ggg gaa ttg aag cgc tac att 869
 Asp Ala Val Lys Gly Lys Lys Trp His Gly Glu Leu Lys Arg Tyr Ile
 110 115 120
 gtc atc aag cat tgatctcttt tatgatggac ggagggctgt gtaatgactg 921
 Val Ile Lys His
 125
 tcgtggggttt ttgcgtatta ttatgttctg catttatcca tgcacgtgg aactatcttt 981
 ctaaaaaagc cgatggaggc gttccgttta tctggctgtt cacagcgatt gcagccgtca 1041
 tctacacgcc gttggccata ggtgtcgtca tatatgaaaa gcctgagatc ggcacatctggc 1101
 agcttgtcat catcatggcg agcatccttg ctacattggg cttttttctt gttcttcaaa 1161
 aaggatacaa aaaggcgat ctctcccttg tctatccgat cgcgaggggg acaggccccgc 1221
 tgctcacctg catgctggcg gtcgcctttt ttggcgagac gttgacgctg cccgctatta 1281
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 aagaatcagg ctcgttcaca ccggttcttt acgggctggc 1381

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 <213> Bacillus licheniformis

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 Ala Val Lys Phe Arg Thr Asp Ala Asn Thr Tyr Thr Lys Ser Ala Thr
 35 40 45
 Ser Ile Val Val Thr Gly Lys Ser Pro Val Thr Gly Thr Met Ile Ala
 50 55 60
 Val Arg Leu Ile Asn Lys Lys Gly Thr Val Leu Ile Tyr Arg Asp Val
 65 70 75 80

10294.204.ST25.txt

His Leu Thr Arg Gly Lys Pro His Phe Arg Val Ser Phe Pro Thr Lys
 85 90 95

Lys Leu Lys Pro Gly Lys Tyr Asp Val Trp Val Asp Ala Val Lys Gly
 100 105 110

Lys Lys Trp His Gly Glu Leu Lys Arg Tyr Ile Val Ile Lys His
 115 120 125

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 <212> DNA
 <213> Bacillus licheniformis

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 <222> (501)..(1187)

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 acacagaaag gggagaagga tctttgaaaa agcaggagaa tttgcgcctg catggggaat 180
 gatcggaaacg cttgtcggtc tcgtcatgat gctcaaaaac ctgaacaagc cggaaacgct 240
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 gctgtttata ccgatcgccg cgaagcttga agaaaagacg gagaatgaaa tctttaagaa 360
 gcaagtcatg atcgaaggca tcatcggcat ccaatcggga agaaatccgc gaaatcttga 420
 aagtcagctt gtcgttttca gttcaaaaga agaatggaca aaaaagcggg cggaccgcat 480
 gaaacaaaag gacaggcctc atg aag ctt aga cat gaa cga agg aag cgc gag 533
 Met Lys Leu Arg His Glu Arg Arg Lys Arg Glu
 1 5 10
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 Gln Gly Arg Lys Ser Pro Asn Trp Ile Ile Thr Phe Ser Asp Leu Ile
 15 20 25
 acg ctc atc ctc gtg ttc ttt att tta ctg ttt tcg atg tcg caa atc 629
 Thr Leu Ile Leu Val Phe Phe Ile Leu Leu Phe Ser Met Ser Gln Ile
 30 35 40
 gat tta aac aaa ttc aaa gca gca gtc ggt tca ttt caa gac agg gcc 677
 Asp Leu Asn Lys Phe Lys Ala Ala Val Gly Ser Phe Gln Asp Arg Ala
 45 50 55
 gac ggc aaa tcc gcc gca gag ttg aaa aaa gac gcg ggc gat cag aag 725
 Asp Gly Lys Ser Ala Ala Glu Leu Lys Lys Asp Ala Gly Asp Gln Lys
 60 65 70 75
 gct gaa aaa acg gct aaa agc caa gat gat tta tta aag aaa atc aat 773
 Ala Glu Lys Thr Ala Lys Ser Gln Asp Asp Leu Leu Lys Lys Ile Asn
 80 85 90
 gac tat att gaa aaa aac gaa ctg tca agt ttg att gcg gcc aag cgt 821
 Asp Tyr Ile Glu Lys Asn Glu Leu Ser Ser Leu Ile Ala Ala Lys Arg
 95 100 105
 gac gaa cgg ggc gtc att ctc gtc ctt cag gaa gcg gtt ttg ttt gat 869
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10294.204.ST25.txt

Asp Glu Arg Gly Val Ile Leu Val Leu Gln Glu Ala Val Leu Phe Asp
 110 115 120
 tca ggg aaa gcg gat ctg aaa gac caa gct cac ccg ctt ttg cat aaa 917
 Ser Gly Lys Ala Asp Leu Lys Asp Gln Ala His Pro Leu Leu His Lys
 125 130 135
 atc gcc gtc ctt ctc aaa tcg gtg tcc aac ccg att cgt gtg gag ggg 965
 Ile Ala Val Leu Leu Lys Ser Val Ser Asn Pro Ile Arg Val Glu Gly
 140 145 150 155
 cat acg gac agc cgc ccg att tcg act tac cgt ttt cca tcc aat tgg 1013
 His Thr Asp Ser Arg Pro Ile Ser Thr Tyr Arg Phe Pro Ser Asn Trp
 160 165 170
 gag ctt tct gca gca agg gcg agc act gtg atc ggc tac ttt acg tcg 1061
 Glu Leu Ser Ala Ala Arg Ala Ser Thr Val Ile Gly Tyr Phe Thr Ser
 175 180 185
 aag gaa aag ctc gac tcg tcg cgt ttt ctt gcc atc ggt tat gcg gat 1109
 Lys Glu Lys Leu Asp Ser Ser Arg Phe Leu Ala Ile Gly Tyr Ala Asp
 190 195 200
 aca aaa ccg gtc agg gac aac gcg act gag agc cat atg aag gaa aac 1157
 Thr Lys Pro Val Arg Asp Asn Arg Thr Glu Ser His Met Lys Glu Asn
 205 210 215
 agg cgc gtc gag att gtc atc gca aaa caa taatgagaag aaagcaaggt 1207
 Arg Arg Val Glu Ile Val Ile Ala Lys Gln 220 225
 cttgcacaaa agcaaggcct tttctgtgtg ccgcaatttt catattaagt ggtacgctgg 1267
 gcagagcgaa tcggataaag ggcttttgga acggtttgtg cgtttttttc cgttatttcg 1327
 gtttttcttg gaattggagg atacaaatct tccgggtcgg accagttggc aggaagccgg 1387
 acagatgcct gtttccccca ttttttcagc cttttttcag gcattttctc ctctggttcc 1447
 atccctttca tttcaagcca gattcttgcc catgccctcg gtacgacgcg ccaaagtgcg 1507
 tagccgcctc cgccgacagc gatccatctt ccgctgcaat aggtgtgtgc aagttcgtga 1567
 gcgagctttg gaatctcttc gtaaattctc atcgtcgtgc acaagtgtgt cagcggatcg 1627
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 <213> Bacillus licheniformis

<400> 228

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 20 25 30

Phe Phe Ile Leu Leu Phe Ser Met Ser Gln Ile Asp Leu Asn Lys Phe
 35 40 45

Lys Ala Ala Val Gly Ser Phe Gln Asp Arg Ala Asp Gly Lys Ser Ala
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50

55

60

Ala Glu Leu Lys Lys Asp Ala Gly Asp Gln Lys Ala Glu Lys Thr Ala
65 70 75 80

Lys Ser Gln Asp Asp Leu Leu Lys Lys Ile Asn Asp Tyr Ile Glu Lys
85 90 95

Asn Glu Leu Ser Ser Leu Ile Ala Ala Lys Arg Asp Glu Arg Gly Val
100 105 110

Ile Leu Val Leu Gln Glu Ala Val Leu Phe Asp Ser Gly Lys Ala Asp
115 120 125

Leu Lys Asp Gln Ala His Pro Leu Leu His Lys Ile Ala Val Leu Leu
130 135 140

Lys Ser Val Ser Asn Pro Ile Arg Val Glu Gly His Thr Asp Ser Arg
145 150 155 160

Pro Ile Ser Thr Tyr Arg Phe Pro Ser Asn Trp Glu Leu Ser Ala Ala
165 170 175

Arg Ala Ser Thr Val Ile Gly Tyr Phe Thr Ser Lys Glu Lys Leu Asp
180 185 190

Ser Ser Arg Phe Leu Ala Ile Gly Tyr Ala Asp Thr Lys Pro Val Arg
195 200 205

Asp Asn Arg Thr Glu Ser His Met Lys Glu Asn Arg Arg Val Glu Ile
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Val Ile Ala Lys Gln
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acagcagaga gaacgtgtca gttttatgaa cttttcacag cgatttttcc cggatgcggc 240
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10294.204.ST25.txt																		
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ggcaaggaaa	ggagtgaaaa	atg	gct	gcg	gaa	aaa	gta	ttt	tcg	aaa	aat	aaa						533
		Met	Ala	Ala	Glu	Lys	Val	Phe	Ser	Lys	Asn	Lys						
		1				5					10							
atc	att	gga	gga	aaa	aga	atg	tca	tat	atg	aaa	cgt	tcc	atc	tct	gtc			581
Ile	Ile	Gly	Gly	Lys	Arg	Met	Ser	Tyr	Met	Lys	Arg	Ser	Ile	Ser	Val			
		15						20					25					
ttc	atc	gcc	tgt	ttt	atg	gta	gcg	gcg	ctt	ggc	atc	agc	ggg	atc	att			629
Phe	Ile	Ala	Cys	Phe	Met	Val	Ala	Ala	Leu	Gly	Ile	Ser	Gly	Ile	Ile			
		30					35					40						
gca	ccg	aaa	gcg	gct	gcc	gct	tct	aaa	aca	ccc	ggt	gct	gta	aac	gga			677
Ala	Pro	Lys	Ala	Ala	Ala	Ala	Ser	Lys	Thr	Pro	Val	Ala	Val	Asn	Gly			
	45					50					55							
cag	ctt	acc	tta	aaa	ggt	acg	cag	ctc	gtc	aat	caa	aac	gga	aaa	gcg			725
Gln	Leu	Thr	Leu	Lys	Gly	Thr	Gln	Leu	Val	Asn	Gln	Asn	Gly	Lys	Ala			
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ggt	cag	ctg	aaa	gga	atc	agc	tcc	cac	ggt	cta	cag	tgg	tat	ggc	gat			773
Val	Gln	Leu	Lys	Gly	Ile	Ser	Ser	His	Gly	Leu	Gln	Trp	Tyr	Gly	Asp			
				80					85					90				
tat	gtc	aac	aaa	gac	tcg	tta	aaa	tgg	ctg	aga	gac	gac	tgg	ggc	atc			821
Tyr	Val	Asn	Lys	Asp	Ser	Leu	Lys	Trp	Leu	Arg	Asp	Asp	Trp	Gly	Ile			
			95					100					105					
aat	gtc	ttc	cgc	gcg	gcc	atg	tat	aca	gct	gaa	ggc	ggc	tat	att	gac			869
Asn	Val	Phe	Arg	Ala	Ala	Met	Tyr	Thr	Ala	Glu	Gly	Gly	Tyr	Ile	Asp			
		110					115					120						
aat	ccg	tcg	ggt	aaa	aac	aaa	gtg	aag	gaa	gcc	gtc	gaa	gcg	gca	aaa			917
Asn	Pro	Ser	Val	Lys	Asn	Lys	Val	Lys	Glu	Ala	Val	Glu	Ala	Ala	Lys			
	125					130					135							
gaa	ctc	gga	atc	tat	gtg	atc	att	gac	tgg	cac	ata	ctg	agc	gat	ggc			965
Glu	Leu	Gly	Ile	Tyr	Val	Ile	Ile	Asp	Trp	His	Ile	Leu	Ser	Asp	Gly			
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10294.204.ST25.txt

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aaa gga gcg ccg att ttc gtc aca gaa tgg gga acg agc gat gct tca Lys Gly Ala Pro Ile Phe Val Thr Glu Trp Gly Thr Ser Asp Ala Ser	270 275	280	1349
gga aac ggc ggg gtc tac ctt gac caa tcc agg gag tgg ctg aaa tat Gly Asn Gly Gly Val Tyr Leu Asp Gln Ser Arg Glu Trp Leu Lys Tyr	285 290	295	1397
tta gac agc aaa aaa atc agc tgg gta aac tgg aac tta tcc gac aaa Leu Asp Ser Lys Lys Ile Ser Trp Val Asn Trp Asn Leu Ser Asp Lys	300 305	310	1445
caa gag tcg tca gca gct tta aac cca ggc gcc tct aaa aac gga gga Gln Glu Ser Ser Ala Ala Leu Asn Pro Gly Ala Ser Lys Asn Gly Gly	320 325	330	1493
tgg tcg caa tcc gac ttg tcc cca tca ggc aaa ttc gtc agg gat aac Trp Ser Gln Ser Asp Leu Ser Pro Ser Gly Lys Phe Val Arg Asp Asn	335 340	345	1541
atc cgc agc ggg tca aac ggt tcg tca gga gac tct gga tcg aat tcg Ile Arg Ser Gly Ser Asn Gly Ser Ser Gly Asp Ser Gly Ser Asn Ser	350 355	360	1589
aaa ggg tca gat caa aaa gac caa aaa aag gat cag gat aaa cca ggt Lys Gly Ser Asp Gln Lys Asp Gln Lys Lys Asp Gln Asp Lys Pro Gly	365 370	375	1637
caa gac agc ggc gct gca gcc aac acg ata gca gta caa tac aga gcg Gln Asp Ser Gly Ala Ala Ala Asn Thr Ile Ala Val Gln Tyr Arg Ala	380 385	390	1685
ggg gac aac aat gta aac ggc aac caa atc cgc cct cag ctc aac att Gly Asp Asn Asn Val Asn Gly Asn Gln Ile Arg Pro Gln Leu Asn Ile	400 405	410	1733
aaa aac aac agc aaa aaa acc gtg tct tta aat cga atc act gtc cgc Lys Asn Asn Ser Lys Lys Thr Val Ser Leu Asn Arg Ile Thr Val Arg	415 420	425	1781
tac tgg tat aaa acg aat cgc aaa gga caa aat ttt gac tgc gac tat Tyr Trp Tyr Lys Thr Asn Arg Lys Gly Gln Asn Phe Asp Cys Asp Tyr	430 435	440	1829
gcc caa atc ggc tgc agc aaa atc acg cac aaa ttc gtt caa tta aaa Ala Gln Ile Gly Cys Ser Lys Ile Thr His Lys Phe Val Gln Leu Lys	445 450	455	1877
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cac aat gac ggc tgg agc aat tat gcc caa agc ggc gac tat tca ttt His Asn Asp Gly Trp Ser Asn Tyr Ala Gln Ser Gly Asp Tyr Ser Phe	495 500	505	2021
ttt aat tca aac acg ttt aaa aat acg aaa aaa atc acg ttg tat gag Phe Asn Ser Asn Thr Phe Lys Asn Thr Lys Lys Ile Thr Leu Tyr Glu			2069

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510

515

520

aac gga aag ctg att tgg ggc act gaa cct aaa taacggcact ttgacggaca 2122
 Asn Gly Lys Leu Ile Trp Gly Thr Glu Pro Lys
 525 530
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 <213> Bacillus licheniformis

<400> 230

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20 25 30

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35 40 45

Ala Ala Ser Lys Thr Pro Val Ala Val Asn Gly Gln Leu Thr Leu Lys
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Gly Thr Gln Leu Val Asn Gln Asn Gly Lys Ala Val Gln Leu Lys Gly
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Ile Ser Ser His Gly Leu Gln Trp Tyr Gly Asp Tyr Val Asn Lys Asp
85 90 95

Ser Leu Lys Trp Leu Arg Asp Asp Trp Gly Ile Asn Val Phe Arg Ala
100 105 110

Ala Met Tyr Thr Ala Glu Gly Gly Tyr Ile Asp Asn Pro Ser Val Lys
115 120 125

Asn Lys Val Lys Glu Ala Val Glu Ala Ala Lys Glu Leu Gly Ile Tyr
130 135 140

Val Ile Ile Asp Trp His Ile Leu Ser Asp Gly Asn Pro Asn Gln Asn
145 150 155 160

10294.204.ST25.txt

Lys Ala Lys Ala Lys Glu Phe Phe Asn Glu Met Ser Arg Leu Tyr Gly
 165 170 175
 Lys Thr Pro Asn Val Ile Phe Glu Ile Ala Asn Glu Pro Asn Gly Asp
 180 185 190
 Val Asn Trp Asn Arg Asp Ile Lys Pro Tyr Ala Glu Glu Ile Leu Ser
 195 200 205
 Val Ile Arg Lys Asn Ser Pro Lys Asn Ile Val Ile Val Gly Thr Gly
 210 215 220
 Thr Trp Ser Gln Asp Val Asn Asp Ala Ala Asp Asn Gln Leu Lys Asp
 225 230 235 240
 Gly Asn Val Met Tyr Ala Leu His Phe Tyr Ala Gly Thr His Gly Gln
 245 250 255
 Ser Leu Arg Asp Lys Ala Asp Tyr Ala Leu Ser Lys Gly Ala Pro Ile
 260 265 270
 Phe Val Thr Glu Trp Gly Thr Ser Asp Ala Ser Gly Asn Gly Gly Val
 275 280 285
 Tyr Leu Asp Gln Ser Arg Glu Trp Leu Lys Tyr Leu Asp Ser Lys Lys
 290 295 300
 Ile Ser Trp Val Asn Trp Asn Leu Ser Asp Lys Gln Glu Ser Ser Ala
 305 310 315 320
 Ala Leu Asn Pro Gly Ala Ser Lys Asn Gly Gly Trp Ser Gln Ser Asp
 325 330 335
 Leu Ser Pro Ser Gly Lys Phe Val Arg Asp Asn Ile Arg Ser Gly Ser
 340 345 350
 Asn Gly Ser Ser Gly Asp Ser Gly Ser Asn Ser Lys Gly Ser Asp Gln
 355 360 365
 Lys Asp Gln Lys Lys Asp Gln Asp Lys Pro Gly Gln Asp Ser Gly Ala
 370 375 380
 Ala Ala Asn Thr Ile Ala Val Gln Tyr Arg Ala Gly Asp Asn Asn Val
 385 390 395 400
 Asn Gly Asn Gln Ile Arg Pro Gln Leu Asn Ile Lys Asn Asn Ser Lys
 405 410 415
 Lys Thr Val Ser Leu Asn Arg Ile Thr Val Arg Tyr Trp Tyr Lys Thr
 420 425 430

10294.204.ST25.txt

Asn Arg Lys Gly Gln Asn Phe Asp Cys Asp Tyr Ala Gln Ile Gly Cys
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Ser Lys Ile Thr His Lys Phe Val Gln Leu Lys Lys Ala Val Asn Gly
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Ala Asp Thr Tyr Leu Glu Val Gly Phe Lys Asn Gly Thr Leu Ala Pro
 465 470 475 480

Gly Ala Asp Thr Gly Glu Ile Gln Ile Arg Leu His Asn Asp Gly Trp
 485 490 495

Ser Asn Tyr Ala Gln Ser Gly Asp Tyr Ser Phe Phe Asn Ser Asn Thr
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Trp Gly Thr Glu Pro Lys
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 cgagtccgtc atggacgaac tctgtttcaa atccttcttt tgcaaaaaac atctctgtca 240
 tagtacatac gcttaaatta tcttcaatca ttaatatatt catcgtaaaa gtgcctccgc 300
 tagacaaacg ttagattcat ttacatagg gccagccat ttctcaattc cattctgaac 360
 atttaaaggt ctggcaacag tttggtcata atttattcat aagtagcggc taagatgaaa 420
 tcaagcataa ggcaaaaagtc ctgctgccgt tagatttggc agcaataata aatgaaatag 480
 atacggagga atcacgcgtt atg aat ttt ttc aaa cga gcc ttt tgg agc atg 533
 Met Asn Phe Phe Lys Arg Ala Phe Trp Ser Met
 1 5 10
 aaa gcg aaa aaa gga aaa aca ctt tta caa ttg ttt gtt ttc acg atg 581
 Lys Ala Lys Lys Gly Lys Thr Leu Leu Gln Leu Phe Val phe Thr Met
 15 20 25
 att tgc gtg ctc gtg ctg aca gga att acg atc cag tgc gca gcc gtg 629
 Ile Cys Val Leu Val Leu Thr Gly Ile Thr Ile Gln Ser Ala Ala Val
 30 35 40

10294.204.ST25.txt

aaa tcg agc gaa ctg gcg agg gaa cag ctc gga ggc agc gtc acg ctc Lys Ser Ser Glu Leu Ala Arg Glu Gln Leu Gly Gly Ser Val Thr Leu 45 50 55	677
aaa gtt gac agg gaa aaa atg atg aaa gaa cag cag gac tca gga gac Lys Val Asp Arg Glu Lys Met Met Lys Glu Gln Gln Asp Ser Gly Asp 60 65 70 75	725
cgg aaa agg ttt gaa tcg acc ccc gtt tct ctc aaa tca gcc gag aaa Arg Lys Arg Phe Glu Ser Thr Pro Val Ser Leu Lys Ser Ala Glu Lys 80 85 90	773
ctt gcg agc ctt tac cat gtc aaa agc tat aac ttc atc tcc tca aca Leu Ala Ser Leu Tyr His Val Lys Ser Tyr Asn Phe Ile Ser Ser Thr 95 100 105	821
tct gct tta gcg gac aac ttc gat ccg atc gaa agc ggt gac gag gat Ser Ala Leu Ala Asp Asn Phe Asp Pro Ile Glu Ser Gly Asp Glu Asp 110 115 120	869
tca acg gac tca aac agc gat cag ccg gcc gga tcg ggc ggc aat gaa Ser Thr Asp Ser Asn Ser Asp Gln Pro Ala Gly Ser Gly Gly Asn Glu 125 130 135	917
cag ggc ggc cgg caa atg atg cag gct gac gta tca atc gaa ggt gtg Gln Gly Gly Arg Gln Met Met Gln Ala Asp Val Ser Ile Glu Gly Val 140 145 150 155	965
aca agc aca gcc ctc gtc gac gaa ttt gcc gac ggg acg tcc aag atc Thr Ser Thr Ala Leu Val Asp Glu Phe Ala Asp Gly Thr Ser Lys Ile 160 165 170	1013
acg gaa ggc cgt gct tta aca aag gat gat gtg aat gaa aaa gtc gcc Thr Glu Gly Arg Ala Leu Thr Lys Asp Asp Val Asn Glu Lys Val Ala 175 180 185	1061
gtg att gaa gaa acg ctt gcc gaa gaa aac gag ctg aag gtc ggc gat Val Ile Glu Glu Thr Leu Ala Glu Glu Asn Glu Leu Lys Val Gly Asp 190 195 200	1109
acg atc aaa gtc aaa gcg agc agc gat gaa gat gca acg atc aat tta Thr Ile Lys Val Lys Ala Ser Ser Asp Glu Asp Ala Thr Ile Asn Leu 205 210 215	1157
aaa atc gtc gga atc tat aaa acg act tca tcc gga gac aat caa gcg Lys Ile Val Gly Ile Tyr Lys Thr Thr Ser Ser Gly Asp Asn Gln Ala 220 225 230 235	1205
caa aac ttc gcc ttt tta aac cct tat aac aaa atc tat aca cca tat Gln Asn Phe Ala Phe Leu Asn Pro Tyr Asn Lys Ile Tyr Thr Pro Tyr 240 245 250	1253
acg gcg gca tcg gcc tta aaa ggc gac gat tat caa aac gcg ata gat Thr Ala Ala Ser Ala Leu Lys Gly Asp Asp Tyr Gln Asn Ala Ile Asp 255 260 265	1301
gaa gcg gtc tac aat atg gac gac gcc tcc aac atc gac gct ttc att Glu Ala Val Tyr Asn Met Asp Asp Ala Ser Asn Ile Asp Ala Phe Ile 270 275 280	1349
gcg gct gcc aag aaa aca ggc att gat ttg gat aca ttc aca ttg gac Ala Ala Ala Lys Lys Thr Gly Ile Asp Leu Asp Thr Phe Thr Leu Asp 285 290 295	1397
gcc aat gac cag ttg tac cag cag atg gtc ggc ccg att gaa aat gtc Ala Asn Asp Gln Leu Tyr Gln Gln Met Val Gly Pro Ile Glu Asn Val 300 305 310 315	1445

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gcc tcc ttc tcg aaa aat gtc gtc tat ctt gtc acg gtc gcc ggg gcg 1493
 Ala Ser Phe Ser Lys Asn Val Val Tyr Leu Val Thr Val Ala Gly Ala
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 gtg att ctc gga ctg atc gtc atg atg tca atc agg gag aga aaa tac 1541
 Val Ile Leu Gly Leu Ile Val Met Met Ser Ile Arg Glu Arg Lys Tyr
 335 340 345
 gaa atg ggt gtt ctg atg gcg atc ggc gaa aaa cgc cgg aaa ctc atc 1589
 Glu Met Gly Val Leu Met Ala Ile Gly Glu Lys Arg Arg Lys Leu Ile
 350 355 360
 gga cag ttt tta acc gaa atc tta atg atc gca gtg ctt gcc atc ggg 1637
 Gly Gln Phe Leu Thr Glu Ile Leu Met Ile Ala Val Leu Ala Ile Gly
 365 370 375
 atc tca gca tta acc ggc agc ctg att gca aag caa atc ggg aac cag 1685
 Ile Ser Ala Leu Thr Gly Ser Leu Ile Ala Lys Gln Ile Gly Asn Gln
 380 385 390 395
 ctc ttg agc cag caa atc gaa caa acg tca gct agc cag tct gca ggc 1733
 Leu Leu Ser Gln Gln Ile Glu Gln Thr Ser Ala Ser Gln Ser Ala Gly
 400 405 410
 gga atg atg ggc cca ggc ggc gga ggc ttc ttc gga caa agt act gct 1781
 Gly Met Met Gly Pro Gly Gly Gly Gly Phe Phe Gly Gln Ser Thr Ala
 415 420 425
 caa gtc tca gcc att gat cag ctc gac att caa gta tcc ttc ggg aac 1829
 Gln Val Ser Ala Ile Asp Gln Leu Asp Ile Gln Val Ser Phe Gly Asn
 430 435 440
 tta atg gca ctt ggc gga atc ggc ctt tta att gcg atg ttc gcg aca 1877
 Leu Met Ala Leu Gly Gly Ile Gly Leu Leu Ile Ala Met Phe Ala Thr
 445 450 455
 ctc ctt ccg tcc ata tct gtt tta agg ctc cat ccg aaa acg att tta 1925
 Leu Leu Pro Ser Ile Ser Val Leu Arg Leu His Pro Lys Thr Ile Leu
 460 465 470 475
 aca aaa caa gaa tagaagaag tgaagattat gggcagtatt ttagaatttc 1977
 Thr Lys Gln Glu
 agaatgtcgg ctattggtat aaaaatcagg atcagcctct attcgaggat atcagcattc 2037
 aattcagcca aggactctta tatacgattg tcgggacttc cggttccggc aaaaccacct 2097
 ttttatcggtt ggcgggcgga cttgacgcgc caaaagaggg gaacatcctc taaaaaggag 2157
 aaaacatttc aaaaatcgga ctgaccagct tccgcaatca atatgtatcg atcgtttttc 2217
 agtcctataa cctgctgccg tatatgacgg ctctccaaaa tatcacgtcg gccatggaaa 2277
 tcaccggatc tcagggtcaaa aacaaggaac aatacgcttt ggagatgctc gaaaagggtcg 2337
 gcatcggcga aaagcaggcc agacagaaag tattgacatt aagcggcggc cagcagcagc 2397
 gtgtctccat catcagagcg ttctgctgtg acacggattt 2437
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 <400> 232

10294.204.ST25.txt

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 Leu Thr Gly Ile Thr Ile Gln Ser Ala Ala Val Lys Ser Ser Glu Leu
 35 40 45
 Ala Arg Glu Gln Leu Gly Gly Ser Val Thr Leu Lys Val Asp Arg Glu
 50 55 60
 Lys Met Met Lys Glu Gln Gln Asp Ser Gly Asp Arg Lys Arg Phe Glu
 65 70 75 80
 Ser Thr Pro Val Ser Leu Lys Ser Ala Glu Lys Leu Ala Ser Leu Tyr
 85 90 95
 His Val Lys Ser Tyr Asn Phe Ile Ser Ser Thr Ser Ala Leu Ala Asp
 100 105 110
 Asn Phe Asp Pro Ile Glu Ser Gly Asp Glu Asp Ser Thr Asp Ser Asn
 115 120 125
 Ser Asp Gln Pro Ala Gly Ser Gly Gly Asn Glu Gln Gly Gly Arg Gln
 130 135 140
 Met Met Gln Ala Asp Val Ser Ile Glu Gly Val Thr Ser Thr Ala Leu
 145 150 155 160
 Val Asp Glu Phe Ala Asp Gly Thr Ser Lys Ile Thr Glu Gly Arg Ala
 165 170 175
 Leu Thr Lys Asp Asp Val Asn Glu Lys Val Ala Val Ile Glu Glu Thr
 180 185 190
 Leu Ala Glu Glu Asn Glu Leu Lys Val Gly Asp Thr Ile Lys Val Lys
 195 200 205
 Ala Ser Ser Asp Glu Asp Ala Thr Ile Asn Leu Lys Ile Val Gly Ile
 210 215 220
 Tyr Lys Thr Thr Ser Ser Gly Asp Asn Gln Ala Gln Asn Phe Ala Phe
 225 230 235 240
 Leu Asn Pro Tyr Asn Lys Ile Tyr Thr Pro Tyr Thr Ala Ala Ser Ala
 245 250 255
 Leu Lys Gly Asp Asp Tyr Gln Asn Ala Ile Asp Glu Ala Val Tyr Asn
 260 265 270

10294.204.ST25.txt

Met Asp Asp Ala Ser Asn Ile Asp Ala Phe Ile Ala Ala Ala Lys Lys
 275 280 285

Thr Gly Ile Asp Leu Asp Thr Phe Thr Leu Asp Ala Asn Asp Gln Leu
 290 295 300

Tyr Gln Gln Met Val Gly Pro Ile Glu Asn Val Ala Ser Phe Ser Lys
 305 310 315 320

Asn Val Val Tyr Leu Val Thr Val Ala Gly Ala Val Ile Leu Gly Leu
 325 330 335

Ile Val Met Met Ser Ile Arg Glu Arg Lys Tyr Glu Met Gly Val Leu
 340 345 350

Met Ala Ile Gly Glu Lys Arg Arg Lys Leu Ile Gly Gln Phe Leu Thr
 355 360 365

Glu Ile Leu Met Ile Ala Val Leu Ala Ile Gly Ile Ser Ala Leu Thr
 370 375 380

Gly Ser Leu Ile Ala Lys Gln Ile Gly Asn Gln Leu Leu Ser Gln Gln
 385 390 395 400

Ile Glu Gln Thr Ser Ala Ser Gln Ser Ala Gly Gly Met Met Gly Pro
 405 410 415

Gly Gly Gly Gly Phe Phe Gly Gln Ser Thr Ala Gln Val Ser Ala Ile
 420 425 430

Asp Gln Leu Asp Ile Gln Val Ser Phe Gly Asn Leu Met Ala Leu Gly
 435 440 445

Gly Ile Gly Leu Leu Ile Ala Met Phe Ala Thr Leu Leu Pro Ser Ile
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Ser Val Leu Arg Leu His Pro Lys Thr Ile Leu Thr Lys Gln Glu
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 <222> (501)..(1289)

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10294.204.ST25.txt

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ctgttcttgt catcagctct ttgttttttc caacgagcat gccgctcgtc tttaccttgc	300
cggagctggg cgccatggct tccgccgtcc ttttgatgat catcatttcc aacgacgggg	360
acacgaactg gtttgaaggc gcgacattgc tggccgctta tatcatcatg ggaatcggtt	420
ttttccttct ttaaaaaaat cgggataaac agagagcatc cggaatacaa taaggaaaaa	480
gaaacagaaa gagtgatagt atg aaa aag ctt ttg tgt ttt acg ctg act gcg	533
Met Lys Lys Leu Leu Cys Phe Thr Leu Thr Ala	10
1	
ttt tta tcc ttt agt ttt ttc gct gta cag gaa gct gac gca gcc aag	581
Phe Leu Ser Phe Ser Phe Phe Ala Val Gln Glu Ala Asp Ala Ala Lys	25
15	
ccg atc aag att cca agc tct gtc acg aat att tcc aaa gag aac aca	629
Pro Ile Lys Ile Pro Ser Ser Val Thr Asn Ile Ser Lys Glu Asn Thr	40
30	
tac cct aac gcc tct cag gat cag ccg agg ctg cag ccg agc gaa tta	677
Tyr Pro Asn Ala Ser Gln Asp Gln Pro Arg Leu Gln Pro Ser Glu Leu	55
45	
gcc gaa gag ctg ctg aaa aca acc gat att gcg att gaa aat ccg cat	725
Ala Glu Glu Leu Leu Lys Thr Thr Asp Ile Ala Ile Glu Asn Pro His	75
60	
ctg att aaa atg ctg aat gag tca agc att tcc ggc aca ccg ctg gca	773
Leu Ile Lys Met Leu Asn Glu Ser Ser Ile Ser Gly Thr Pro Leu Ala	90
80	
atc ggc tat cgg gcg acg att tat ttg ggc aga tgg gcg cta ggt tac	821
Ile Gly Tyr Arg Ala Thr Ile Tyr Leu Gly Arg Trp Ala Leu Gly Tyr	100
95	
acc tcg aat gaa acc gtt gcg aac tgg gaa tac cgc aaa atc aac aca	869
Thr Ser Asn Glu Thr Val Ala Asn Trp Glu Tyr Arg Lys Ile Asn Thr	115
110	
aac cgc ttt gac aac cgg ggc ggc aaa gca cct gca gaa ctc acg tat	917
Asn Arg Phe Asp Asn Arg Gly Gly Lys Ala Pro Ala Glu Leu Thr Tyr	135
125	
tcc cag gaa cag acg agc aaa atc aaa ggc ggc tta aca gcg aaa gtt	965
Ser Gln Glu Gln Thr Ser Lys Ile Lys Gly Gly Leu Thr Ala Lys Val	155
140	
cca aag gcg gaa gat gtc aaa aat atg atg atg ctc aaa gcc atg gaa	1013
Pro Lys Ala Glu Asp Val Lys Asn Met Met Met Leu Lys Ala Met Glu	165
160	
aaa aca aag ctg ccg ctc gcc ttt gaa aca gtg gtc ggc tcc ggt aca	1061
Lys Thr Lys Leu Pro Leu Ala Phe Glu Thr Val Val Gly Ser Gly Thr	185
175	
aaa cgc gat cag att tat aaa gtg cag ccg aaa aaa ctg gga aat tta	1109
Lys Arg Asp Gln Ile Tyr Lys Val Gln Pro Lys Lys Leu Gly Asn Leu	195
190	
cac gcc tat gca cct gcc gtc aat gaa aaa gga aaa gtc acc tac ggc	1157
His Ala Tyr Ala Pro Ala Val Asn Glu Lys Gly Lys Val Thr Tyr Gly	215
205	
210	

10294.204.ST25.txt

gaa gtg tac atc gta tta aaa ggc aac aaa aga aag cta gtc gtc aaa 1205
 Glu Val Tyr Ile Val Leu Lys Gly Asn Lys Arg Lys Leu Val Val Lys 235
 220 225 230

aat atc acc tcg caa gga atc ggc gct tgg att cct gta cag gat cac 1253
 Asn Ile Thr Ser Gln Gly Ile Gly Ala Trp Ile Pro Val Gln Asp His 250
 240 245 250

ctg aca ttc ggc ttt cag ctc agc cat cag ccg aaa taaaaaagca 1299
 Leu Thr Phe Gly Phe Gln Leu Ser His Gln Pro Lys 260
 255 260

agcctttgcg gcttgctttt ttcatactct tgctgttctg gaagtaaaat caacatcttg 1359

ataatagctg tttttgacga gcacattcgg tccgaggcac cggacgtgcg ggcagtgcca 1419

gttgagtctt ttggcaagct ctgtttttct ccacttcgcg taggcgcttg gcaggctgtc 1479

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aaaaatattg acgttcaggc gcgatctgcc gtcagggtcg tttctgacgg tgacgttttt 1599

cgcttcgcbc agccgctgta agaggcgctg atcttcagga tcagggtctgc acgcgtaaaa 1659

cggcagagtg ccgaacagca tccacgtatt ttcgtcgcga atgtcaagaa ggcggtggat 1719

cgctttttctc atgtctttta agcttaaaga ttcaagtgcg cttgcaaagt cgctcggata 1779

catcggatgg 1789

<210> 234
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 <212> PRT
 <213> Bacillus licheniformis

<400> 234

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Ser Ser Val Thr Asn Ile Ser Lys Glu Asn Thr Tyr Pro Asn Ala Ser
 35 40 45

Gln Asp Gln Pro Arg Leu Gln Pro Ser Glu Leu Ala Glu Glu Leu Leu
 50 55 60

Lys Thr Thr Asp Ile Ala Ile Glu Asn Pro His Leu Ile Lys Met Leu
 65 70 75 80

Asn Glu Ser Ser Ile Ser Gly Thr Pro Leu Ala Ile Gly Tyr Arg Ala
 85 90 95

Thr Ile Tyr Leu Gly Arg Trp Ala Leu Gly Tyr Thr Ser Asn Glu Thr
 100 105 110

Val Ala Asn Trp Glu Tyr Arg Lys Ile Asn Thr Asn Arg Phe Asp Asn
 115 120 125

10294.204.ST25.txt

Arg Gly Gly Lys Ala Pro Ala Glu Leu Thr Tyr Ser Gln Glu Gln Thr
 130 135 140

Ser Lys Ile Lys Gly Gly Leu Thr Ala Lys Val Pro Lys Ala Glu Asp
 145 150 155 160

Val Lys Asn Met Met Met Leu Lys Ala Met Glu Lys Thr Lys Leu Pro
 165 170 175

Leu Ala Phe Glu Thr Val Val Gly Ser Gly Thr Lys Arg Asp Gln Ile
 180 185 190

Tyr Lys Val Gln Pro Lys Lys Leu Gly Asn Leu His Ala Tyr Ala Pro
 195 200 205

Ala Val Asn Glu Lys Gly Lys Val Thr Tyr Gly Glu Val Tyr Ile Val
 210 215 220

Leu Lys Gly Asn Lys Arg Lys Leu Val Val Lys Asn Ile Thr Ser Gln
 225 230 235 240

Gly Ile Gly Ala Trp Ile Pro Val Gln Asp His Leu Thr Phe Gly Phe
 245 250 255

Gln Leu Ser His Gln Pro Lys
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<210> 235
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 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
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<400> 235
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 tttgtccgct atttttcaca ggctgcgctg atcgggtctcg ttcgcccttt gacgacggcc 180
 ggaatggctg ctgctgggtg cttggctcgtg tatgtgctgt tgacgggttcc ggggtctgatc 240
 ccattttatg gtgtcagttt gtttgctctt gtatcgatgt ttatcgcacaca tcgctgtttt 300
 ttgcgtctgga aaggctagct gaactgtgca aaaatgagaa aatcgggcaa aaaaatatca 360
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 agtgcaattg aataaaaaatg gaagccgtaa tagaatccct tttgagtaag cgttttacaaa 480
 aatgggtgaag ggagaagatg atg aaa aaa gga aag aaa agg tgg aag aac ctg 533
 Met Lys Lys Gly Lys Lys Arg Trp Lys Asn Leu
 1 5 10

10294.204.ST25.txt

ttg gcc gcg tca tct ctt tta tta atc acg cta gtg acc ggc ttc tcg Leu Ala Ala Ser Ser Leu Leu Leu Ile Thr Leu Val Thr Gly Phe Ser 15 20 25	581
gag caa gct gag gca gac ggg cgg acg gct gcg cag gca agg caa atg Glu Gln Ala Glu Ala Asp Gly Arg Thr Ala Ala Gln Ala Arg Gln Met 30 35 40	629
gaa tcg ctt aac agg ggg ctt gtc gct gtt aaa acg ggg aac ggt gtc Glu Ser Leu Asn Arg Gly Leu Val Ala Val Lys Thr Gly Asn Gly Val 45 50 55	677
ttt gtc agc tgg cgg ctt ctg gga acc gag ccg tct tct gtt tca ttt Phe Val Ser Trp Arg Leu Leu Gly Thr Glu Pro Ser Ser Val Ser Phe 60 65 70 75	725
aat gtg tat cga aac gga aag aag ctg aac ggt tct ccg att aca tcg Asn Val Tyr Arg Asn Gly Lys Lys Leu Asn Gly Ser Pro Ile Thr Ser 80 85 90	773
agc aca aac tat cag gat gca ggc ggg gat ttg aac gcc gtt tac cag Ser Thr Asn Tyr Gln Asp Ala Gly Gly Asp Leu Asn Ala Val Tyr Gln 95 100 105	821
gtg cgc gcc gtt ttg aac ggc agg gag cag gct cct tct gaa tcc gtc Val Arg Ala Val Leu Asn Gly Arg Glu Gln Ala Pro Ser Glu Ser Val 110 115 120	869
ggc gta ttg aat aaa caa tat aaa tct gtt ccg ctg caa aaa ccg gcc Gly Val Leu Asn Lys Gln Tyr Lys Ser Val Pro Leu Gln Lys Pro Ala 125 130 135	917
gga gga aaa acg cct gat ggg gtg tca tac aca tac agc gcc aat gat Gly Gly Lys Thr Pro Asp Gly Val Ser Tyr Thr Tyr Ser Ala Asn Asp 140 145 150 155	965
gcg agc gta ggc gac ctt gat gga gac ggc caa tat gaa atc att ctc Ala Ser Val Gly Asp Leu Asp Gly Asp Gly Gln Tyr Glu Ile Ile Leu 160 165 170	1013
aag tgg gat cct tcc aat tca aag gat aat tca cag gac gga tac acg Lys Trp Asp Pro Ser Asn Ser Lys Asp Asn Ser Gln Asp Gly Tyr Thr 175 180 185	1061
gga gat gtg ctg att gac gca tac aag ctt gac ggc acc atg atg tgg Gly Asp Val Leu Ile Asp Ala Tyr Lys Leu Asp Gly Thr Met Met Trp 190 195 200	1109
aga atc aac ctt ggc aaa aat att cgc gcc ggc gcc cat tat acg cag Arg Ile Asn Leu Gly Lys Asn Ile Arg Ala Gly Ala His Tyr Thr Gln 205 210 215	1157
ttt ctc gtc tat gac ttt gac ggc gat gga aaa gcg gaa atc gcc atg Phe Leu Val Tyr Asp Phe Asp Gly Asp Gly Lys Ala Glu Ile Ala Met 220 225 230 235	1205
aag acg gca gac ggg acg aag gac ggc aaa ggg aag gtg atc ggc aat Lys Thr Ala Asp Gly Thr Lys Asp Gly Lys Gly Lys Val Ile Gly Asn 240 245 250	1253
gca aac gcc gat tac cgc aat gcc caa ggc cga att ttg tca ggg cct Ala Asn Ala Asp Tyr Arg Asn Ala Gln Gly Arg Ile Leu Ser Gly Pro 255 260 265	1301
gag tat ttg acg gtt ttt aaa ggc gat aca ggc gct gag ctt aca acg Glu Tyr Leu Thr Val Phe Lys Gly Asp Thr Gly Ala Glu Leu Thr Thr 270 275 280	1349

10294.204.ST25.txt

gtc aac tac gaa cct gcc cgg gga aat gta gcc gat tgg gga gac agc Val Asn Tyr Glu Pro Ala Arg Gly Asn Val Ala Asp Trp Gly Asp Ser 285 290 295	1397
tac ggc aac agg gtt gac cgc ttt ctg gcc ggt gtc gca tac ctt gac Tyr Gly Asn Arg Val Asp Arg Phe Leu Ala Gly Val Ala Tyr Leu Asp 300 305 310 315	1445
ggg gag cgg ccg agt ttt gtc atg gca cgc ggt tat tac acg aga aca Gly Glu Arg Pro Ser Phe Val Met Ala Arg Gly Tyr Tyr Thr Arg Thr 320 325 330	1493
gtg cta gtc gct tac aac ttc aga ggc gga aag ctg acc aag ctg tgg Val Leu Val Ala Tyr Asn Phe Arg Gly Gly Lys Leu Thr Lys Leu Trp 335 340 345	1541
acg ttc gat tcg gat gct ccc gga aat ggc gcc tat gcc ggt caa ggc Thr Phe Asp Ser Asp Ala Pro Gly Asn Gly Ala Tyr Ala Gly Gln Gly 350 355 360	1589
aac cac agt ttg agc gtc gcc gac gtt gac gga gat gga aag gac gag Asn His Ser Leu Ser Val Ala Asp Val Asp Gly Asp Gly Lys Asp Glu 365 370 375	1637
atc ata tac gga gcg atg gct gtc gat cat gac gga aaa ggc ctc tac Ile Ile Tyr Gly Ala Met Ala Val Asp His Asp Gly Lys Gly Leu Tyr 380 385 390 395	1685
tca acc ggc tgg gga cat ggg gat gcc atg cat aca ggg aac ctg gac Ser Thr Gly Trp Gly His Gly Asp Ala Met His Thr Gly Asn Leu Asp 400 405 410	1733
ccg tca agg cct gga ctg gaa gtc ttc caa gtc cat gaa aac agc aat Pro Ser Arg Pro Gly Leu Glu Val Phe Gln Val His Glu Asn Ser Asn 415 420 425	1781
tct cct tat ggc ttg tcc ttc cgc gat gcg aaa aca gga aag atc atc Ser Pro Tyr Gly Leu Ser Phe Arg Asp Ala Lys Thr Gly Lys Ile Ile 430 435 440	1829
tgg gga gtt cac gca ggt aaa gat gtc gga cgc gga atg gcc gct gat Trp Gly Val His Ala Gly Lys Asp Val Gly Arg Gly Met Ala Ala Asp 445 450 455	1877
atc gat ccg cgc tac gaa gga gcg gaa gta tgg gcg aac ggc agt ctt Ile Asp Pro Arg Tyr Glu Gly Ala Glu Val Trp Ala Asn Gly Ser Leu 460 465 470 475	1925
tat acg gca aaa ggc gta aaa atc gga aac aca ttg cct tca tca acg Tyr Thr Ala Lys Gly Val Lys Ile Gly Asn Thr Leu Pro Ser Ser Thr 480 485 490	1973
aac ttc ggc atc tgg tgg gac ggc gat ctc caa aga gag ctt ctg gac Asn Phe Gly Ile Trp Trp Asp Gly Asp Leu Gln Arg Glu Leu Leu Asp 495 500 505	2021
agc aac aga att gat aaa tgg gat tat caa aat tcg cga acc gtc aac Ser Asn Arg Ile Asp Lys Trp Asp Tyr Gln Asn Ser Arg Thr Val Asn 510 515 520	2069
ttg ctg aca gcg tcc gga gct tcg gca aat aac gga aca aaa gcg acg Leu Leu Thr Ala Ser Gly Ala Ser Ala Asn Asn Gly Thr Lys Ala Thr 525 530 535	2117
ccg tcc ctg cag gcg gac att ctc gga gac tgg cgc gaa gaa gtg gtc Pro Ser Leu Gln Ala Asp Ile Leu Gly Asp Trp Arg Glu Glu Val Val 540 545 550 555	2165

10294.204.ST25.txt

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 Trp Arg Ala Glu Asp Ser Ser Glu Leu Arg Ile Tyr Thr Thr Thr Asp
 560 565 570
 gtg acg gag cac cgc atg tat acg ctg atg cat gat gca gtc tat cgc 2261
 Val Thr Glu His Arg Met Tyr Thr Leu Met His Asp Ala Val Tyr Arg
 575 580 585
 ctc ggt atc gcc tgg cag aat gtc ggc tac aac cag cct ccg cac acc 2309
 Leu Gly Ile Ala Trp Gln Asn Val Gly Tyr Asn Gln Pro Pro His Thr
 590 595 600
 ggc ttt tat tta ggc gaa ggc atg cag aca ccg gag aag ccg aac att 2357
 Gly Phe Tyr Leu Gly Glu Gly Met Gln Thr Pro Glu Lys Pro Asn Ile
 605 610 615
 tat aca cgc tgatgataaa ggggagctgc ataatgaagc gatatgttcg 2406
 Tyr Thr Arg
 620
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 <213> Bacillus licheniformis

<400> 236

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20 25 30

Asp Gly Arg Thr Ala Ala Gln Ala Arg Gln Met Glu Ser Leu Asn Arg
35 40 45

Gly Leu Val Ala Val Lys Thr Gly Asn Gly Val Phe Val Ser Trp Arg
50 55 60

Leu Leu Gly Thr Glu Pro Ser Ser Val Ser Phe Asn Val Tyr Arg Asn
65 70 75 80

Gly Lys Lys Leu Asn Gly Ser Pro Ile Thr Ser Ser Thr Asn Tyr Gln
85 90 95

10294.204.ST25.txt

Asp Ala Gly Gly Asp Leu Asn Ala Val Tyr Gln Val Arg Ala Val Leu
 100 105 110

Asn Gly Arg Glu Gln Ala Pro Ser Glu Ser Val Gly Val Leu Asn Lys
 115 120 125

Gln Tyr Lys Ser Val Pro Leu Gln Lys Pro Ala Gly Gly Lys Thr Pro
 130 135 140

Asp Gly Val Ser Tyr Thr Tyr Ser Ala Asn Asp Ala Ser Val Gly Asp
 145 150 155 160

Leu Asp Gly Asp Gly Gln Tyr Glu Ile Ile Leu Lys Trp Asp Pro Ser
 165 170 175

Asn Ser Lys Asp Asn Ser Gln Asp Gly Tyr Thr Gly Asp Val Leu Ile
 180 185 190

Asp Ala Tyr Lys Leu Asp Gly Thr Met Met Trp Arg Ile Asn Leu Gly
 195 200 205

Lys Asn Ile Arg Ala Gly Ala His Tyr Thr Gln Phe Leu Val Tyr Asp
 210 215 220

Phe Asp Gly Asp Gly Lys Ala Glu Ile Ala Met Lys Thr Ala Asp Gly
 225 230 235 240

Thr Lys Asp Gly Lys Gly Lys Val Ile Gly Asn Ala Asn Ala Asp Tyr
 245 250 255

Arg Asn Ala Gln Gly Arg Ile Leu Ser Gly Pro Glu Tyr Leu Thr Val
 260 265 270

Phe Lys Gly Asp Thr Gly Ala Glu Leu Thr Thr Val Asn Tyr Glu Pro
 275 280 285

Ala Arg Gly Asn Val Ala Asp Trp Gly Asp Ser Tyr Gly Asn Arg Val
 290 295 300

Asp Arg Phe Leu Ala Gly Val Ala Tyr Leu Asp Gly Glu Arg Pro Ser
 305 310 315 320

Phe Val Met Ala Arg Gly Tyr Tyr Thr Arg Thr Val Leu Val Ala Tyr
 325 330 335

Asn Phe Arg Gly Gly Lys Leu Thr Lys Leu Trp Thr Phe Asp Ser Asp
 340 345 350

Ala Pro Gly Asn Gly Ala Tyr Ala Gly Gln Gly Asn His Ser Leu Ser
 355 360 365

10294.204.ST25.txt

Val Ala Asp Val Asp Gly Asp Gly Lys Asp Glu Ile Ile Tyr Gly Ala
 370 375 380
 Met Ala Val Asp His Asp Gly Lys Gly Leu Tyr Ser Thr Gly Trp Gly
 385 390 395 400
 His Gly Asp Ala Met His Thr Gly Asn Leu Asp Pro Ser Arg Pro Gly
 405 410 415
 Leu Glu Val Phe Gln Val His Glu Asn Ser Asn Ser Pro Tyr Gly Leu
 420 425 430
 Ser Phe Arg Asp Ala Lys Thr Gly Lys Ile Ile Trp Gly Val His Ala
 435 440 445
 Gly Lys Asp Val Gly Arg Gly Met Ala Ala Asp Ile Asp Pro Arg Tyr
 450 455 460
 Glu Gly Ala Glu Val Trp Ala Asn Gly Ser Leu Tyr Thr Ala Lys Gly
 465 470 475 480
 Val Lys Ile Gly Asn Thr Leu Pro Ser Ser Thr Asn Phe Gly Ile Trp
 485 490 495
 Trp Asp Gly Asp Leu Gln Arg Glu Leu Leu Asp Ser Asn Arg Ile Asp
 500 505 510
 Lys Trp Asp Tyr Gln Asn Ser Arg Thr Val Asn Leu Leu Thr Ala Ser
 515 520 525
 Gly Ala Ser Ala Asn Asn Gly Thr Lys Ala Thr Pro Ser Leu Gln Ala
 530 535 540
 Asp Ile Leu Gly Asp Trp Arg Glu Glu Val Val Trp Arg Ala Glu Asp
 545 550 555 560
 Ser Ser Glu Leu Arg Ile Tyr Thr Thr Thr Asp Val Thr Glu His Arg
 565 570 575
 Met Tyr Thr Leu Met His Asp Ala Val Tyr Arg Leu Gly Ile Ala Trp
 580 585 590
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 595 600 605
 Glu Gly Met Gln Thr Pro Glu Lys Pro Asn Ile Tyr Thr Arg
 610 615 620

<210> 237
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 <212> DNA

10294.204.ST25.txt

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1688)

<400> 237

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aacggttaca ctaaaaaacg caatgaaatt caacgacagc aagacattca tcagctgctc      360
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gaaaaaaggg agtgtcttca ttg gtg ccg ctt atg att atg gta tgt ttt ctc      533
                        Leu Val Pro Leu Met Ile Met Val Cys Phe Leu
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atc ctg ctt ctt gcg ctc gat ttc cat ttt ggc cgc aaa gcc ttt gag      581
Ile Leu Leu Leu Ala Leu Asp Phe His Phe Gly Arg Lys Ala Phe Glu
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aag aaa gcc tac gag ccc gtt ttt tca gag aag aaa agc gat att gaa      629
Lys Lys Ala Tyr Glu Pro Val Phe Ser Glu Lys Lys Ser Asp Ile Glu
                        30          35          40

ctg att cat aat gga gaa gac ttg tgt gag cgg ctg ctg gat gac atc      677
Leu Ile His Asn Gly Glu Asp Leu Cys Glu Arg Leu Leu Asp Asp Ile
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cgc cag gcc gaa tcg tcg gtg cat gtc atg ttt tat att gtg aag aac      725
Arg Gln Ala Glu Ser Ser Val His Val Met Phe Tyr Ile Val Lys Asn
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gat gac atc agc ctt gaa ttt ttg aag gtg ctg aag gat aaa gcg aaa      773
Asp Asp Ile Ser Leu Glu Phe Leu Lys Val Leu Lys Asp Lys Ala Lys
                        80          85          90

tcc ggc gta tgc gta cga ttg ctg atc gac cgg atc ggc gcg atg aag      821
Ser Gly Val Cys Val Arg Leu Leu Ile Asp Arg Ile Gly Ala Met Lys
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gtg aag aaa aaa acg ctc tcc ggc ctg aaa caa agc ggt gtg cac gtt      869
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ttt ttc gcc aac aag ccg ggc ttc ccc tat ttc ttt tac cgg ctg aat      917
Phe Phe Ala Asn Lys Pro Gly Phe Pro Tyr Phe Phe Tyr Arg Leu Asn
                        125          130          135

gcg agg aat cat cga aaa atc gcc gtc ata gac gga aag atc ggc tat      965
Ala Arg Asn His Arg Lys Ile Ala Val Ile Asp Gly Gly Lys Ile Gly Tyr
                        140          145          150          155

gtg ggc gga ttt aac atc gcg aaa gaa tac ctt ggt aaa aaa gcg gaa      1013
Val Gly Gly Phe Asn Ile Ala Lys Glu Tyr Leu Gly Lys Lys Lys Ala Glu
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10294.204.ST25.txt

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cag gca aag ccg gcc aac agc gta ttt ccg ccg ctg cag caa gga gct Gln Ala Lys Pro Ala Asn Ser Val Phe Pro Pro Leu Gln Gln Gly Ala 205 210 215	1157
gtc acc cat aca acc cat gcg aca aag gga ttt tct cta gag gaa aaa Val Thr His Thr Thr His Ala Thr Lys Gly Phe Ser Leu Glu Glu Lys 220 225 230 235	1205
tac att tca ttt atc gaa cag gca aaa gaa aga atc atg att tgc acg Tyr Ile Ser Phe Ile Glu Gln Ala Lys Glu Arg Ile Met Ile Cys Thr 240 245 250	1253
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cat gat aaa gac tgg aca aag caa ttc ttc gac gtc gtc aag gaa agc His Asp Lys Asp Trp Thr Lys Gln Phe Phe Asp Val Val Lys Glu Ser 350 355 360	1589
att gaa cac gcc gag ctt ctg aca aag gag cgg tat gcg aag cgg ccg Ile Glu His Ala Glu Leu Leu Thr Lys Glu Arg Tyr Ala Lys Arg Pro 365 370 375	1637
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Ser Val His Val Met Phe Tyr Ile Val Lys Asn Asp Asp Ile Ser Leu
65 70 75 80

Glu Phe Leu Lys Val Leu Lys Asp Lys Ala Lys Ser Gly Val Cys Val
85 90 95

Arg Leu Leu Ile Asp Arg Ile Gly Ala Met Lys Val Lys Lys Lys Thr
100 105 110

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115 120 125

Pro Gly Phe Pro Tyr Phe Phe Tyr Arg Leu Asn Ala Arg Asn His Arg
130 135 140

Lys Ile Ala Val Ile Asp Gly Lys Ile Gly Tyr Val Gly Gly Phe Asn
145 150 155 160

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165 170 175

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His Ala Thr Lys Gly Phe Ser Leu Glu Glu Lys Tyr Ile Ser Phe Ile
 225 230 235 240

Glu Gln Ala Lys Glu Arg Ile Met Ile Cys Thr Pro Tyr Tyr Ile Pro
 245 250 255

Ser Pro Ala Leu Gln Gln Ala Val Leu Ser Ala Arg Glu Arg Gly Val
 260 265 270

Ile Val Ser Val Leu Val Pro Met Lys Pro Asp His Pro Leu Val Lys
 275 280 285

Glu Ala Ala Tyr Thr His Phe Pro Ala Leu Leu Lys Ala Gly Cys Tyr
 290 295 300

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 305 310 315 320

Asp Asp Arg His Val Met Ile Gly Thr Ser Asn Phe Asp Asn Arg Ser
 325 330 335

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 340 345 350

Thr Lys Gln Phe Phe Asp Val Val Lys Glu Ser Ile Glu His Ala Glu
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 aagtcttctt ttacacttaa atgtatagac gtctatacgt gtttcaccct ctgcacaacc 300

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Glu	Val	Ala	Lys	Ala	Asp	Ser	Gly	Lys	Asn	Tyr	Lys	Ile	Ile	Gly	Tyr	
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Trp	Glu	Gly	Arg	His	Gly	Asn	Pro	Asp	Pro	Thr	Gly	Pro	Asn	Pro	Gln	
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Asp	Phe	Ala	Pro	Asp	Gly	Gly	Asn	Pro	Glu	Pro	Pro	Ser	Ser	Ala	Pro		
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Phe	Glu	Asn	Arg	Ser	Ile	Ser	Val	Lys	Glu	Thr	Ser	Ala	Glu	Ile	Gly		
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gcg gat gga aag ctc cat gcc gga cca acg gta gag gtc acg acg aat 2117
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tct gac caa gcc tgt tca tat gac gaa tgg aaa gag acg agc gca tac 2165
 Ser Asp Gln Ala Cys Ser Tyr Asp Glu Trp Lys Glu Thr Ser Ala Tyr
 540 545 550 555

aca ggc gga gag cgg gtt gca ttt aac gga aaa gtg tat gaa gcg aaa 2213
 Thr Gly Gly Glu Arg Val Ala Phe Asn Gly Lys Val Tyr Glu Ala Lys
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 Trp Trp Thr Lys Gly Asp Arg Pro Asp Gln Ser Gly Glu Trp Gly Val
 575 580 585

tgg cgg ctg atc gga ggc tgc gaa taagagaaag tcaaattggat agaaaacgat 2315
 Trp Arg Leu Ile Gly Gly Cys Glu
 590 595

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<213> Bacillus licheniformis

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Asp Ser Gly Lys Asn Tyr Lys Ile Ile Gly Tyr Tyr Pro Ser Trp Gly
 35 40 45

Ala Tyr Gly Arg Asp Phe Gln Val Trp Asp Met Asp Val Ser Lys Val
 50 55 60

Ser His Ile Asn Tyr Ala Phe Ala Asp Ile Cys Trp Glu Gly Arg His
 65 70 75 80

Gly Asn Pro Asp Pro Thr Gly Pro Asn Pro Gln Thr Trp Ser Cys Gln
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85

90

95

Asp Glu Asn Gly Val Ile Asp Ala Pro Asn Gly Thr Ile Val Met Gly
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Asp Pro Trp Ile Asp Ala Gln Lys Ser Asn Pro Gly Asp Val Trp Asp
115 120 125

Glu Pro Ile Arg Gly Asn Phe Lys Gln Leu Leu Lys Leu Lys Lys Ser
130 135 140

His Pro His Leu Lys Thr Phe Ile Ser Val Gly Gly Trp Thr Trp Ser
145 150 155 160

Asn Arg Phe Ser Asp Val Ala Ala Asp Pro Ala Ala Arg Glu Asn Phe
165 170 175

Ala Ala Ser Ala Val Glu Phe Leu Arg Lys Tyr Gly Phe Asp Gly Val
180 185 190

Asp Leu Asp Trp Glu Tyr Pro Val Ser Gly Gly Leu Pro Gly Asn Ser
195 200 205

Thr Arg Pro Glu Asp Lys Arg Asn Tyr Thr Leu Leu Leu Gln Glu Val
210 215 220

Arg Lys Lys Leu Asp Ala Ala Glu Ala Lys Asp Gly Lys Glu Tyr Leu
225 230 235 240

Leu Thr Ile Ala Ser Gly Ala Ser Pro Asp Tyr Val Ser Asn Thr Glu
245 250 255

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260 265 270

Asp Phe Asn Gly Gly Trp Gln Ser Ile Ser Ala His Asn Ala Pro Leu
275 280 285

Phe Tyr Asp Pro Lys Ala Lys Glu Ala Gly Val Pro Asn Ala Glu Thr
290 295 300

Tyr Asn Ile Glu Asn Thr Val Lys Arg Tyr Lys Glu Ala Gly Val Lys
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Gly Asp Lys Leu Val Leu Gly Thr Pro Phe Tyr Gly Arg Gly Trp Ser
325 330 335

Gly Cys Glu Pro Gly Gly His Gly Glu Tyr Gln Lys Cys Gly Pro Ala
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Lys Glu Gly Thr Trp Glu Lys Gly Val Phe Asp Phe Ser Asp Leu Glu
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355

360

365

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 370 375 380

Ala Lys Val Pro Phe Leu Tyr Asn Ala Glu Asn Gly Asn Phe Ile Thr
 385 390 395 400

Tyr Asp Asp Glu Gln Ser Phe Gly His Lys Thr Asp Phe Ile Lys Ala
 405 410 415

Asn Gly Leu Ser Gly Ala Met Phe Trp Asp Phe Ser Gly Asp Ser Asn
 420 425 430

Arg Thr Leu Leu Asn Lys Leu Ala Ala Asp Leu Asp Phe Ala Pro Asp
 435 440 445

Gly Gly Asn Pro Glu Pro Pro Ser Ser Ala Pro Val Asn Val Arg Val
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Thr Gly Lys Thr Ala Thr Ser Val Ser Leu Ala Trp Asp Ala Pro Ser
 465 470 475 480

Ser Gly Ala Asn Ile Ala Glu Tyr Val Val Ser Phe Glu Asn Arg Ser
 485 490 495

Ile Ser Val Lys Glu Thr Ser Ala Glu Ile Gly Gly Leu Lys Pro Gly
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Thr Ala Tyr Ser Phe Thr Val Ser Ala Lys Asp Ala Asp Gly Lys Leu
 515 520 525

His Ala Gly Pro Thr Val Glu Val Thr Thr Asn Ser Asp Gln Ala Cys
 530 535 540

Ser Tyr Asp Glu Trp Lys Glu Thr Ser Ala Tyr Thr Gly Gly Glu Arg
 545 550 555 560

Val Ala Phe Asn Gly Lys Val Tyr Glu Ala Lys Trp Trp Thr Lys Gly
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Gly Cys Glu
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gtaggagagg atgatgcaga atg aag aca aaa caa acg gtt aat gcc ctt att 533
Met Lys Thr Lys Gln Thr Val Asn Ala Leu Ile
1 5 10

ttt att gtg gtt tta ttt tta att gtt cat gtc ttt caa tcg ctt gaa 581
Phe Ile Val Val Leu Phe Leu Ile Val His Val Phe Gln Ser Leu Glu
15 20 25

gca gcg ggc aat acg ccg ctt gaa cag ctg gcg gaa ggt ttg agc cgc 629
Ala Ala Gly Asn Thr Pro Leu Glu Gln Leu Ala Glu Gly Leu Ser Arg
30 35 40

cat gat gtc gag ctt gaa gag tgg acc atg cat aca aaa aaa cag ctt 677
His Asp Val Glu Leu Glu Glu Trp Thr Met His Thr Lys Lys Gln Leu
45 50 55

acc cta agt gaa aaa gat ttt ttt gca aaa ctg aaa cat ttc aag aaa 725
Thr Leu Ser Glu Lys Asp Phe Phe Ala Lys Leu Lys His Phe Lys Lys
60 65 70 75

cag cat cga caa tat gaa tgg act tta acg cgg gaa gac gac gat aca 773
Gln His Arg Gln Tyr Glu Trp Thr Leu Thr Arg Glu Asp Asp Asp Thr
80 85 90

gtt aaa gcg aca ggt gtt ttt cag gac aaa aaa aat cat atc aat tcc 821
Val Lys Ala Thr Gly Val Phe Gln Asp Lys Lys Asn His Ile Asn Ser
95 100 105

aaa ata cat ttg gta tcc acc cac aaa aac cag aga ctt gtt tcg tat 869
Lys Ile His Leu Val Ser Thr His Lys Asn Gln Arg Leu Val Ser Tyr
110 115 120

tta ttg tat gag caa aaa ggc gcg gga cca cgg gaa aac tgg aat gct 917
Leu Leu Tyr Glu Gln Lys Gly Ala Gly Pro Arg Glu Asn Trp Asn Ala
125 130 135

aca tat aag cag ttt gaa cgg gat gca ttc gac ata atg cga gaa aag 965
Thr Tyr Lys Gln Phe Glu Arg Asp Ala Phe Asp Ile Met Arg Glu Lys
140 145 150 155

acc gca att ttt act tgt cta aag ggc cat tta aat ggt atg atg aat 1013
Thr Ala Ile Phe Thr Cys Leu Lys Gly His Leu Asn Gly Met Met Asn
160 165 170

gtt gtt ttg caa aaa aaa gca aat gag cta gta cat gaa ttt gat gca 1061
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10294.204.ST25.txt

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190                               195                               200

tac act aac gag tgg aaa gaa tcc atc aag aca gaa aaa cac cgt atg      1157
Tyr Thr Asn Glu Trp Lys Glu Ser Ile Lys Thr Glu Lys His Arg Met
205                               210                               215

aat ttg caa gtc tcg ctt aga aat gcg gga atg ggc gaa aaa ctt acc      1205
Asn Leu Gln Val Ser Leu Arg Asn Ala Gly Met Gly Glu Lys Leu Thr
220                               225                               230

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Val Thr Val Gly Thr Pro Ile Val Thr Thr Glu Tyr
240                               245

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Pro Leu Glu Gln Leu Ala Glu Gly Leu Ser Arg His Asp Val Glu Leu
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Glu Glu Trp Thr Met His Thr Lys Lys Gln Leu Thr Leu Ser Glu Lys
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Asp Phe Phe Ala Lys Leu Lys His Phe Lys Lys Gln His Arg Gln Tyr
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Glu Trp Thr Leu Thr Arg Glu Asp Asp Thr Val Lys Ala Thr Gly
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10294.204.ST25.txt
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Ser Thr His Lys Asn Gln Arg Leu Val Ser Tyr Leu Leu Tyr Glu Gln
 115 120 125

Lys Gly Ala Gly Pro Arg Glu Asn Trp Asn Ala Thr Tyr Lys Gln Phe
 130 135 140

Glu Arg Asp Ala Phe Asp Ile Met Arg Glu Lys Thr Ala Ile Phe Thr
 145 150 155 160

Cys Leu Lys Gly His Leu Asn Gly Met Met Asn Val Val Leu Gln Lys
 165 170 175

Lys Ala Asn Glu Leu Val His Glu Phe Asp Ala Lys Ser Val Glu Asp
 180 185 190

Leu Ile Glu Pro Asn Phe Val Ser Ile Ser Ala Tyr Thr Asn Glu Trp
 195 200 205

Lys Glu Ser Ile Lys Thr Glu Lys His Arg Met Asn Leu Gln Val Ser
 210 215 220

Leu Arg Asn Ala Gly Met Gly Glu Lys Leu Thr Val Thr Val Gly Thr
 225 230 235 240

Pro Ile Val Thr Thr Glu Tyr
 245

<210> 243
 <211> 1948
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 <213> Bacillus licheniformis

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 cataacatca agtgaaccaa agtggttcaac tgctgaatta atcagctttt tcacgtcctc 120
 ttcggaagac acgtcagctt ctatcgcaag ggcgtttccg cccgctgctt gaatattgtc 180
 gacggccttc cgtgcgcctc cgggatcgct gtgataattg acaaccacat tcattctttc 240
 ttttccaaac cggttctgcaa ccgccttgcc tatacctttt gaagagccgg tcacaattgc 300
 tgtttttctt tttaaatcac tatacaacct aaacaccctt caatttcttt tctccatgta 360
 cattaccggt tatcaatata tgatcaaaca aaatgttaat acacaccttt agtatgatct 420
 tttttaaaca tatggaaaat tcagaattat tttgttaata tctaacttgt acttacaaca 480
 aaataaggaa gtgatatgat ttg gtt agt aaa aag agt gtt aaa cga ggt ttg 533

10294.204.ST25.txt

Leu Val Ser Lys Lys Ser Val Lys Arg Gly Leu
 1 5 10

atc aca ggt ctc att ggt att tct att tat tct tta ggt atg cac ccg 581
 Ile Thr Gly Leu Ile Gly Ile Ser Ile Tyr Ser Leu Gly Met His Pro
 15 20 25

gcc caa gcc gcg cca tcg cct cat act cct gtt tca agc gat cct tca 629
 Ala Gln Ala Ala Pro Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser
 30 35 40

tac aaa gcg gaa aca tcg gtt act tat gac cca aac att aag agc gat 677
 Tyr Lys Ala Glu Thr Ser Val Thr Tyr Asp Pro Asn Ile Lys Ser Asp
 45 50 55

caa tac ggc ttg tat tca aaa gcg ttt aca ggc acc ggc aaa gtg aat 725
 Gln Tyr Gly Leu Tyr Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Asn
 60 65 70 75

gaa aca aag gaa aaa gcg gaa aaa aag tca ccc gcc aaa gct cct tac 773
 Glu Thr Lys Glu Lys Ala Glu Lys Lys Ser Pro Ala Lys Ala Pro Tyr
 80 85 90

agc att aaa tcg gtg att ggt tct gat gat cgg aca agg gtc acc aac 821
 Ser Ile Lys Ser Val Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn
 95 100 105

aca acc gca tat ccg tac aga gcg atc gtt cat att tca agc agc atc 869
 Thr Thr Ala Tyr Pro Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile
 110 115 120

ggt tca tgc acc gga tgg atg atc ggt ccg aaa acc gtc gca aca gcc 917
 Gly Ser Cys Thr Gly Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala
 125 130 135

gga cac tgc atc tat gac aca tca agc ggt tca ttt gcc ggt aca gcc 965
 Gly His Cys Ile Tyr Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala
 140 145 150 155

act gtt tcg ccg gga ccg aac ggg aca agc tat cct tac ggc tca gtt 1013
 Thr Val Ser Pro Gly Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val
 160 165 170

aaa tcg acg cgc tac ttt att ccg tca gga tgg aga agc gga aac acc 1061
 Lys Ser Thr Arg Tyr Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr
 175 180 185

aat tac gat tac ggc gca atc gaa cta agc gaa ccg atc ggc aat act 1109
 Asn Tyr Asp Tyr Gly Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr
 190 195 200

gtc gga tac ttc gga tac tcg tac act act tca tca ctt gtt ggg aca 1157
 Val Gly Tyr Phe Gly Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Thr
 205 210 215

act gtt acc atc agc ggc tac cca ggc gat aaa aca gca ggc aca caa 1205
 Thr Val Thr Ile Ser Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln
 220 225 230 235

tgg cag cat tca gga ccg att gcc atc tcc gaa acg tat aaa ttg cag 1253
 Trp Gln His Ser Gly Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln
 240 245 250

tac gca atg gac acg tac gga gga caa agc ggt tca ccg gta ttc gaa 1301
 Tyr Ala Met Asp Thr Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu
 255 260 265

caa agc agc tcc aga acg aac tgc agc ggt ccg tgc tcg ctt gcc gta 1349

10294.204.ST25.txt

Gln Ser Ser Ser Arg Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val
 270 275 280

cac aca aat gga gta tac ggc ggc tcc tcg tac aac aga ggc acc cgg 1397
 His Thr Asn Gly Val Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg
 285 290 295

att aca aaa gag gtg ttc gac aat ttg acc aac tgg aaa aac agc gca 1445
 Ile Thr Lys Glu Val Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala
 300 305 310 315

caa taatacacga agacagcccg cttccttttg gaacgggctg tcacatctaa 1498
 Gln

cggccgtata ctttaatttcc ttttaagcctg tacttttttg catctattga tatcgtgaaa 1558

tttgaaggac cgctgatcgg caaataatag acaagctgaa actccgcttc ctcaccaggt 1618

ttaatggttt tccagattga tagagtcact ctgatgcggt ggaaatctac tgtcagtcgg 1678

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ctaaaccgag gggaagtgga tgtcggcgca tcaaattcga taaaagaacc tcccgtaatc 1798

gtgacatcgc tgttgttgat cagcttcac accgggtgga tcgggtaatt ttgatctcct 1858

aacggaaagt tcgtcaactc tacttctgca tctagtgatt catcaggcaa aggtgatgtg 1918

ctgagtcgat tatcgtatgg tgttgtatcc 1948

<210> 244
 <211> 316
 <212> PRT
 <213> Bacillus licheniformis

<400> 244

Leu Val Ser Lys Lys Ser Val Lys Arg Gly Leu Ile Thr Gly Leu Ile
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Gly Ile Ser Ile Tyr Ser Leu Gly Met His Pro Ala Gln Ala Ala Pro
 20 25 30

Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Ala Glu Thr
 35 40 45

Ser Val Thr Tyr Asp Pro Asn Ile Lys Ser Asp Gln Tyr Gly Leu Tyr
 50 55 60

Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Asn Glu Thr Lys Glu Lys
 65 70 75 80

Ala Glu Lys Lys Ser Pro Ala Lys Ala Pro Tyr Ser Ile Lys Ser Val
 85 90 95

Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn Thr Thr Ala Tyr Pro
 100 105 110

Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly
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115

120

125

Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr
 130 135 140

Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly
 145 150 155 160

Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr
 165 170 175

Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly
 180 185 190

Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly
 195 200 205

Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Thr Thr Val Thr Ile Ser
 210 215 220

Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly
 225 230 235 240

Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr
 245 250 255

Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg
 260 265 270

Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val
 275 280 285

Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val
 290 295 300

Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln
 305 310 315

<210> 245
 <211> 1231
 <212> DNA
 <213> Bacillus licheniformis

<220>
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 <222> (501)..(731)

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 aatgggcgtc caccttgaaa tcacccgcgc gtccggagga aggagttttt ggaggccttt 120
 tctatataag gggagggagg agccaaaacg gggacctttc cgaaattatg tcaagccggt 180

10294.204.ST25.txt

ccccaaggtg ctccaggcca gatcctgaaa atggaacctc aggttattcg gggtaggacc 240
 tgctaaacca tgagggagga ataaaggaat ggaccggaaa gcccgcttcg tccaggaatt 300
 tatgtcccac cgccttgtgc cggaggacct cattcaaaaa attgatgaaa accttttcga 360
 ttccaacccg cctgaaccgt cgatgccacc aaaggacctt gtccacgcat atgctgcaat 420
 ctttctatac ctttgcttcg gcggcaaagg aaggggaccgg agaccctttt aaaaagaagc 480
 ccgaagaacc agggacaagc ttg agc gag ctt gcc aaa acg tat cca gaa aaa 533
 Leu Ser Glu Leu Ala Lys Thr Tyr Pro Glu Lys
 1 5 10
 aca aaa acg ctg ctt gaa tcc ttt acg gat gaa gaa ttg gat cgt gaa 581
 Thr Lys Thr Leu Leu Glu Ser Phe Thr Asp Glu Glu Leu Asp Arg Glu
 15 20 25
 gtc gat ttg acc ggc gtc ttc gga cga aaa gta gcc ggc gaa cag cta 629
 Val Asp Leu Thr Gly Val Phe Gly Arg Lys Val Ala Gly Glu Gln Leu
 30 35 40
 ctg cag ctc gcg atc gga cac gaa att cac cac aaa ggc aat ctg ttt 677
 Leu Gln Leu Ala Ile Gly His Glu Ile His His Lys Gly Asn Leu Phe
 45 50 55
 gtt tat gtc cgt gaa atg gga cac acg gat ctg cct ttg tat gta aag 725
 Val Tyr Val Arg Glu Met Gly His Thr Asp Leu Pro Leu Tyr Val Lys
 60 65 70 75
 att cat tgatcctgag agccctcctt gaaagaaaac cggttaaaaa ggaatacgaa 781
 Ile His
 agcaccgagg agtacacatt atgagtaaaa gctaaaggag ggtgtcaggt gaatacgag 841
 cgtgcccagg aaatcgtcga atcaccgat atggttgatg ttacttataa cggcaggccg 901
 atttatattc agcgtgtcga cgaacaaaat gaaaccgcaa gaatctttcc gctcggccag 961
 ccggagaacg agcaggaagt gccgctcgca aatttgaaag aacattaaaa agaaaccctt 1021
 tctgaggaag gggttttgtt ttggatttgc ctgccacaca gccatcaaaa aaacaccgga 1081
 aagaccgagt gtttaattta taattttcgc aagtcctctt actgccagcc tcagcacata 1141
 aaacaatggc tcaagcaa at cgacgagata aagataatcc catttgatcat cattacgttt 1201
 attttttttc ttcaacgaat gtttctcctt 1231

<210> 246
 <211> 77
 <212> .PRT
 <213> Bacillus licheniformis

<400> 246

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 20 25 30

Val Phe Gly Arg Lys Val Ala Gly Glu Gln Leu Leu Gln Leu Ala Ile
 35 40 45

10294.204.ST25.txt

Gly His Glu Ile His His Lys Gly Asn Leu Phe Val Tyr Val Arg Glu
 50 55 60

Met Gly His Thr Asp Leu Pro Leu Tyr Val Lys Ile His
 65 70 75

<210> 247
 <211> 1597
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1097)

<400> 247
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 cattccccgaa attaaatcgt ctttttccaa aaaaagtgcg cgaaaaaagc gaaaaccgcg 180
 ccaagcggaa tacaggagat cattgcggtt ccgttgacca gcccgtcagc cccgcttatt 240
 ttcagggcctt cccggtagcc tattaataaag tggatgatcg ataggacata acataagagc 300
 atcatatagt aaggattcat ttgtataccc tcctctattc gctttactat attacattca 360
 atagagggaa agattatgcc tgtttaagta ggaaaaagaa caaatatta tagacgaaaa 420
 gattttcaat tacaatacat gtttttaaaa atatttccac tataatcaaa atgaaagata 480
 aatttagggg gtcatacaaa atg aaa aaa agg ctg atg tca cta ttg gtc tgc 533
 Met Lys Lys Arg Leu Met Ser Leu Leu Val Cys
 1 5 10
 atc ctg gtt tta gtg ccg gca gca gga gct ttt gcc gcg ccg aaa cag 581
 Ile Leu Val Leu Val Pro Ala Ala Gly Ala Phe Ala Ala Pro Lys Gln
 15 20 25
 gcc gag ctt aaa gat tat ctt gaa gaa ata gga atg aca gaa aaa gaa 629
 Ala Glu Leu Lys Asp Tyr Leu Glu Glu Ile Gly Met Thr Glu Lys Glu
 30 35 40
 ttg gaa gcc tat ttg cag gat aca tat gat gag agt tta aaa ggt ttt 677
 Leu Glu Ala Tyr Leu Gln Asp Thr Tyr Asp Glu Ser Leu Lys Gly Phe
 45 50 55
 gac tcg gtg gaa gag ttg aaa gac ttt tta ggg caa aga ctg act aaa 725
 Asp Ser Val Glu Glu Leu Lys Asp Phe Leu Gly Gln Arg Leu Thr Lys
 60 65 70 75
 aag ctt ttg gca tcc tat ttg aaa gaa tac gga ttg agc gaa aaa gaa 773
 Lys Leu Leu Ala Ser Tyr Leu Lys Glu Tyr Gly Leu Ser Glu Lys Glu
 80 85 90
 gcg gct gac cta ttt gtt gaa aat ggc tat atg gaa agc ggc caa aac 821
 Ala Ala Asp Leu Phe Val Glu Asn Gly Tyr Met Glu Ser Gly Gln Asn
 95 100 105
 att ctc gac gtg ttt atg ttt gaa tac gaa ttg gac gat gcg ctc tac 869
 Ile Leu Asp Val Phe Met Phe Glu Tyr Glu Leu Asp Ala Leu Tyr
 110 115 120

10294.204.ST25.txt

acc gtg aca tat gaa gaa gac gat ttt cag atc gga aac atg ttt caa 917
 Thr Val Thr Tyr Glu Glu Asp Asp Phe Gln Ile Gly Asn Met Phe Gln
 125 130 135

gaa ttg ggt gtg gat gat cag gag tgg gaa aga ctc gtg aat cac ctc 965
 Glu Leu Gly Val Asp Asp Gln Glu Trp Glu Arg Leu Val Asn His Leu
 140 145 150 155

cga aaa gtg cgc gat aac aat ccg aac ctt gaa aat gac ttg atg gct 1013
 Arg Lys Val Arg Asp Asn Asn Pro Asn Leu Glu Asn Asp Leu Met Ala
 160 165 170

ctt gga gaa cgt ctt gaa gcg gta gcc gat ttc gag tct gta tca gag 1061
 Leu Gly Glu Arg Leu Glu Ala Val Ala Asp Phe Glu Ser Val Ser Glu
 175 180 185

ctg tca gct cag gat atc gct gaa tgc tgt cca ttt taacgatctt 1107
 Leu Ser Ala Gln Asp Ile Ala Glu Cys Cys Pro Phe
 190 195

cagaagacgc tcgaagtga aacgaatatt atcttggttaa gacggaaaga aaaaagaagt 1167
 gtctttgacg acgcttggtca gtgctgaaga tctgaaggga gcaagcctcc tagtggaagt 1227
 atacgatctg cagggcaatt tcattttgga tgtattgctg acgcctgaaa tgatcggatc 1287
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 gcattacgca gaatgggtcga tctttggcgc cgttctgatg tttggcggat tgtttatggt 1467
 cagaaggctt cgaaaagcgg ctttaacattt tacttcccat tctaagtctg tatagaatgg 1527
 gaagttttta taaggagtga aaggaaatta aggcacatcg aaaaaagatc atctggcttg 1587
 cagccattgc 1597

<210> 248
 <211> 199
 <212> PRT
 <213> Bacillus licheniformis

<400> 248
 Met Lys Lys Arg Leu Met Ser Leu Leu Val Cys Ile Leu Val Leu Val
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Pro Ala Ala Gly Ala Phe Ala Ala Pro Lys Gln Ala Glu Leu Lys Asp
 20 25 30

Tyr Leu Glu Glu Ile Gly Met Thr Glu Lys Glu Leu Glu Ala Tyr Leu
 35 40 45

Gln Asp Thr Tyr Asp Glu Ser Leu Lys Gly Phe Asp Ser Val Glu Glu
 50 55 60

Leu Lys Asp Phe Leu Gly Gln Arg Leu Thr Lys Lys Leu Leu Ala Ser
 65 70 75 80

Tyr Leu Lys Glu Tyr Gly Leu Ser Glu Lys Glu Ala Ala Asp Leu Phe

10294.204.ST25.txt
90

85

95

Val Glu Asn Gly Tyr Met Glu Ser Gly Gln Asn Ile Leu Asp Val Phe
 100 105 110

Met Phe Glu Tyr Glu Leu Asp Asp Ala Leu Tyr Thr Val Thr Tyr Glu
 115 120 125

Glu Asp Asp Phe Gln Ile Gly Asn Met Phe Gln Glu Leu Gly Val Asp
 130 135 140

Asp Gln Glu Trp Glu Arg Leu Val Asn His Leu Arg Lys Val Arg Asp
 145 150 155 160

Asn Asn Pro Asn Leu Glu Asn Asp Leu Met Ala Leu Gly Glu Arg Leu
 165 170 175

Glu Ala Val Ala Asp Phe Glu Ser Val Ser Glu Leu Ser Ala Gln Asp
 180 185 190

Ile Ala Glu Cys Cys Pro Phe
 195